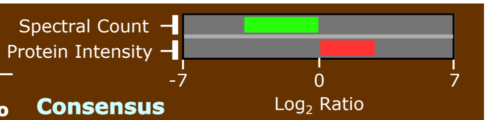
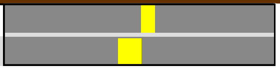
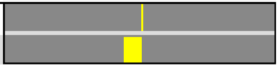
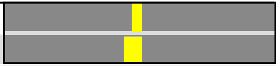
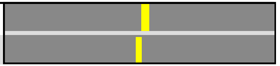
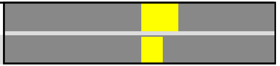
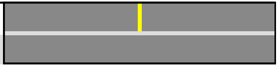
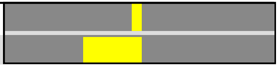
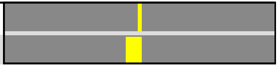
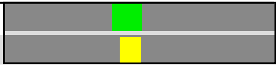
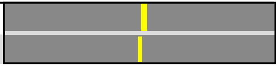
Supplementary File 2. Statistically processed spectral count and protein summed intensity values obtained for Hendrickson *et al*.

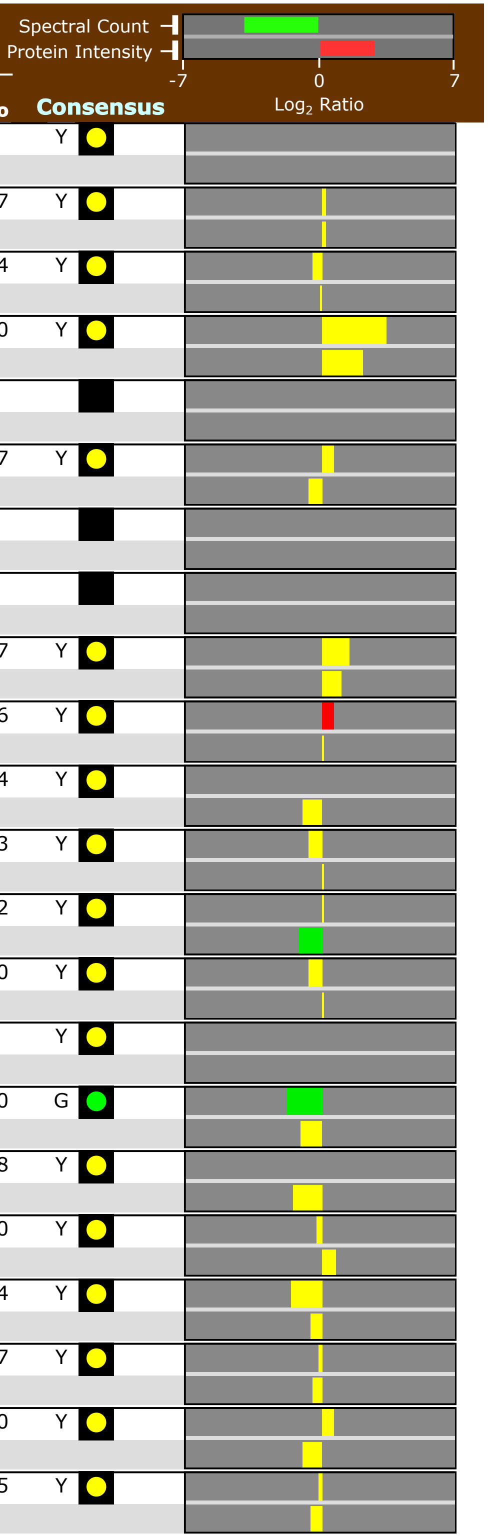
For details of how these values were calculated, significance cut-offs, color- coding, *etc.* see the proteomic methods in Supplementary File1.

This PDF file is based on a FileMaker™ database maintained in an electronic archive hosted by the Department of Microbiology at the University of Washington. Readers with access to FileMaker™ Ver. 10 or above who wish to use the database in its native format should contact *mhackett@u.washington.edu*.

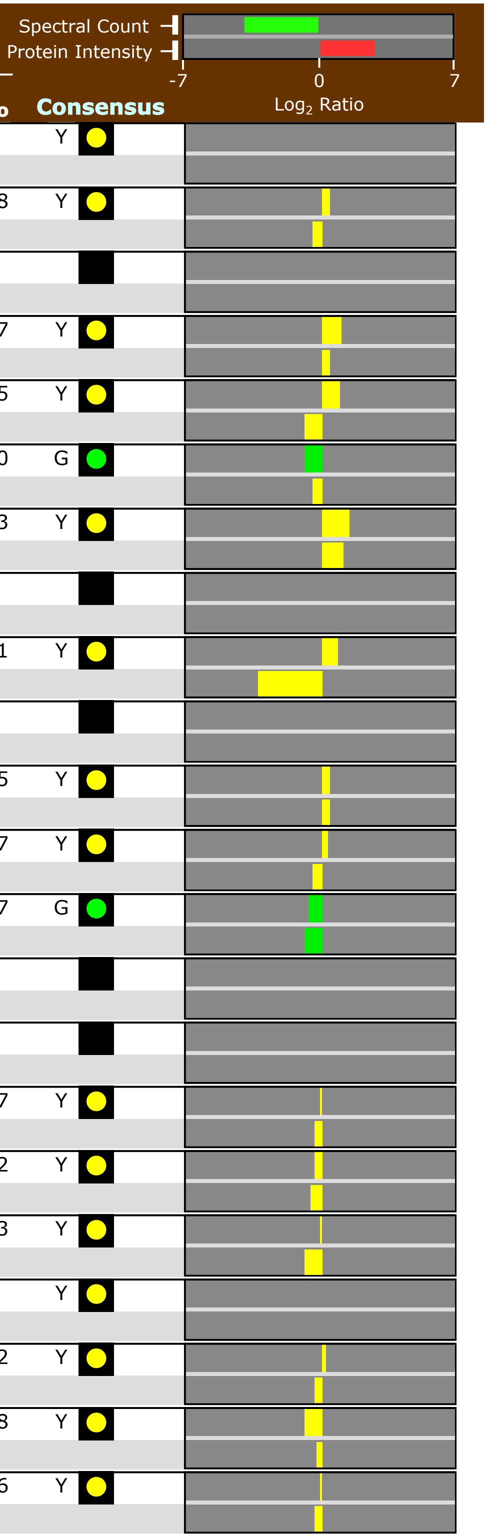


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity							
ORF	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	**Consensus**		
MFLA0001	1.96 E-2	5.358	4.648	6.046	0.710	Y	🟡	🟡	Y	1.11 E-1	22.995	23.671	24.372	-1.187	Y	🟡	
	chromosomal replication initiator protein DnaA [Methylobacillus flagellatus KT]637936882 YP_544113																
MFLA0002		7.702	7.525	8.616	0.083	Y	🟡	🟡	Y	5.47 E-2	27.021	27.774	28.446	-0.865	Y	🟡	
	" DNA polymerase III, beta subunit [Methylobacillus flagellatus KT]637936883 YP_544114 """																
MFLA0003	1.15 E-10	8.560	9.028	9.813	-0.462	Y	🟡	🟡	Y	1.23 E-2	28.072	28.941	29.571	-0.897	Y	🟡	
	" DNA gyrase, B subunit [Methylobacillus flagellatus KT]637936884 YP_544115 """																
MFLA0004		0.521		0.521		Y	🟡	🟡	Y		19.163		19.163		Y	🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637936885 YP_544116																
MFLA0005		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	sulphate transporter [Methylobacillus flagellatus KT]637936886 YP_544117																
MFLA0006		3.664	2.000	4.060	0.363	Y	🟡	🟡	Y	1.41 E-1	21.663	20.961	22.354	-0.332	Y	🟡	
	" glycoside hydrolase family 2, sugar binding [Methylobacillus flagellatus KT]637936887 YP_544118 """																
MFLA0007		3.328	1.807	3.759	1.521	Y	🟡	🟡	Y		20.571	20.244	21.417	0.328	Y	🟡	
	cyclase/dehydrase [Methylobacillus flagellatus KT]637936888 YP_544119																
MFLA0008		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	DNA-directed DNA polymerase [Methylobacillus flagellatus KT]637936889 YP_544120																
MFLA0009		3.328	2.540	3.987	1.862	Y	🟡	🟡	Y	7.7 E-2	21.650	21.635	22.643	1.094	Y	🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637936891 YP_544121																
MFLA0010		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	transport-associated [Methylobacillus flagellatus KT]637936892 YP_544122																
MFLA0011		4.595	4.820	5.712	-0.232	Y	🟡	🟡	Y	2.28 E-1	23.099	23.040	24.070	0.030	Y	🟡	
	Malate dehydrogenase (acceptor) [Methylobacillus flagellatus KT]637936893 YP_544123																
MFLA0012		2.259	2.797	3.553	-0.486	Y	🟡	🟡	Y	1.37 E-2	17.630	20.595	20.769	-3.030	Y	🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637936894 YP_544124																
MFLA0013		3.901	5.132	5.644	-0.226	Y	🟡	🟡	Y	2.05 E-2	23.046	24.831	25.199	-0.786	Y	🟡	
	Protein-methionine-S-oxide reductase [Methylobacillus flagellatus KT]637936895 YP_544125																
MFLA0014		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637936896 YP_544126																
MFLA0015			2.140	2.140		Y	🟡	🟡	Y			21.181	21.181		Y	🟡	
	GCN5-related N-acetyltransferase [Methylobacillus flagellatus KT]637936897 YP_544127																
MFLA0016	0	10.829	12.337	12.772	-1.500	G	🟢	🟡	Y	1.66 E-2	29.606	30.689	31.246	-1.148	G	🟢	
	histone-like DNA-binding protein [Methylobacillus flagellatus KT]637936898 YP_544128																
MFLA0017		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637936899 YP_544129																
MFLA0018	6.97 E-3	5.899	5.249	6.610	0.660	R	🔴	🟡	Y	2.58 E-1	24.343	24.418	25.381	-0.278	Y	🟡	
	MscS Mechanosensitive ion channel [Methylobacillus flagellatus KT]637936900 YP_544130																
MFLA0019		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	CBS domain containing membrane protein [Methylobacillus flagellatus KT]637936901 YP_544131																
MFLA0020		4.235	3.991	5.118	0.251	Y	🟡	🟡	Y	7.11 E-2	22.548	22.765	23.661	-0.227	Y	🟡	
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637936902 YP_544132 """																
MFLA0021		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	coenzyme PQQ biosynthesis protein A [Methylobacillus flagellatus KT]637936903 YP_544133																
MFLA0022		3.571	3.945	4.770	-0.356	Y	🟡	🟡	Y	2.27 E-1	21.826	21.690	22.759	-0.011	Y	🟡	
	Zinc finger/thioredoxin putative [Methylobacillus flagellatus KT]637936904 YP_544134																

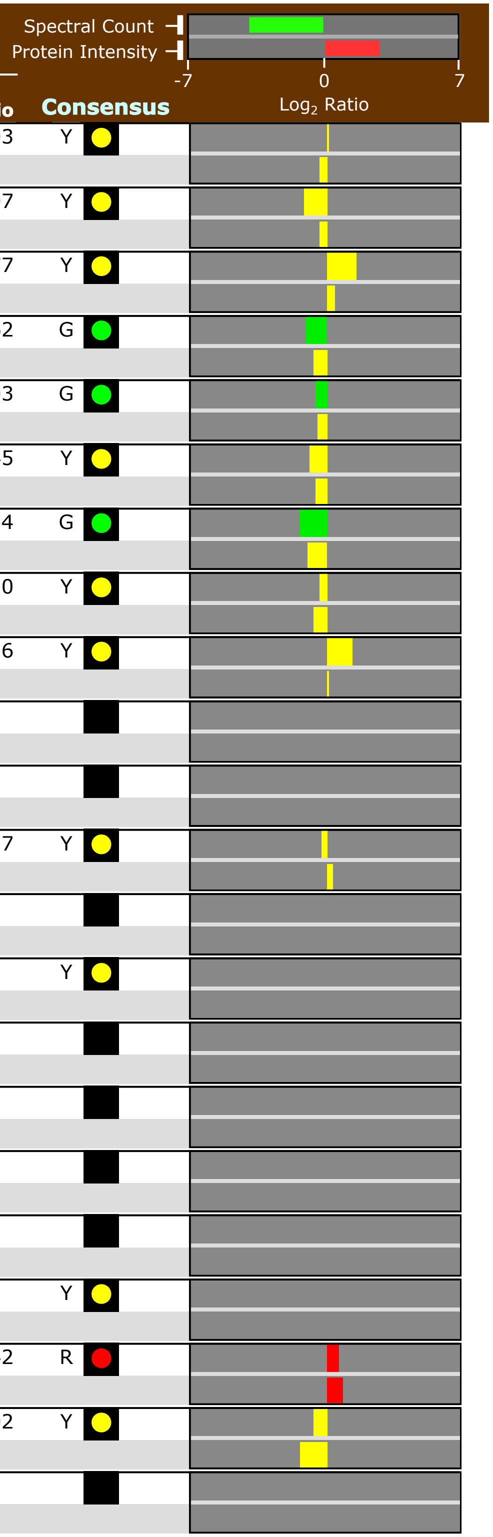
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	**Consensus**	
MFLA0023		1.843		1.843		Y	🟡	🟡	Y		21.732		21.732		Y	🟡
	ribosomal protein L11 methyltransferase [Methylobacillus flagellatus KT]637936905 YP_544135															
MFLA0024	3.4 E-2	6.416	6.251	7.336	0.212	Y	🟡	🟡	Y	9.6 E-2	27.079	26.853	27.971	0.247	Y	🟡
	" acetyl-CoA carboxylase, biotin carboxylase [Methylobacillus flagellatus KT]637936906 YP_544136 """															
MFLA0025		6.510	6.986	7.768	-0.516	Y	🟡	🟡	Y	2.8 E-1	25.386	25.387	26.386	-0.074	Y	🟡
	" acetyl-CoA carboxylase, biotin carboxyl carrier protein [Methylobacillus flagellatus KT]637936907 YP_544137 """															
MFLA0026		4.691	1.346	4.826	3.344	Y	🟡	🟡	Y		22.036	19.956	22.343	2.080	Y	🟡
	" 3-dehydroquinate dehydratase, type II [Methylobacillus flagellatus KT]637936908 YP_544138 """															
MFLA0027		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen [Methylobacillus flagellatus KT]637936909 YP_544139															
MFLA0028		2.328	2.739	3.548	0.590	Y	🟡	🟡	Y	1.17 E-1	20.379	22.087	22.472	-0.657	Y	🟡
	Protein-disulfide reductase [Methylobacillus flagellatus KT]637936910 YP_544140															
MFLA0029		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	CutA1 divalent ion tolerance protein [Methylobacillus flagellatus KT]637936911 YP_544141															
MFLA0030		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	FxsA cytoplasmic membrane protein [Methylobacillus flagellatus KT]637936912 YP_544142															
MFLA0031		4.522	3.117	4.984	1.384	Y	🟡	🟡	Y	9.8 E-2	23.540	22.235	24.030	1.007	Y	🟡
	oxidoreductase FAD/NAD(P)-binding [Methylobacillus flagellatus KT]637936913 YP_544143															
MFLA0032	1.24 E-3	5.285	4.568	5.971	0.642	R	🔴	🟡	Y	1.89 E-1	24.045	23.686	24.876	0.076	Y	🟡
	HemY-like protein [Methylobacillus flagellatus KT]637936914 YP_544144															
MFLA0033	9.34 E-2	4.933	4.951	5.942	0.028	Y	🟡	🟡	Y	4.21 E-2	23.498	24.396	25.016	-1.024	Y	🟡
	" protein of unknown function DUF513, hemX [Methylobacillus flagellatus KT]637936915 YP_544145 """															
MFLA0034		1.398	3.056	3.453	-0.652	Y	🟡	🟡	Y	2.77 E-1	21.813	22.822	23.404	0.073	Y	🟡
	Uroporphyrinogen-III synthase [Methylobacillus flagellatus KT]637936916 YP_544146															
MFLA0035	2.85 E-2	5.429	5.475	6.452	0.054	Y	🟡	🟢	G	5.06 E-3	23.649	24.869	25.385	-1.222	Y	🟡
	porphobilinogen deaminase [Methylobacillus flagellatus KT]637936917 YP_544147															
MFLA0036		1.106	1.807	2.499	-0.702	Y	🟡	🟡	Y		19.207	19.106	20.157	0.100	Y	🟡
	" transcriptional regulator, LytR/AlgR family [Methylobacillus flagellatus KT]637936918 YP_544148 """															
MFLA0037		0.521		0.521		Y	🟡	🟡	Y		17.917		17.917		Y	🟡
	histidine kinase internal region [Methylobacillus flagellatus KT]637936919 YP_544149															
MFLA0038	0	6.082	7.864	8.232	-1.761	G	🟢	🟡	Y	6.49 E-2	26.050	26.872	27.519	-1.090	G	🟢
	argininosuccinate lyase [Methylobacillus flagellatus KT]637936920 YP_544150															
MFLA0039		4.851	4.707	5.781	0.035	Y	🟡	🟡	Y	5.47 E-2	22.531	23.582	24.151	-1.488	Y	🟡
	diguanylate cyclase (GGDEF domain) [Methylobacillus flagellatus KT]637936921 YP_544151															
MFLA0040		2.106	3.435	3.918	-0.264	Y	🟡	🟡	Y	1.42 E-1	20.271	20.707	21.506	0.730	Y	🟡
	Putative oxygen-independent coproporphyrinogen III oxidase [Methylobacillus flagellatus KT]637936922 YP_544152															
MFLA0041		1.106	2.700	3.113	-1.595	Y	🟡	🟡	Y		21.303	21.897	22.630	-0.594	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637936923 YP_544153															
MFLA0042		4.160	4.350	5.258	-0.237	Y	🟡	🟡	Y	1.03 E-1	24.044	24.489	25.284	-0.527	Y	🟡
	Ham1-like protein [Methylobacillus flagellatus KT]637936924 YP_544154															
MFLA0043		4.637	3.979	5.345	0.644	Y	🟡	🟡	Y	3.09 E-2	23.926	24.863	25.469	-1.040	Y	🟡
	ribonuclease PH [Methylobacillus flagellatus KT]637936925 YP_544155															
MFLA0044		3.210	3.334	4.273	-0.167	Y	🟡	🟡	Y	1.33 E-1	21.611	22.003	22.820	-0.575	Y	🟡
	protein serine/threonine phosphatases [Methylobacillus flagellatus KT]637936926 YP_544156															



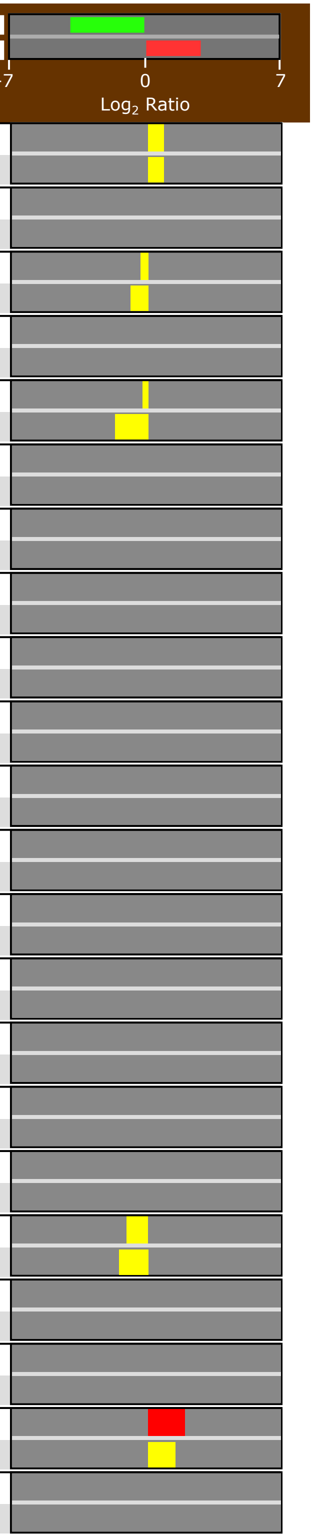
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA0045			1.184	1.184		Y	🟡	🟡	Y			20.903	20.903		Y	🟡
	serine/threonine protein kinase [Methylobacillus flagellatus KT]637936927 YP_544157															
MFLA0046		6.096	5.435	6.803	0.384	Y	🟡	🟡	Y	1.23 E-1	24.205	24.662	25.451	-0.498	Y	🟡
	conserved hypothetical protein 255 [Methylobacillus flagellatus KT]637936928 YP_544158															
MFLA0047		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF475 [Methylobacillus flagellatus KT]637936929 YP_544159															
MFLA0048		3.418	2.573	4.056	0.959	Y	🟡	🟡	Y	1.33 E-1	22.671	22.254	23.477	0.427	Y	🟡
	Guanylate kinase [Methylobacillus flagellatus KT]637936930 YP_544160															
MFLA0049		4.989	4.090	5.609	0.907	Y	🟡	🟡	Y	1.08 E-2	25.443	26.335	26.957	-0.915	Y	🟡
	" DNA-directed RNA polymerase, omega subunit [Methylobacillus flagellatus KT]637936931 YP_544161 """															
MFLA0050	2.32 E-4	5.179	6.055	6.683	-0.865	G	🟢	🟡	Y	8.32 E-2	24.554	25.123	25.866	-0.500	G	🟢
	" (p)ppGpp synthetase I (GTP pyrophosphokinase), SpoT/RelA [Methylobacillus flagellatus KT]637936932 YP_544162 """															
MFLA0051		5.699	1.807	5.794	1.424	Y	🟡	🟡	Y	1.45 E-1	24.332	21.910	24.579	1.073	Y	🟡
	YjgF-like protein [Methylobacillus flagellatus KT]637936933 YP_544163															
MFLA0052		0.000	0.000				■	■			0.000	0.000				■
	ATP-dependent DNA helicase RecG [Methylobacillus flagellatus KT]637936934 YP_544164															
MFLA0053		1.106	0.346	1.775	0.759	Y	🟡	🟡	Y		17.193	20.505	20.643	-3.311	Y	🟡
	Chorismate lyase [Methylobacillus flagellatus KT]637936935 YP_544165															
MFLA0054		0.000	0.000				■	■			0.000	0.000				■
	4-hydroxybenzoate polyprenyl transferase [Methylobacillus flagellatus KT]637936936 YP_544166															
MFLA0055		8.187	7.580	8.915	0.448	Y	🟡	🟡	Y	6.47 E-2	27.973	27.572	28.787	0.425	Y	🟡
	ribosomal protein L13 [Methylobacillus flagellatus KT]637936937 YP_544167															
MFLA0056		8.573	8.203	9.400	0.331	Y	🟡	🟡	Y	8.39 E-2	26.958	27.393	28.192	-0.497	Y	🟡
	ribosomal protein S9 [Methylobacillus flagellatus KT]637936938 YP_544168															
MFLA0057	5.13 E-3	5.163	5.873	6.561	-0.714	G	🟢	🟢	G	8.91 E-3	24.755	25.661	26.278	-0.917	G	🟢
	N-acetyl-gamma-glutamyl-phosphate reductase [Methylobacillus flagellatus KT]637936939 YP_544169															
MFLA0058		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637936940 YP_544170															
MFLA0059		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF583 [Methylobacillus flagellatus KT]637936941 YP_544171															
MFLA0060		3.899	4.032	4.967	-0.098	Y	🟡	🟡	Y	7.44 E-2	24.768	25.223	26.014	-0.427	Y	🟡
	HesB/YadR/YfhF [Methylobacillus flagellatus KT]637936942 YP_544172															
MFLA0061	2.35 E-3	7.023	7.443	8.248	-0.419	Y	🟡	🟡	Y	4.99 E-2	26.401	27.058	27.767	-0.622	Y	🟡
	Citrate synthase I [Methylobacillus flagellatus KT]637936943 YP_544173															
MFLA0062		2.795	2.897	3.847	-0.117	Y	🟡	🟡	Y	1.07 E-1	21.206	21.797	22.532	-0.883	Y	🟡
	protein of unknown function UPF0075 [Methylobacillus flagellatus KT]637936944 YP_544174															
MFLA0063		0.521		0.521		Y	🟡	🟡	Y		18.922		18.922		Y	🟡
	peptidase M23B [Methylobacillus flagellatus KT]637936945 YP_544175															
MFLA0064		8.159	7.946	9.056	0.159	Y	🟡	🟡	Y	1.24 E-1	26.975	27.302	28.147	-0.412	Y	🟡
	tyrosyl-tRNA synthetase [Methylobacillus flagellatus KT]637936946 YP_544176															
MFLA0065		4.467	5.352	5.976	-0.888	Y	🟡	🟡	Y	1.37 E-1	23.763	24.168	24.980	-0.328	Y	🟡
	protein of unknown function DUF150 [Methylobacillus flagellatus KT]637936952 YP_544177															
MFLA0066		8.204	8.258	9.231	-0.093	Y	🟡	🟡	Y	1.53 E-2	27.646	28.027	28.849	-0.386	Y	🟡
	NusA antitermination factor [Methylobacillus flagellatus KT]637936953 YP_544178															



	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA0067		8.477	8.350	9.415	0.099	Y	🟡	🟡	Y	7.77 E-2	27.623	27.983	28.814	-0.403	Y	🟡
	translation initiation factor IF-2 [Methylobacillus flagellatus KT]637936954 YP_544179															
MFLA0068		1.521	3.764	4.040	-1.196	Y	🟡	🟡	Y	1.57 E-1	21.070	22.565	23.003	-0.407	Y	🟡
	ribosome-binding factor A [Methylobacillus flagellatus KT]637936955 YP_544180															
MFLA0069		3.135	2.627	3.903	1.509	Y	🟡	🟡	Y	3.43 E-2	21.307	21.930	22.652	0.377	Y	🟡
	tRNA pseudouridine synthase B [Methylobacillus flagellatus KT]637936956 YP_544181															
MFLA0070	0	6.018	7.260	7.769	-1.070	G	🟢	🟡	Y	1.99 E-2	26.994	27.633	28.349	-0.662	G	🟢
	ribosomal protein S15 [Methylobacillus flagellatus KT]637936957 YP_544182															
MFLA0071	0	9.907	10.465	11.213	-0.586	G	🟢	🟡	Y	7.24 E-2	29.438	29.899	30.687	-0.503	G	🟢
	3' exoribonuclease [Methylobacillus flagellatus KT]637936958 YP_544183															
MFLA0072		6.635	7.343	8.032	-0.906	Y	🟡	🟡	Y	5.55 E-2	26.240	26.838	27.570	-0.645	Y	🟡
	" transcriptional regulators, TraR/DksA family [Methylobacillus flagellatus KT]637936959 YP_544184 """															
MFLA0073	2.36 E-14	5.426	6.845	7.303	-1.419	G	🟢	🟡	Y	1.1 E-2	24.884	25.843	26.442	-0.954	G	🟢
	Methenyltetrahydrofolate cyclohydrolase [Methylobacillus flagellatus KT]637936960 YP_544185															
MFLA0074		5.287	5.534	6.416	-0.417	Y	🟡	🟡	Y	4.5 E-2	23.592	24.337	25.012	-0.710	Y	🟡
	" two component, sigma54 specific, transcriptional regulator, Fis family [Methylobacillus flagellatus KT]637936964 YP_544186 """															
MFLA0075		1.843	0.585	2.347	1.258	Y	🟡	🟡	Y		20.182	20.066	21.125	0.116	Y	🟡
	" general secretion pathway protein, ATPase [Methylobacillus flagellatus KT]637936965 YP_544187 """															
MFLA0076		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	type II and III secretion system protein [Methylobacillus flagellatus KT]637936966 YP_544188															
MFLA0077		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	TPR repeat [Methylobacillus flagellatus KT]637936967 YP_544189															
MFLA0078		0.521	1.915	2.380	-0.314	Y	🟡	🟡	Y	9.25 E-2	19.596	20.286	20.982	0.317	Y	🟡
	type II secretion system protein E [Methylobacillus flagellatus KT]637936968 YP_544190															
MFLA0079		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	type II secretion system protein [Methylobacillus flagellatus KT]637936969 YP_544191															
MFLA0080			1.000	1.000		Y	🟡	🟡	Y			19.484	19.484		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637936970 YP_544192															
MFLA0081		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637936971 YP_544193															
MFLA0082		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637936972 YP_544194															
MFLA0083		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637936973 YP_544195															
MFLA0084		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	methylation [Methylobacillus flagellatus KT]637936974 YP_544196															
MFLA0085			2.991	2.991		Y	🟡	🟡	Y			21.534	21.534		Y	🟡
	UBA/THIF-type NAD/FAD binding fold [Methylobacillus flagellatus KT]637936975 YP_544197															
MFLA0086	1.71 E-3	6.309	5.707	7.039	0.600	R	🔴	🔴	R	8.64 E-3	26.425	25.595	27.069	0.842	R	🔴
	band 7 protein [Methylobacillus flagellatus KT]637936976 YP_544198															
MFLA0087		3.093	3.848	4.519	-0.736	Y	🟡	🟡	Y	4.93 E-2	20.498	22.013	22.446	-1.402	Y	🟡
	protein of unknown function DUF107 [Methylobacillus flagellatus KT]637936977 YP_544199															
MFLA0088		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637936978 YP_544200															



ORF	AM/OH *M Flagellatus* Spectral Count					Regulation				AM/OH *M Flagellatus* Protein Intensity					Consensus	
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio					*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		
MFLA0089		3.656	2.871	4.316	0.786	Y	🟡	🟡	Y	5.54 E-2	22.448	21.592	23.083	0.794	Y	🟡
	LemA [Methylobacillus flagellatus KT]637936979 YP_544201															
MFLA0090		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637936980 YP_544202															
MFLA0091	1.82 E-4	7.628	8.044	8.851	-0.414	Y	🟡	🟡	Y	3.33 E-2	26.128	27.020	27.642	-0.922	Y	🟡
	valyl-tRNA synthetase [Methylobacillus flagellatus KT]637936981 YP_544203															
MFLA0092			2.410	2.410		Y	🟡	🟡	Y			20.836	20.836		Y	🟡
	protein of unknown function UPF0187 [Methylobacillus flagellatus KT]637936982 YP_544204															
MFLA0093		2.106	3.705	4.117	-0.264	Y	🟡	🟡	Y	1.15 E-1	22.145	25.048	25.229	-1.721	Y	🟡
	SirA-like protein [Methylobacillus flagellatus KT]637936983 YP_544205															
MFLA0094		0.000	0.000				■	■			0.000	0.000				■
	Rhodanese-like protein [Methylobacillus flagellatus KT]637936984 YP_544206															
MFLA0095		0.000	0.000				■	■			0.000	0.000				■
	TonB-dependent siderophore receptor [Methylobacillus flagellatus KT]637936985 YP_544207															
MFLA0096		0.000	0.000				■	■			0.000	0.000				■
	" Prolyl 4-hydroxylase, alpha subunit [Methylobacillus flagellatus KT]637936986 YP_544208 """															
MFLA0097		0.000	0.000				■	■			0.000	0.000				■
	Sel1 [Methylobacillus flagellatus KT]637936987 YP_544209															
MFLA0098			0.585	0.585		Y	🟡	🟡	Y			21.187	21.187		Y	🟡
	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase [Methylobacillus flagellatus KT]637936989 YP_544210															
MFLA0099		0.000	0.000				■	■			0.000	0.000				■
	cobalamin 5'-phosphate synthase [Methylobacillus flagellatus KT]637936990 YP_544211															
MFLA0100		2.210		2.210		Y	🟡	🟡	Y		20.973		20.973		Y	🟡
	Phosphoglycerate mutase [Methylobacillus flagellatus KT]637936991 YP_544212															
MFLA0101		0.000	0.000				■	■			0.000	0.000				■
	" aminotransferase, class I and II [Methylobacillus flagellatus KT]637936992 YP_544213 """															
MFLA0102		0.000	0.000				■	■			0.000	0.000				■
	cobalamin biosynthesis protein CobD [Methylobacillus flagellatus KT]637936993 YP_544214															
MFLA0103		0.000	0.000				■	■			0.000	0.000				■
	cobyric acid synthase CobQ [Methylobacillus flagellatus KT]637936994 YP_544215															
MFLA0104		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637936995 YP_544216															
MFLA0105		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637936996 YP_544217															
MFLA0106		3.674	4.814	5.354	-1.145	Y	🟡	🟡	Y	6.56 E-2	23.538	24.595	25.161	-1.548	Y	🟡
	" methionine aminopeptidase, type I [Methylobacillus flagellatus KT]637936997 YP_544218 """															
MFLA0107			1.585	1.585		Y	🟡	🟡	Y			18.700	18.700		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637936998 YP_544219															
MFLA0108		4.492		4.492		Y	🟡	🟡	Y		22.531		22.531		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637936999 YP_544220															
MFLA0109	0	7.700	5.788	8.040	1.914	R	🔴	🟡	Y	2.01 E-2	26.885	25.422	27.331	1.443	R	🔴
	TonB-dependent siderophore receptor [Methylobacillus flagellatus KT]637937000 YP_544221															
MFLA0110		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937001 YP_544222															



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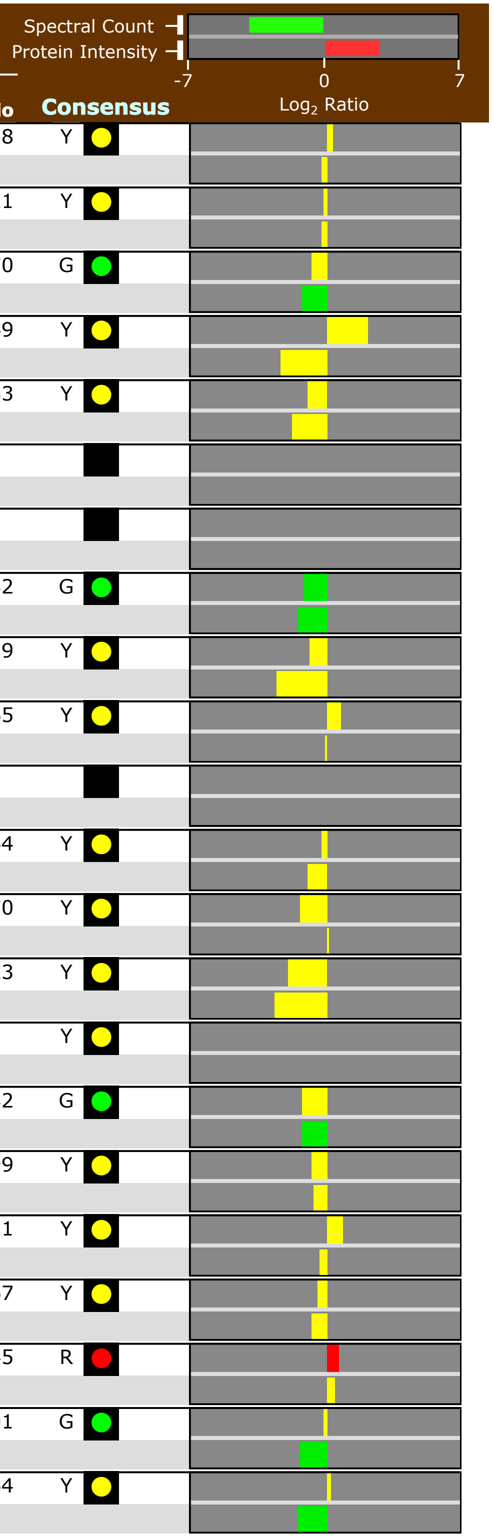
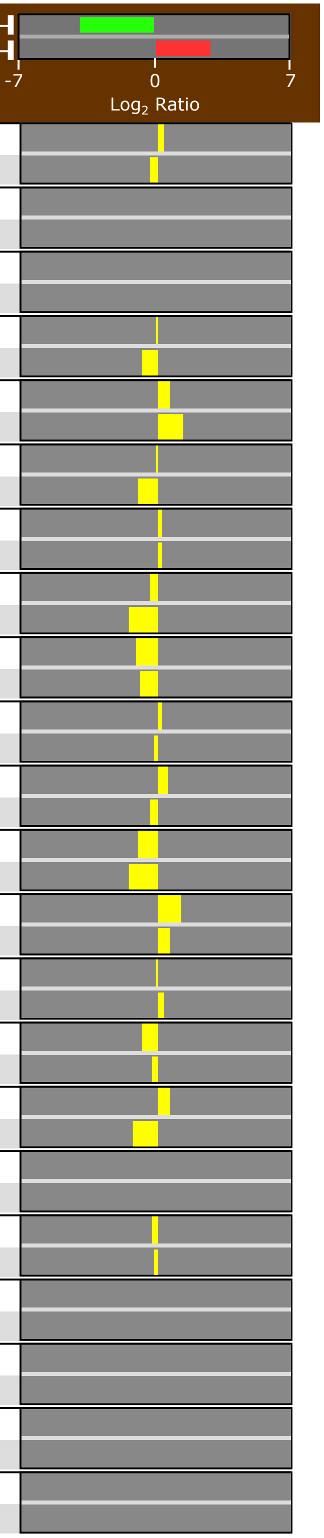
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio					*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		
MFLA0111 *hypothetical protein [Methylobacillus flagellatus KT]637937002 YP_544223*		5.060	4.742	5.909	0.330	Y	🟡	🟡	Y	7.97 E-2	24.088	24.360	25.230	-0.258	Y	🟡
MFLA0112 *hypothetical protein [Methylobacillus flagellatus KT]637937003 YP_544224*		1.106	1.322	2.218	-0.216	Y	🟡	🟡	Y		19.089	19.410	20.258	-0.321	Y	🟡
MFLA0113 *cobalbumin biosynthesis enzyme [Methylobacillus flagellatus KT]637937004 YP_544225*		5.345	6.000	6.709	-0.814	Y	🟡	🟢	G	9.87 E-3	23.660	24.938	25.436	-1.270	G	🟢
MFLA0114 *periplasmic binding protein [Methylobacillus flagellatus KT]637937005 YP_544226*		3.106	2.015	3.661	2.140	Y	🟡	🟡	Y	1.34 E-1	21.398	25.429	25.514	-2.449	Y	🟡
MFLA0115 *" Cob(II)yrinic acid a,c-diamide reductase [Methylobacillus flagellatus KT]637937006 YP_544227 """*		4.017	4.949	5.557	-0.974	Y	🟡	🟡	Y	4.29 E-2	22.413	23.789	24.259	-1.783	Y	🟡
MFLA0116 *hypothetical protein [Methylobacillus flagellatus KT]637937007 YP_544228*		0.000	0.000				■	■			0.000	0.000				■
MFLA0117 *MotA/TolQ/ExbB proton channel [Methylobacillus flagellatus KT]637937008 YP_544229*		0.000	0.000				■	■			0.000	0.000				■
MFLA0118 *CobN/magnesium chelatase [Methylobacillus flagellatus KT]637937009 YP_544230*	3.52 E-12	5.804	6.989	7.515	-1.184	G	🟢	🟢	G	6.36 E-3	24.204	25.679	26.122	-1.482	G	🟢
MFLA0119 *CobB/CobQ-like glutamine amidotransferase [Methylobacillus flagellatus KT]637937010 YP_544231*		4.052	4.732	5.432	-0.854	Y	🟡	🟡	Y	1.66 E-2	21.737	24.237	24.472	-2.619	Y	🟡
MFLA0120 *cob(I)alamin adenosyltransferase [Methylobacillus flagellatus KT]637937011 YP_544232*		3.221	3.579	4.411	0.691	Y	🟡	🟡	Y	2.28 E-1	22.814	23.945	24.487	-0.065	Y	🟡
MFLA0121 *hypothetical protein [Methylobacillus flagellatus KT]637937012 YP_544233*		0.000	0.000				■	■			0.000	0.000				■
MFLA0122 *TonB-dependent receptor [Methylobacillus flagellatus KT]637937013 YP_544234*		10.944	11.130	12.040	-0.251	Y	🟡	🟡	Y	6.6 E-2	29.387	30.197	30.848	-1.044	Y	🟡
MFLA0123 *hypothetical protein [Methylobacillus flagellatus KT]637937014 YP_544235*		1.398	3.754	4.012	-1.355	Y	🟡	🟡	Y	2.48 E-1	22.593	23.547	24.148	0.070	Y	🟡
MFLA0124 *protein of unknown function DUF710 [Methylobacillus flagellatus KT]637937015 YP_544236*		2.025	3.941	4.280	-1.960	Y	🟡	🟡	Y	1.87 E-2	21.481	24.189	24.394	-2.723	Y	🟡
MFLA0125 *hypothetical protein [Methylobacillus flagellatus KT]637937016 YP_544237*		2.135		2.135		Y	🟡	🟡	Y		19.509		19.509		Y	🟡
MFLA0126 *protein of unknown function DUF589 [Methylobacillus flagellatus KT]637937017 YP_544238*		3.610	4.864	5.369	-1.320	Y	🟡	🟢	G	4.29 E-3	23.481	24.760	25.258	-1.282	G	🟢
MFLA0127 *" ferric uptake regulator, FUR family [Methylobacillus flagellatus KT]637937018 YP_544239 """*		8.653	9.238	9.975	-0.817	Y	🟡	🟡	Y	2.52 E-2	27.686	28.352	29.057	-0.699	Y	🟡
MFLA0128 *" threonine dehydratase, biosynthetic [Methylobacillus flagellatus KT]637937019 YP_544240 """*		5.716	4.830	6.340	0.811	Y	🟡	🟡	Y	1.23 E-1	24.713	25.089	25.913	-0.411	Y	🟡
MFLA0129 *ribose 5-phosphate isomerase [Methylobacillus flagellatus KT]637937020 YP_544241*	0	9.681	10.142	10.930	-0.460	Y	🟡	🟡	Y	1.13 E-2	28.023	28.773	29.447	-0.767	Y	🟡
MFLA0130 *" phosphate uptake regulator, PhoU [Methylobacillus flagellatus KT]637937021 YP_544242 """*	6.56 E-4	5.384	4.664	6.068	0.629	R	🔴	🟡	Y	1.29 E-1	24.169	23.223	24.772	0.445	R	🔴
MFLA0131 *Ppx/GppA phosphatase [Methylobacillus flagellatus KT]637937022 YP_544243*		4.517	4.697	5.610	-0.170	Y	🟡	🟢	G	6.36 E-3	22.552	23.930	24.400	-1.401	G	🟢
MFLA0132 *Polyphosphate kinase [Methylobacillus flagellatus KT]637937023 YP_544244*		4.978	4.816	5.899	0.163	Y	🟡	🟢	G	3.73 E-3	22.723	24.186	24.633	-1.464	Y	🟡





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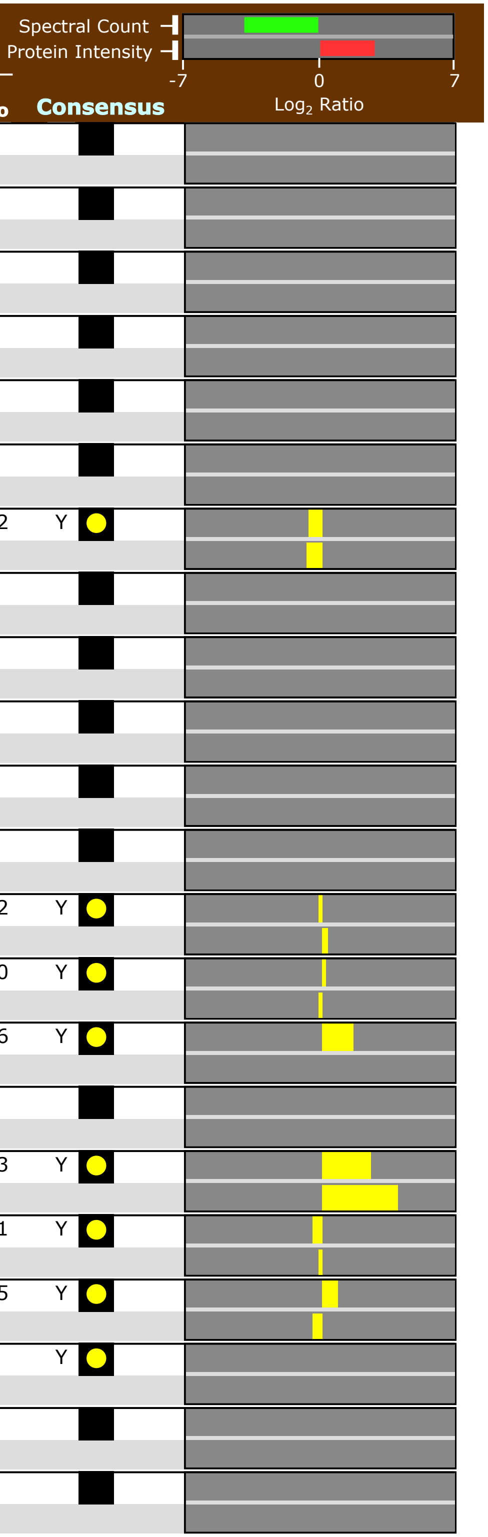
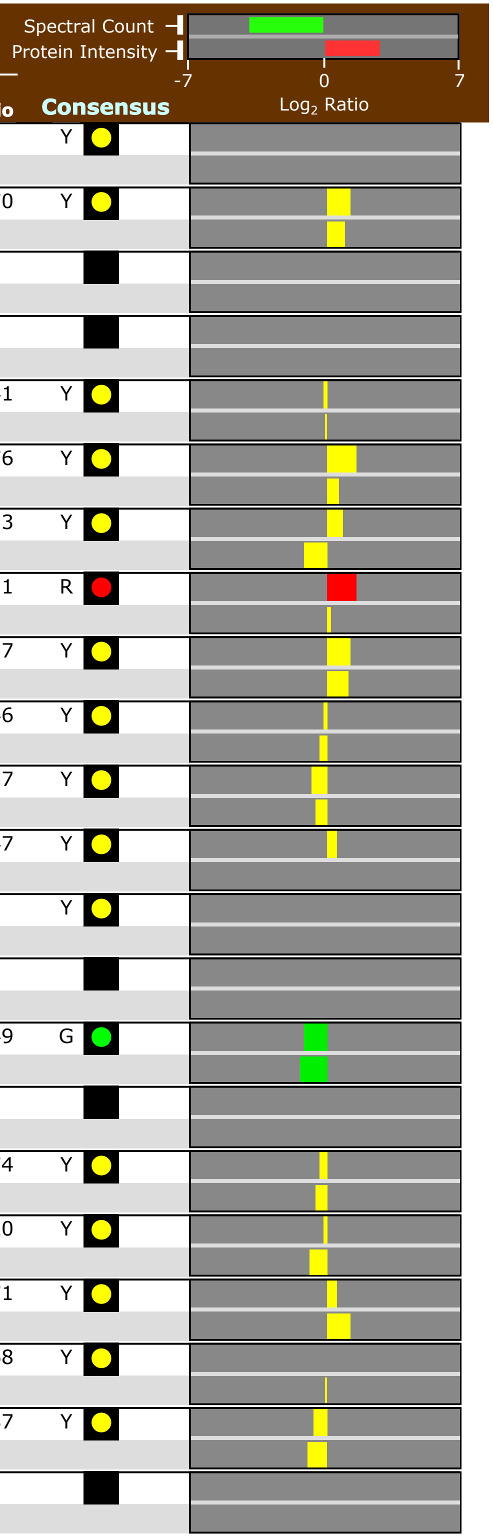
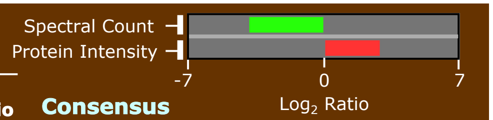
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA0133	1.19 E-2	5.837	5.435	6.650	0.324	Y ● ● Y	1.43 E-1	25.488	25.897	26.707	-0.436	Y ●
	Fe(II) trafficking protein YggX [Methylobacillus flagellatus KT]637937024 YP_544245											
MFLA0134		3.561		3.561		Y ● ● Y		22.275		22.275		Y ●
	TonB-dependent receptor [Methylobacillus flagellatus KT]637937025 YP_544246											
MFLA0135		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937026 YP_544247											
MFLA0136		4.628	4.669	5.649	-0.069	Y ● ● Y	7.54 E-2	22.914	23.597	24.295	-0.786	Y ●
	FAD dependent oxidoreductase [Methylobacillus flagellatus KT]637937027 YP_544248											
MFLA0137		2.843	3.321	4.101	0.647	Y ● ● Y	1.28 E-1	21.357	21.477	22.418	1.279	Y ●
	KpsF/GutQ family protein [Methylobacillus flagellatus KT]637937028 YP_544249											
MFLA0138		4.481	4.337	5.411	-0.138	Y ● ● Y	9.11 E-2	22.022	22.732	23.421	-1.019	Y ●
	Phosphatase kdsC [Methylobacillus flagellatus KT]637937029 YP_544250											
MFLA0139		4.289	4.143	5.218	0.155	Y ● ● Y	2.56 E-2	23.822	23.594	24.712	0.227	Y ●
	protein of unknown function DUF1239 [Methylobacillus flagellatus KT]637937030 YP_544251											
MFLA0140		3.439	3.793	4.627	-0.375	Y ● ● Y	3.77 E-2	23.056	24.208	24.744	-1.457	Y ●
	OstA-like protein [Methylobacillus flagellatus KT]637937031 YP_544252											
MFLA0141		3.408	4.404	4.990	-1.075	Y ● ● Y	1.97 E-2	22.949	23.869	24.481	-0.914	Y ●
	ABC transporter related [Methylobacillus flagellatus KT]637937032 YP_544253											
MFLA0142	5.66 E-2	5.087	4.917	6.004	0.151	Y ● ● Y	2.19 E-1	23.799	23.931	24.866	-0.154	Y ●
	sigma-54 (RpoN) [Methylobacillus flagellatus KT]637937033 YP_544254											
MFLA0143		7.283	6.626	7.992	0.534	Y ● ● Y	1.02 E-1	25.789	26.253	27.040	-0.392	Y ●
	sigma 54 modulation protein/ribosomal protein S30EA [Methylobacillus flagellatus KT]637937034 YP_544255											
MFLA0144		3.656	4.769	5.317	-0.992	Y ● ● Y	2.27 E-2	23.484	24.770	25.266	-1.499	Y ●
	HPr kinase [Methylobacillus flagellatus KT]637937035 YP_544256											
MFLA0145		2.521	2.334	3.430	1.186	Y ● ● Y	1.87 E-1	21.305	21.922	22.646	0.603	Y ●
	Uncharacterised P-loop ATPase protein UPF0042 [Methylobacillus flagellatus KT]637937036 YP_544257											
MFLA0146		4.758	4.766	5.762	-0.108	Y ● ● Y	1.5 E-1	24.076	23.758	24.926	0.262	Y ●
	PTS system fructose subfamily IIA component [Methylobacillus flagellatus KT]637937037 YP_544258											
MFLA0147		3.582	3.764	4.676	-0.757	Y ● ● Y	2.7 E-1	24.029	24.064	25.047	-0.320	Y ●
	HPrNtr [Methylobacillus flagellatus KT]637937038 YP_544259											
MFLA0148		4.609	3.893	5.295	0.636	Y ● ● Y	2.06 E-2	21.868	23.080	23.598	-1.339	Y ●
	Phosphoenolpyruvate-protein phosphotransferase [Methylobacillus flagellatus KT]637937039 YP_544260											
MFLA0149		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937040 YP_544261											
MFLA0150		7.581	7.899	8.749	-0.318	Y ● ● Y	1.07 E-1	27.269	27.472	28.374	-0.222	Y ●
	Oligopeptidase A [Methylobacillus flagellatus KT]637937041 YP_544262											
MFLA0151		0.000	0.000			■ ■		0.000	0.000			■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637937042 YP_544263											
MFLA0152		0.000	0.000			■ ■		0.000	0.000			■
	Twin-arginine translocation pathway signal [Methylobacillus flagellatus KT]637937043 YP_544264											
MFLA0153		0.000	0.000			■ ■		0.000	0.000			■
	ABC transporter related [Methylobacillus flagellatus KT]637937044 YP_544265											
MFLA0154		0.000	0.000			■ ■		0.000	0.000			■
	ABC transporter related [Methylobacillus flagellatus KT]637937045 YP_544266											

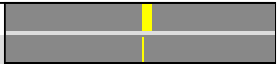
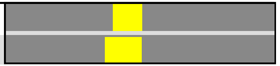
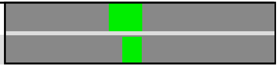
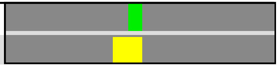
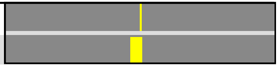
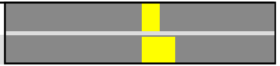
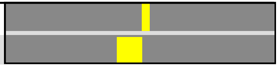
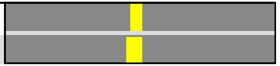
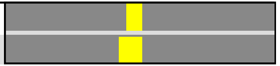
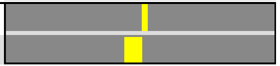


ORF	AM/OH *M Flagellatus* Spectral Count *q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation	AM/OH *M Flagellatus* Protein Intensity *q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA0155		0.000	0.000			■ ■		0.000	0.000			■
	inner-membrane translocator [Methylobacillus flagellatus KT]637937046 YP_544267											
MFLA0156		0.000	0.000			■ ■		0.000	0.000			■
	inner-membrane translocator [Methylobacillus flagellatus KT]637937047 YP_544268											
MFLA0157		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937048 YP_544269											
MFLA0158		0.000	0.000			■ ■		0.000	0.000			■
	" putative N,N-dimethylformamidase [Methylobacillus flagellatus KT]637937049 YP_544270 """											
MFLA0159		0.000	0.000			■ ■		0.000	0.000			■
	" transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637937050 YP_544271 """											
MFLA0160		0.000	0.000			■ ■		0.000	0.000			■
	YaeQ [Methylobacillus flagellatus KT]637937051 YP_544272											
MFLA0161		3.915	4.695	5.357	-0.708	Y ● ● Y	7.63 E-2	23.451	24.372	24.983	-0.792	Y ●
	YbaK/prolyl-tRNA synthetase associated region [Methylobacillus flagellatus KT]637937052 YP_544273											
MFLA0162		0.000	0.000			■ ■		0.000	0.000			■
	alpha/beta hydrolase fold [Methylobacillus flagellatus KT]637937053 YP_544274											
MFLA0163		0.000	0.000			■ ■		0.000	0.000			■
	Methyltransferase type 11 [Methylobacillus flagellatus KT]637937054 YP_544275											
MFLA0164		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937055 YP_544276											
MFLA0165		0.000	0.000			■ ■		0.000	0.000			■
	protein of unknown function DUF890 [Methylobacillus flagellatus KT]637937056 YP_544277											
MFLA0166		0.000	0.000			■ ■		0.000	0.000			■
	ABC-2 [Methylobacillus flagellatus KT]637937057 YP_544278											
MFLA0167		0.521	1.825	2.315	-0.153	Y ● ● Y	1.31 E-1	18.300	19.037	19.716	0.282	Y ●
	response regulator receiver domain protein (CheY-like) [Methylobacillus flagellatus KT]637937058 YP_544279											
MFLA0168		4.101	4.114	5.107	0.174	Y ● ● Y	2.54 E-1	23.240	23.300	24.270	-0.190	Y ●
	secretion protein HlyD [Methylobacillus flagellatus KT]637937059 YP_544280											
MFLA0169		3.637	1.000	3.852	1.620	Y ● ● Y	2.45 E-1	21.574	20.435	22.114	-0.046	Y ●
	" RND efflux system, outer membrane lipoprotein, NodT [Methylobacillus flagellatus KT]637937060 YP_544281 """											
MFLA0170		0.000	0.000			■ ■		0.000	0.000			■
	" transcriptional regulator, TetR family [Methylobacillus flagellatus KT]637937061 YP_544282 """											
MFLA0171		3.521	1.000	3.752	2.521	Y ● ● Y		21.803	17.920	21.898	3.883	Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637937062 YP_544283											
MFLA0172		4.413	4.875	5.663	-0.456	Y ● ● Y	1.51 E-1	23.455	23.643	24.552	-0.151	Y ●
	exodeoxyribonuclease III (xth) [Methylobacillus flagellatus KT]637937063 YP_544284											
MFLA0173		3.532	2.889	4.246	0.794	Y ● ● Y	1.16 E-1	23.482	24.038	24.787	-0.505	Y ●
	nitroreductase [Methylobacillus flagellatus KT]637937064 YP_544285											
MFLA0174		0.813		0.813		Y ● ● Y		20.266		20.266		Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637937065 YP_544286											
MFLA0175		0.000	0.000			■ ■		0.000	0.000			■
	MgtC/SapB transporter [Methylobacillus flagellatus KT]637937066 YP_544287											
MFLA0176		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937067 YP_544288											

	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	**Consensus**
MFLA0177		0.521		0.521		Y 🟡 🟡 Y		20.059		20.059		Y 🟡
	Deoxyguanosinetriphosphate triphosphohydrolase [Methylobacillus flagellatus KT]637937068 YP_544289											
MFLA0178		3.307	1.000	3.573	1.167	Y 🟡 🟡 Y	7.24 E-2	23.217	21.335	23.564	0.870	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937069 YP_544290											
MFLA0179		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	MIP family channel proteins [Methylobacillus flagellatus KT]637937070 YP_544291											
MFLA0180		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	protein of unknown function DUF1275 [Methylobacillus flagellatus KT]637937071 YP_544292											
MFLA0181	1.05 E-1	6.110	6.342	7.231	-0.232	Y 🟡 🟡 Y	2.69 E-1	25.321	25.285	26.303	-0.141	Y 🟡
	" two component, sigma54 specific, transcriptional regulator, Fis family [Methylobacillus flagellatus KT]637937072 YP_544293 """											
MFLA0182		5.114	3.611	5.550	1.504	Y 🟡 🟡 Y	1.21 E-1	22.693	22.001	23.388	0.576	Y 🟡
	periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637937073 YP_544294											
MFLA0183		3.038	2.095	3.642	0.786	Y 🟡 🟡 Y	4.09 E-2	20.965	22.037	22.598	-1.233	Y 🟡
	putative proline rich signal peptide protein [Methylobacillus flagellatus KT]637937074 YP_544295											
MFLA0184	1.84 E-11	6.411	4.945	6.856	1.465	R 🔴 🟡 Y	1.69 E-1	23.967	23.805	24.888	0.211	R 🔴
	sun protein [Methylobacillus flagellatus KT]637937075 YP_544296											
MFLA0185		4.266	2.816	4.716	1.245	Y 🟡 🟡 Y	7.19 E-2	24.267	23.223	24.838	1.137	Y 🟡
	" peptidase M48, Ste24p [Methylobacillus flagellatus KT]637937076 YP_544297 """											
MFLA0186	7.33 E-2	4.828	5.065	5.952	-0.218	Y 🟡 🟡 Y	2.02 E-1	23.493	23.721	24.612	-0.446	Y 🟡
	methionyl-tRNA formyltransferase [Methylobacillus flagellatus KT]637937077 YP_544298											
MFLA0187	1.44 E-1	4.587	5.217	5.936	-0.802	Y 🟡 🟡 Y	2.21 E-1	24.298	24.510	25.408	-0.637	Y 🟡
	Peptide deformylase [Methylobacillus flagellatus KT]637937078 YP_544299											
MFLA0188		6.223	5.688	6.980	0.531	Y 🟡 🟡 Y	2.73 E-1	25.671	25.650	26.661	-0.047	Y 🟡
	Peptidoglycan-binding LysM [Methylobacillus flagellatus KT]637937079 YP_544300											
MFLA0189		1.106		1.106		Y 🟡 🟡 Y		18.772		18.772		Y 🟡
	" DNA processing protein DprA, putative [Methylobacillus flagellatus KT]637937080 YP_544301 """											
MFLA0190		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	protein of unknown function DUF494 [Methylobacillus flagellatus KT]637937081 YP_544302											
MFLA0191	3.4 E-16	6.201	7.326	7.870	-1.210	G 🟢 🟢 G	8.35 E-3	25.048	26.504	26.952	-1.449	G 🟢
	" 5,10-methylenetetrahydrofolate reductase [Methylobacillus flagellatus KT]637937082 YP_544303 """											
MFLA0192		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	membrane protein of unknown function [Methylobacillus flagellatus KT]637937083 YP_544304											
MFLA0193	0	9.243	9.611	10.439	-0.414	Y 🟡 🟡 Y	4.29 E-2	29.142	29.675	30.433	-0.574	Y 🟡
	adenosylhomocysteinase [Methylobacillus flagellatus KT]637937084 YP_544305											
MFLA0194		8.175	8.311	9.244	-0.160	Y 🟡 🟡 Y	3.23 E-2	28.043	28.873	29.517	-0.920	Y 🟡
	Methionine adenosyltransferase [Methylobacillus flagellatus KT]637937085 YP_544306											
MFLA0195		2.980	3.616	4.333	0.457	Y 🟡 🟡 Y	3.27 E-2	21.849	21.684	22.768	1.171	Y 🟡
	lipid A biosynthesis acyltransferase [Methylobacillus flagellatus KT]637937086 YP_544307											
MFLA0196		3.386	3.385	4.386	-0.006	Y 🟡 🟡 Y	2.72 E-1	22.261	22.281	23.271	-0.068	Y 🟡
	Diaminopimelate epimerase [Methylobacillus flagellatus KT]637937087 YP_544308											
MFLA0197		5.096	5.704	6.432	-0.701	Y 🟡 🟡 Y	8.46 E-2	25.561	26.283	26.967	-0.987	Y 🟡
	protein of unknown function DUF484 [Methylobacillus flagellatus KT]637937088 YP_544309											
MFLA0198		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	Tyrosine recombinase XerC [Methylobacillus flagellatus KT]637937089 YP_544310											

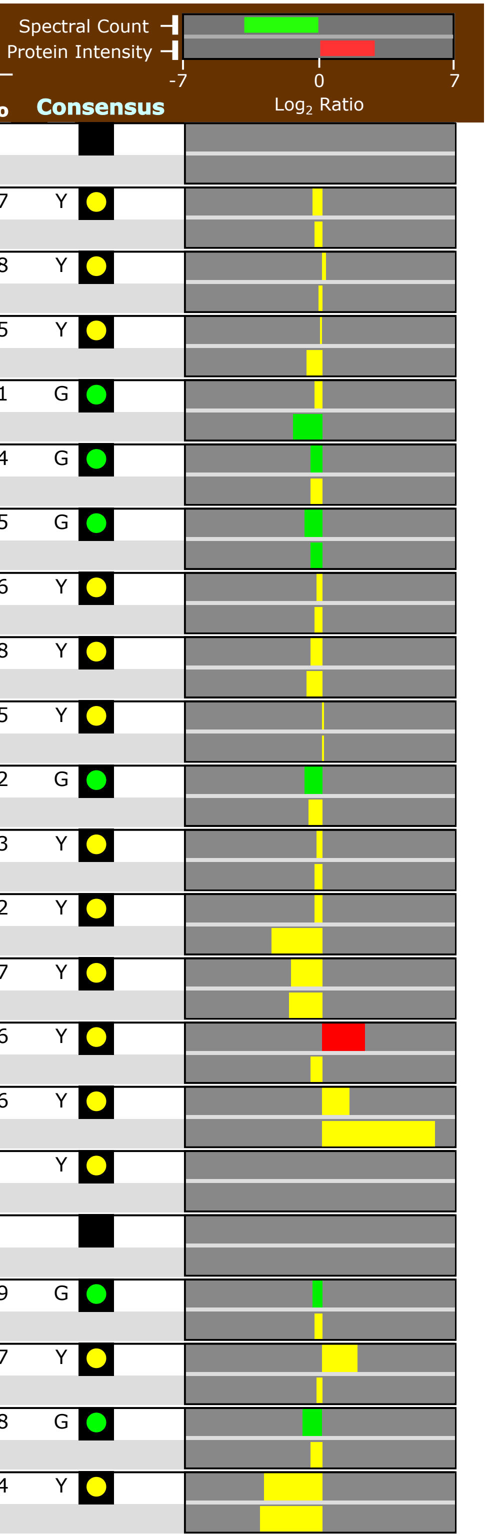


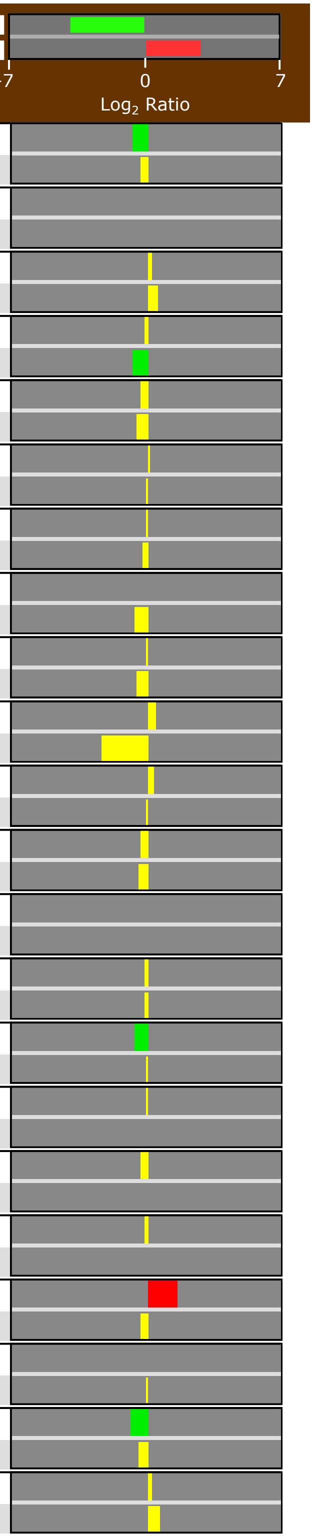


ORF	AM/OH *M Flagellatus* Spectral Count					Regulation				AM/OH *M Flagellatus* Protein Intensity					Consensus		
	q-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio					*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio			
MFLA0199		3.135	3.240	4.189	0.897	Y	🟡	🟡	Y	5.65 E-2	18.605	22.347	22.451	-2.723	Y	🟡	
	molybdenum cofactor biosynthesis protein C [Methylobacillus flagellatus KT]637937090 YP_544311																
MFLA0200		2.106	1.585	2.869	0.521	Y	🟡	🟡	Y		20.801	20.685	21.744	0.115	Y	🟡	
	" peptidase M48, Ste24p [Methylobacillus flagellatus KT]637937091 YP_544312 """																
MFLA0201		0.000	0.000				■	■			0.000	0.000				■	
	" transmembrane proetin, twin-arginine translocation pathway signal [Methylobacillus flagellatus KT]637937092 YP_544313 """																
MFLA0202		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637937093 YP_544314																
MFLA0203		8.168	7.896	9.038	0.175	Y	🟡	🟡	Y	2.58 E-1	27.470	27.508	28.489	-0.016	Y	🟡	
	" Alcohol dehydrogenase, zinc-binding [Methylobacillus flagellatus KT]637937094 YP_544315 """																
MFLA0204		2.307	2.700	3.517	-1.533	Y	🟡	🟡	Y	1.53 E-2	21.965	22.903	23.509	-1.940	Y	🟡	
	" Chromosomal replication initiator, DnaA [Methylobacillus flagellatus KT]637937095 YP_544316 """																
MFLA0205	0	6.311	8.244	8.579	-1.726	G	🟢	🟢	G	7.38 E-3	25.196	26.143	26.746	-0.955	G	🟢	
	phosphoribosylformylglycinamidine cyclo-ligase [Methylobacillus flagellatus KT]637937096 YP_544317																
MFLA0206	1.43 E-7	6.298	5.210	6.854	1.124	R	🔴	🟡	Y	7.93 E-2	24.296	23.694	25.027	0.541	R	🔴	
	hypothetical protein [Methylobacillus flagellatus KT]637937097 YP_544318																
MFLA0207		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637937098 YP_544319																
MFLA0208	1.68 E-3	5.505	6.183	6.883	-0.668	G	🟢	🟡	Y	2.09 E-2	24.547	26.025	26.467	-1.461	G	🟢	
	Fmu (Sun) [Methylobacillus flagellatus KT]637937099 YP_544320																
MFLA0209		0.000	0.000				■	■			0.000	0.000				■	
	sodium:dicarboxylate symporter [Methylobacillus flagellatus KT]637937100 YP_544321																
MFLA0210		7.689	7.878	8.787	-0.091	Y	🟡	🟡	Y	1.46 E-1	29.556	30.168	30.894	-0.587	Y	🟡	
	blue (type 1) copper domain [Methylobacillus flagellatus KT]637937101 YP_544322																
MFLA0211		4.362	2.897	4.808	0.912	Y	🟡	🟡	Y	5.8 E-2	22.302	20.511	22.669	1.663	Y	🟡	
	acriflavin resistance protein [Methylobacillus flagellatus KT]637937102 YP_544323																
MFLA0212		4.824	4.444	5.647	0.381	Y	🟡	🟡	Y	3.45 E-2	23.854	25.151	25.644	-1.305	Y	🟡	
	secretion protein HlyD [Methylobacillus flagellatus KT]637937103 YP_544324																
MFLA0213		1.398		1.398		Y	🟡	🟡	Y		19.129		19.129		Y	🟡	
	" negative regulator of AmpC, AmpD [Methylobacillus flagellatus KT]637937104 YP_544325 """																
MFLA0214	1.07 E-2	4.816	5.432	6.157	-0.610	Y	🟡	🟡	Y	4.87 E-2	23.389	24.062	24.764	-0.772	Y	🟡	
	" two component, sigma54 specific, transcriptional regulator, Fis family [Methylobacillus flagellatus KT]637937105 YP_544326 """																
MFLA0215		1.843	3.759	4.098	-0.784	Y	🟡	🟡	Y	1.07 E-1	19.660	21.927	22.199	-1.185	Y	🟡	
	periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637937106 YP_544327																
MFLA0216		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637937107 YP_544328																
MFLA0217		0.000	0.000				■	■			0.000	0.000				■	
	sigma-24 (FecI-like) [Methylobacillus flagellatus KT]637937108 YP_544329																
MFLA0218		0.000	0.000				■	■			0.000	0.000				■	
	putative transmembrane protein [Methylobacillus flagellatus KT]637937109 YP_544330																
MFLA0219		3.674	3.458	4.570	0.264	Y	🟡	🟡	Y	2.41 E-2	20.500	21.395	22.016	-0.881	Y	🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637937110 YP_544331																
MFLA0220		0.000	0.000				■	■			0.000	0.000				■	
	permease YjgP/YjgQ [Methylobacillus flagellatus KT]637937111 YP_544332																

ORF	AM/OH *M Flagellatus* Spectral Count					Regulation				AM/OH *M Flagellatus* Protein Intensity					Consensus	
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio					*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		
MFLA0221		1.521	2.807	3.303	-1.287	Y	🟡	🟡	Y		21.774	22.062	22.925	-0.289	Y	🟡
	permease YjgP/YjgQ [Methylobacillus flagellatus KT]637937112 YP_544333															
MFLA0222		8.246	8.129	9.189	-0.002	Y	🟡	🟡	Y	2.42 E-1	28.232	28.186	29.210	0.012	Y	🟡
	Leucyl aminopeptidase [Methylobacillus flagellatus KT]637937113 YP_544334															
MFLA0223			0.000	0.000		Y	🟡	🟡	Y			18.790	18.790		Y	🟡
	" DNA polymerase III chi subunit, HolC [Methylobacillus flagellatus KT]637937114 YP_544335 """															
MFLA0224	4.53 E-4	5.816	4.997	6.464	0.872	R	🔴	🟡	Y	1.67 E-1	22.333	21.713	23.056	0.331	R	🔴
	hypothetical protein [Methylobacillus flagellatus KT]637937115 YP_544336															
MFLA0225		0.000	0.000				■	■			0.000	0.000				■
	glycine cleavage system H protein [Methylobacillus flagellatus KT]637937116 YP_544337															
MFLA0226		0.000	0.000				■	■			0.000	0.000				■
	" peptidase S11, D-alanyl-D-alanine carboxypeptidase 1 [Methylobacillus flagellatus KT]637937117 YP_544338 """															
MFLA0227	4.16 E-2	7.382	7.339	8.361	0.021	Y	🟡	🟡	Y	2.25 E-2	26.344	27.053	27.742	-0.717	Y	🟡
	DNA topoisomerase [Methylobacillus flagellatus KT]637937118 YP_544339															
MFLA0228		4.179	2.471	4.564	1.712	Y	🟡	🟡	Y	5.48 E-2	22.188	21.929	23.064	0.271	Y	🟡
	PP-loop [Methylobacillus flagellatus KT]637937119 YP_544340															
MFLA0229		4.080	4.930	5.567	-0.901	Y	🟡	🟡	Y	4.59 E-2	23.167	23.914	24.588	-0.855	Y	🟡
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637937120 YP_544341															
MFLA0230			1.710	1.710		Y	🟡	🟡	Y			21.241	21.241		Y	🟡
	protein of unknown function DUF185 [Methylobacillus flagellatus KT]637937121 YP_544342															
MFLA0231		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937122 YP_544343															
MFLA0232		4.556	4.972	5.779	-0.543	Y	🟡	🟡	Y	1.14 E-1	23.401	24.201	24.856	-2.078	Y	🟡
	" GTP-binding protein, HSR1-related [Methylobacillus flagellatus KT]637937123 YP_544344 """															
MFLA0233		5.055	3.788	5.556	0.976	Y	🟡	🟡	Y	2.03 E-1	23.719	23.311	24.530	0.155	Y	🟡
	ResB-like protein [Methylobacillus flagellatus KT]637937124 YP_544345															
MFLA0234		0.000	0.000				■	■			0.000	0.000				■
	cytochrome c assembly protein [Methylobacillus flagellatus KT]637937125 YP_544346															
MFLA0235		3.364	2.322	3.935	0.041	Y	🟡	🟡	Y	8.39 E-2	20.933	20.340	21.667	-0.417	Y	🟡
	" ATP-binding region, ATPase-like protein [Methylobacillus flagellatus KT]637937126 YP_544347 """															
MFLA0236	2.99 E-2	5.201	5.219	6.210	-0.081	Y	🟡	🟡	Y	2.72 E-1	24.670	24.644	25.657	0.046	Y	🟡
	methylation [Methylobacillus flagellatus KT]637937127 YP_544348															
MFLA0237		5.277	4.485	5.935	0.907	Y	🟡	🟡	Y	4.29 E-2	22.209	23.774	24.194	-1.707	Y	🟡
	ABC transporter related [Methylobacillus flagellatus KT]637937128 YP_544349															
MFLA0238		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF140 [Methylobacillus flagellatus KT]637937129 YP_544350															
MFLA0239		6.460	6.194	7.333	0.163	Y	🟡	🟡	Y	2.7 E-1	25.540	25.510	26.525	-0.000	Y	🟡
	Mammalian cell entry related [Methylobacillus flagellatus KT]637937130 YP_544351															
MFLA0240	1.16 E-2	6.284	6.176	7.231	0.194	Y	🟡	🟡	Y	9.56 E-2	27.283	27.891	28.619	-0.608	Y	🟡
	toluene tolerance [Methylobacillus flagellatus KT]637937131 YP_544352															
MFLA0241		0.000	0.000				■	■			0.000	0.000				■
	STAS domain [Methylobacillus flagellatus KT]637937132 YP_544353															
MFLA0242		4.210	3.385	4.856	0.798	Y	🟡	🟡	Y	1.9 E-1	22.269	22.650	23.472	-0.553	Y	🟡
	ABC transporter related [Methylobacillus flagellatus KT]637937133 YP_544354															

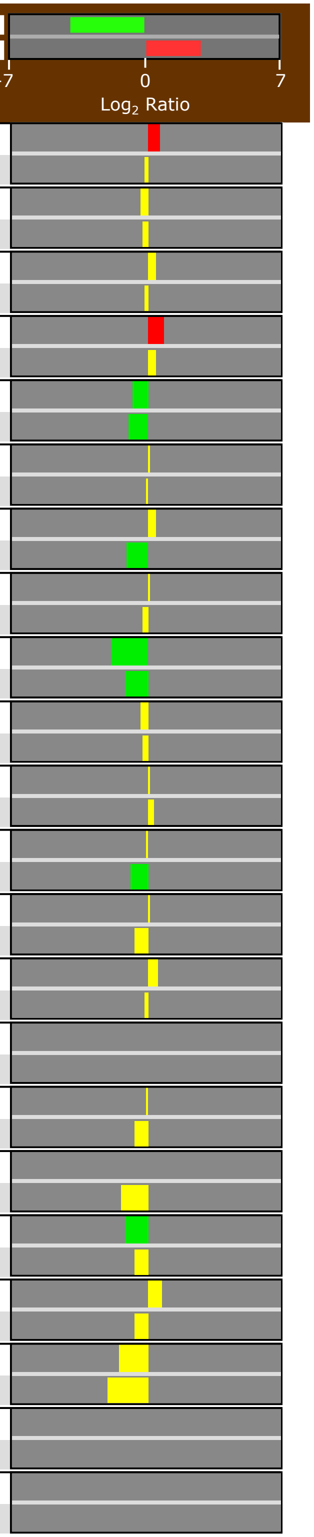
ORF	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA0243		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	ABC-2 [Methylobacillus flagellatus KT]637937134 YP_544355															
MFLA0244		2.502	2.941	3.738	-0.460	Y	🟡	🟡	Y	6.85 E-2	22.875	23.303	24.105	-0.437	Y	🟡
	BolA-like protein [Methylobacillus flagellatus KT]637937135 YP_544356															
MFLA0245		6.347	5.974	7.173	0.178	Y	🟡	🟡	Y	2.32 E-1	27.037	27.136	28.088	-0.198	Y	🟡
	Glutaredoxin-related protein [Methylobacillus flagellatus KT]637937136 YP_544357															
MFLA0246	4.46 E-2	5.214	5.207	6.210	-0.133	Y	🟡	🟡	Y	1.61 E-2	23.315	24.137	24.784	-0.815	Y	🟡
	UDP-N-acetylglucosamine 1-carboxyvinyltransferase [Methylobacillus flagellatus KT]637937137 YP_544358															
MFLA0247	1.11 E-2	5.298	5.760	6.548	-0.426	Y	🟡	🟢	G	8.62 E-3	23.852	25.361	25.795	-1.501	G	🟢
	ATP phosphoribosyltransferase [Methylobacillus flagellatus KT]637937138 YP_544359															
MFLA0248	1.47 E-7	7.342	7.922	8.661	-0.586	G	🟢	🟡	Y	4.29 E-2	26.948	27.502	28.252	-0.564	G	🟢
	Histidinol dehydrogenase [Methylobacillus flagellatus KT]637937139 YP_544360															
MFLA0249	1.56 E-3	4.783	5.674	6.296	-0.893	G	🟢	🟢	G	6.36 E-3	23.691	24.314	25.036	-0.625	G	🟢
	histidinol-phosphate aminotransferase [Methylobacillus flagellatus KT]637937140 YP_544361															
MFLA0250	0	11.768	12.040	12.910	-0.274	Y	🟡	🟡	Y	1.69 E-3	31.314	31.760	32.554	-0.446	Y	🟡
	Orotidine 5'-phosphate decarboxylase [Methylobacillus flagellatus KT]637937141 YP_544362															
MFLA0251	2.28 E-2	5.084	5.665	6.404	-0.571	Y	🟡	🟡	Y	2.56 E-2	23.418	24.198	24.860	-0.768	Y	🟡
	Imidazoleglycerol-phosphate dehydratase [Methylobacillus flagellatus KT]637937142 YP_544363															
MFLA0252		3.619	3.488	4.555	0.070	Y	🟡	🟡	Y	2.2 E-1	23.988	23.927	24.958	0.075	Y	🟡
	" imidazole glycerol phosphate synthase, glutamine amidotransferase subunit [Methylobacillus flagellatus KT]637937143 YP_544364 """															
MFLA0253	2.12 E-12	6.849	7.730	8.356	-0.880	G	🟢	🟡	Y	1.08 E-2	26.134	26.856	27.540	-0.732	G	🟢
	Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [Methylobacillus flagellatus KT]637937144 YP_544365															
MFLA0254	1.03 E-1	5.156	5.462	6.317	-0.293	Y	🟡	🟡	Y	1.26 E-1	24.624	24.934	25.787	-0.353	Y	🟡
	" imidazoleglycerol phosphate synthase, cyclase subunit [Methylobacillus flagellatus KT]637937145 YP_544366 """															
MFLA0255		3.053	3.315	4.190	-0.443	Y	🟡	🟡	Y	5.13 E-2	18.856	21.725	21.910	-2.622	Y	🟡
	Phosphoribosyl-AMP cyclohydrolase [Methylobacillus flagellatus KT]637937146 YP_544367															
MFLA0256		2.543	2.907	3.736	-1.579	Y	🟡	🟡	Y	1.78 E-2	21.250	21.974	22.657	-1.727	Y	🟡
	phosphoribosyl-ATP pyrophosphohydrolase [Methylobacillus flagellatus KT]637937147 YP_544368															
MFLA0257	1.64 E-8	5.687	3.471	5.969	2.212	R	🔴	🟡	Y	1.79 E-1	22.882	23.191	24.045	-0.596	Y	🟡
	histidine triad (HIT) protein [Methylobacillus flagellatus KT]637937148 YP_544369															
MFLA0258		3.328	3.730	4.543	1.362	Y	🟡	🟡	Y	1.61 E-2	24.849	20.626	24.924	5.836	Y	🟡
	" twin-arginine translocation protein, TatA/E family [Methylobacillus flagellatus KT]637937149 YP_544370 """															
MFLA0259			1.322	1.322		Y	🟡	🟡	Y			22.383	22.383		Y	🟡
	twin-arginine translocation protein TatB [Methylobacillus flagellatus KT]637937150 YP_544371															
MFLA0260		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	Sec-independent protein translocase TatC [Methylobacillus flagellatus KT]637937151 YP_544372															
MFLA0261	4.5 E-3	6.079	6.613	7.371	-0.536	G	🟢	🟡	Y	7.24 E-2	25.955	26.438	27.216	-0.449	G	🟢
	" peptidase S1 and S6, chymotrypsin/Hap [Methylobacillus flagellatus KT]637937152 YP_544373 """															
MFLA0262		4.903	3.032	5.251	1.842	Y	🟡	🟡	Y	2.23 E-1	21.933	21.637	22.792	-0.347	Y	🟡
	protein of unknown function DUF34 [Methylobacillus flagellatus KT]637937153 YP_544374															
MFLA0263	0	8.435	9.384	9.986	-0.951	G	🟢	🟡	Y	8.26 E-2	27.822	28.375	29.125	-0.648	G	🟢
	glutathione S-transferase-like protein [Methylobacillus flagellatus KT]637937154 YP_544375															
MFLA0264		0.521	4.540	4.626	-2.956	Y	🟡	🟡	Y	6.47 E-2	21.089	25.304	25.379	-3.184	Y	🟡
	Stringent starvation protein B [Methylobacillus flagellatus KT]637937155 YP_544376															



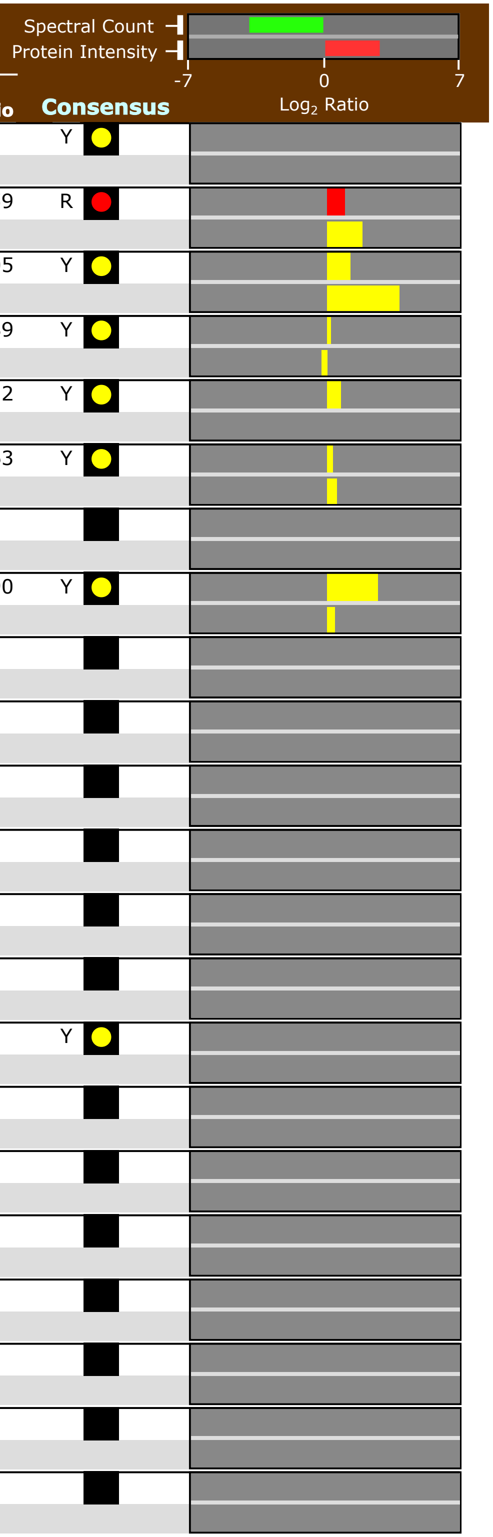


	AM/OH *M Flagellatus* Spectral Count							AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation		*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA0265	0	12.327	13.069	13.746	-0.769	G ●	● Y	4.29 E-3	33.109	33.547	34.345	-0.438	G ●
	translation elongation factor Tu [Methylobacillus flagellatus KT]637937160 YP_544377												
MFLA0266		0.000	0.000			■	■		0.000	0.000			■
	SecE subunit of protein translocation complex [Methylobacillus flagellatus KT]637937162 YP_544378												
MFLA0267		7.122	6.869	8.001	0.181	Y ●	● Y	5.9 E-2	27.294	26.767	28.054	0.497	Y ●
	NusG antitermination factor [Methylobacillus flagellatus KT]637937163 YP_544379												
MFLA0268	1.03 E-1	6.058	6.207	7.134	-0.168	Y ●	● G	8.35 E-3	27.562	28.365	29.018	-0.801	G ●
	ribosomal protein L11 [Methylobacillus flagellatus KT]637937164 YP_544380												
MFLA0269		10.362	10.737	11.562	-0.367	Y ●	● Y	7.9 E-2	30.038	30.623	31.360	-0.608	Y ●
	ribosomal protein L1 [Methylobacillus flagellatus KT]637937165 YP_544381												
MFLA0270		8.125	8.035	9.081	0.065	Y ●	● Y	2.53 E-1	28.686	28.718	29.702	-0.063	Y ●
	ribosomal protein L10 [Methylobacillus flagellatus KT]637937166 YP_544382												
MFLA0271		10.175	10.248	11.212	-0.086	Y ●	● Y	7.24 E-2	29.578	29.895	30.745	-0.341	Y ●
	ribosomal protein L7/L12 [Methylobacillus flagellatus KT]637937167 YP_544383												
MFLA0272		10.761	10.793	11.777	-0.050	Y ●	● Y	3.48 E-2	30.310	30.926	31.650	-0.663	Y ●
	" DNA-directed RNA polymerase, beta subunit [Methylobacillus flagellatus KT]637937168 YP_544384 """												
MFLA0273		10.631	10.712	11.672	-0.093	Y ●	● Y	2.7 E-2	29.891	30.466	31.207	-0.602	Y ●
	" DNA-directed RNA polymerase, subunit beta-prime [Methylobacillus flagellatus KT]637937169 YP_544385 """												
MFLA0274		6.383	7.198	7.848	0.416	Y ●	● Y	6.08 E-2	21.827	25.277	25.404	-2.429	Y ●
	ribosomal protein S12 [Methylobacillus flagellatus KT]637937170 YP_544386												
MFLA0275	1.4 E-2	7.083	6.839	7.966	0.265	Y ●	● Y	1.05 E-1	28.386	28.533	29.461	-0.143	Y ●
	ribosomal protein S7 [Methylobacillus flagellatus KT]637937171 YP_544387												
MFLA0276		10.227	10.623	11.438	-0.400	Y ●	● Y	3.92 E-2	30.608	31.077	31.861	-0.480	Y ●
	translation elongation factor G [Methylobacillus flagellatus KT]637937172 YP_544388												
MFLA0277		0.000	0.000			■	■		0.000	0.000			■
	translation elongation factor Tu [Methylobacillus flagellatus KT]637937173 YP_544389												
MFLA0278	2.63 E-2	6.925	7.075	8.002	-0.180	Y ●	● Y	1.21 E-1	27.997	28.180	29.091	-0.175	Y ●
	ribosomal protein S10 [Methylobacillus flagellatus KT]637937174 YP_544390												
MFLA0279	2.75 E-8	6.662	7.385	8.068	-0.697	G ●	● Y	2.17 E-1	28.232	28.337	29.285	-0.100	Y ●
	ribosomal protein L3 [Methylobacillus flagellatus KT]637937175 YP_544391												
MFLA0280	6.51 E-2	8.955	9.083	10.020	-0.128	Y ●	● Y	2.1 E-1	29.661	29.614	30.638	0.038	Y ●
	ribosomal protein L4/L1e [Methylobacillus flagellatus KT]637937176 YP_544392												
MFLA0281		6.304	6.468	7.389	-0.354	Y ●	● Y	2.58 E-1	27.679	27.638	28.659	-0.026	Y ●
	Ribosomal protein L25/L23 [Methylobacillus flagellatus KT]637937177 YP_544393												
MFLA0282		8.192	8.405	9.302	-0.196	Y ●	● Y	2.64 E-1	29.181	29.190	30.186	-0.016	Y ●
	ribosomal protein L2 [Methylobacillus flagellatus KT]637937178 YP_544394												
MFLA0283	0	7.054	5.504	7.478	1.548	R ●	● Y	5.97 E-2	26.721	27.076	27.910	-0.381	Y ●
	ribosomal protein S19 [Methylobacillus flagellatus KT]637937179 YP_544395												
MFLA0284	1.13 E-1	7.866	7.811	8.839	0.050	Y ●	● Y	1.31 E-1	28.701	28.812	29.758	-0.102	Y ●
	ribosomal protein L22 [Methylobacillus flagellatus KT]637937180 YP_544396												
MFLA0285	0	7.430	8.200	8.865	-0.925	G ●	● Y	2.34 E-1	28.119	28.272	29.197	-0.466	G ●
	ribosomal protein S3 [Methylobacillus flagellatus KT]637937181 YP_544397												
MFLA0286	1.21 E-1	6.362	6.195	7.281	0.164	Y ●	● Y	1.03 E-1	28.889	28.255	29.607	0.583	Y ●
	ribosomal protein L16 [Methylobacillus flagellatus KT]637937182 YP_544398												

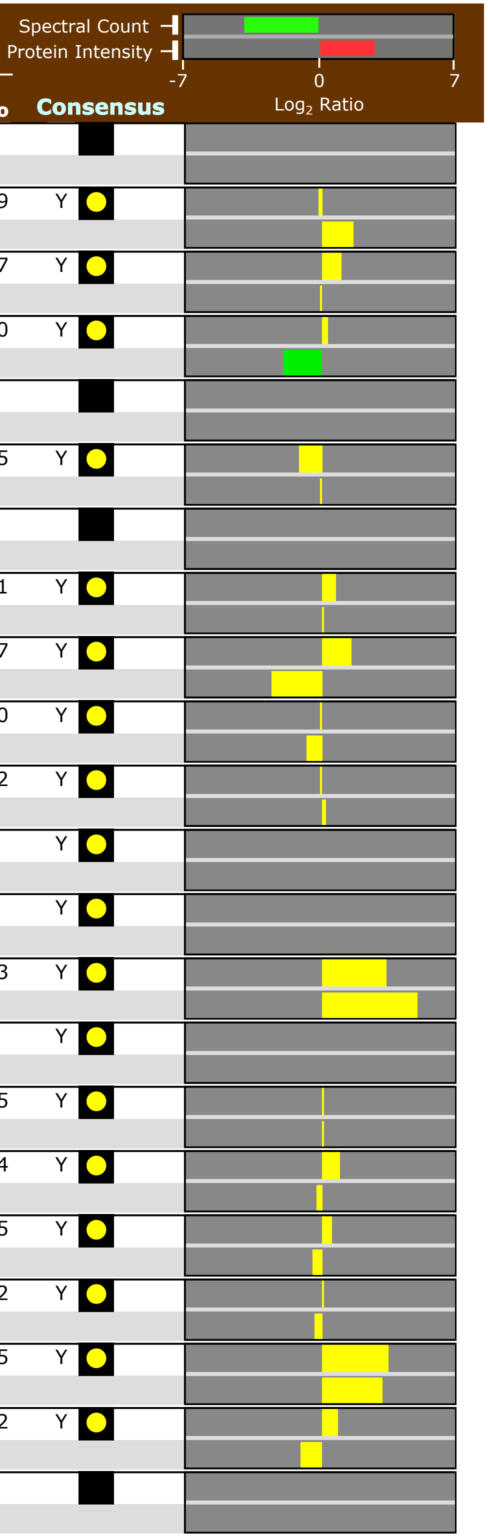
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA0287	1.38 E-3	6.376	5.772	7.105	0.591	R	🔴	🟡	Y	1.36 E-1	26.805	27.000	27.906	-0.226	Y	🟡
	ribosomal protein L29 [Methylobacillus flagellatus KT]637937183 YP_544399															
MFLA0288		5.966	5.729	6.853	-0.368	Y	🟡	🟡	Y	2.02 E-1	25.534	25.712	26.626	-0.294	Y	🟡
	ribosomal protein S17 [Methylobacillus flagellatus KT]637937184 YP_544400															
MFLA0289	3.82 E-3	7.180	6.759	7.985	0.430	Y	🟡	🟡	Y	1.07 E-1	28.046	28.289	29.173	-0.222	Y	🟡
	ribosomal protein L14 [Methylobacillus flagellatus KT]637937185 YP_544401															
MFLA0290	1.61 E-10	7.781	7.019	8.450	0.754	R	🔴	🟡	Y	7.14 E-2	27.942	27.520	28.746	0.415	R	🔴
	ribosomal protein L24 [Methylobacillus flagellatus KT]637937186 YP_544402															
MFLA0291	0	8.036	8.802	9.469	-0.754	G	🟢	🟢	G	2.75 E-5	28.600	29.618	30.197	-1.018	G	🟢
	ribosomal protein L5 [Methylobacillus flagellatus KT]637937187 YP_544403															
MFLA0292	1.71 E-2	7.081	6.968	8.025	0.098	Y	🟡	🟡	Y	1.79 E-1	27.136	27.202	28.170	-0.075	Y	🟡
	ribosomal protein S14 [Methylobacillus flagellatus KT]637937188 YP_544404															
MFLA0293	1.44 E-14	9.299	8.916	10.120	0.422	Y	🟡	🟢	G	6.19 E-3	26.883	28.025	28.564	-1.143	Y	🟡
	ribosomal protein S8 [Methylobacillus flagellatus KT]637937189 YP_544405															
MFLA0294		9.008	8.911	9.960	0.087	Y	🟡	🟡	Y	8.3 E-2	29.205	29.544	30.385	-0.350	Y	🟡
	ribosomal protein L6 [Methylobacillus flagellatus KT]637937190 YP_544406															
MFLA0295	0	6.284	8.288	8.609	-1.932	G	🟢	🟢	G	9.51 E-3	26.329	27.547	28.063	-1.221	G	🟢
	ribosomal protein L18 [Methylobacillus flagellatus KT]637937191 YP_544407															
MFLA0296		8.242	8.658	9.465	-0.366	Y	🟡	🟡	Y	1.99 E-2	28.089	28.421	29.264	-0.336	Y	🟡
	ribosomal protein S5-like protein [Methylobacillus flagellatus KT]637937192 YP_544408															
MFLA0297		7.318	7.149	8.236	0.150	Y	🟡	🟡	Y	7.24 E-2	27.283	27.023	28.159	0.260	Y	🟡
	ribosomal protein L30 [Methylobacillus flagellatus KT]637937193 YP_544409															
MFLA0298	7.93 E-2	6.807	6.876	7.842	-0.082	Y	🟡	🟢	G	9.69 E-3	27.722	28.635	29.250	-0.927	Y	🟡
	ribosomal protein L15 [Methylobacillus flagellatus KT]637937194 YP_544410															
MFLA0299		1.843	3.086	3.594	0.147	Y	🟡	🟡	Y	1.2 E-1	22.350	24.055	24.441	-0.651	Y	🟡
	SecY protein [Methylobacillus flagellatus KT]637937195 YP_544411															
MFLA0300	5.1 E-2	5.631	5.166	6.417	0.473	Y	🟡	🟡	Y	1.12 E-1	25.058	25.245	26.155	-0.182	Y	🟡
	translation initiation factor IF-1 [Methylobacillus flagellatus KT]637937196 YP_544412															
MFLA0301		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	ribosomal protein L36 [Methylobacillus flagellatus KT]637937197 YP_544413															
MFLA0302	1.23 E-1	8.175	8.241	9.208	-0.064	Y	🟡	🟡	Y	1.01 E-2	27.274	27.961	28.658	-0.687	Y	🟡
	ribosomal protein S13 [Methylobacillus flagellatus KT]637937198 YP_544414															
MFLA0303		8.269	8.057	9.167	-0.001	Y	🟡	🟡	Y	1.77 E-2	27.434	28.815	29.283	-1.354	Y	🟡
	ribosomal protein S11 [Methylobacillus flagellatus KT]637937199 YP_544415															
MFLA0304	0	9.611	10.726	11.274	-1.163	G	🟢	🟡	Y	6.37 E-2	29.040	29.693	30.404	-0.703	G	🟢
	" DNA-directed RNA polymerase, alpha subunit [Methylobacillus flagellatus KT]637937200 YP_544416 """															
MFLA0305		5.084	4.388	5.777	0.701	Y	🟡	🟡	Y	4.72 E-2	27.012	27.704	28.400	-0.657	Y	🟡
	ribosomal protein L17 [Methylobacillus flagellatus KT]637937201 YP_544417															
MFLA0306		4.017	5.466	5.916	-1.483	Y	🟡	🟡	Y	2.99 E-2	22.462	24.414	24.745	-2.089	Y	🟡
	magnesium transporter [Methylobacillus flagellatus KT]637937202 YP_544418															
MFLA0307		1.521		1.521		Y	🟡	🟡	Y		20.216		20.216		Y	🟡
	MscS Mechanosensitive ion channel [Methylobacillus flagellatus KT]637937203 YP_544419															
MFLA0308		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937204 YP_544420															



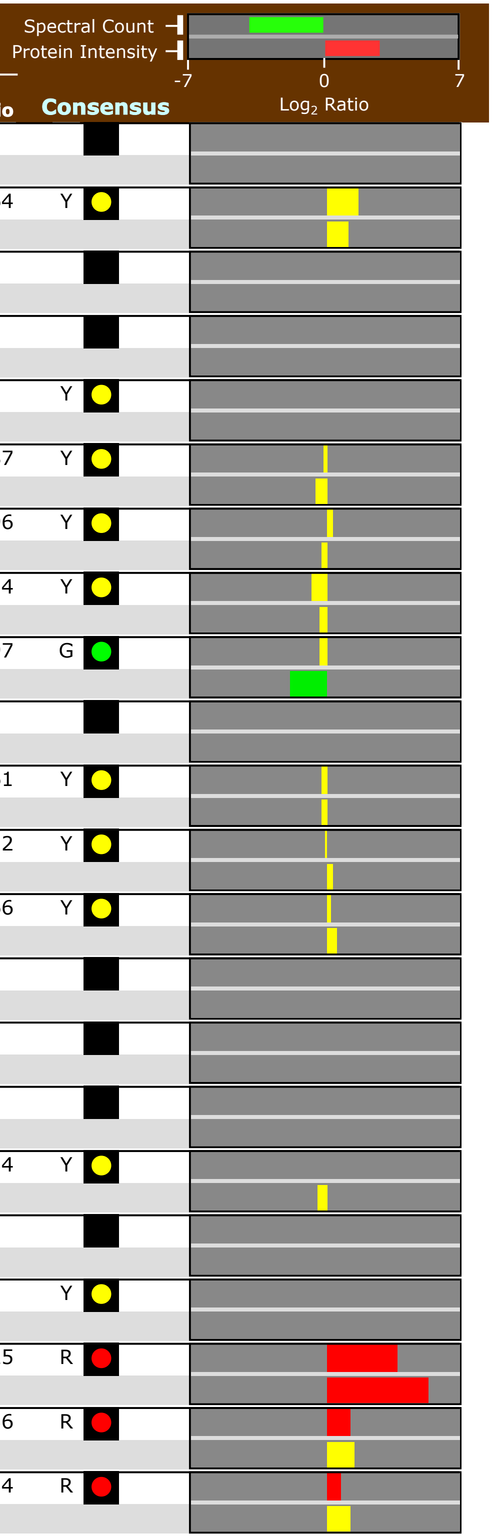
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA0309		2.106		2.106		Y	🟡	🟡	Y		19.947		19.947		Y	🟡
	" transcriptional regulator, TetR family [Methylobacillus flagellatus KT]637937205 YP_544421 """															
MFLA0310	5.13 E-3	5.806	3.931	6.153	0.874	R	🔴	🟡	Y	7.16 E-2	24.905	22.118	25.100	1.759	R	🔴
	conserved hypothetical signal peptide protein [Methylobacillus flagellatus KT]637937206 YP_544422															
MFLA0311		5.057	3.923	5.598	1.169	Y	🟡	🟡	Y	3.67 E-2	25.773	22.107	25.882	3.705	Y	🟡
	ribosomal protein L33 [Methylobacillus flagellatus KT]637937207 YP_544423															
MFLA0312		6.789	6.644	7.718	0.245	Y	🟡	🟡	Y	2.17 E-1	27.470	27.640	28.557	-0.289	Y	🟡
	ribosomal protein L28 [Methylobacillus flagellatus KT]637937208 YP_544424															
MFLA0313		4.908	4.015	5.529	0.712	Y	🟡	🟡	Y	2.64 E-1	23.541	23.497	24.519	0.012	Y	🟡
	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut) [Methylobacillus flagellatus KT]637937209 YP_544425															
MFLA0314	8.64 E-2	5.474	5.164	6.327	0.311	Y	🟡	🟡	Y	1.29 E-2	24.086	23.629	24.876	0.463	Y	🟡
	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase [Methylobacillus flagellatus KT]637937210 YP_544426															
MFLA0315		0.000	0.000				■	■			0.000	0.000				■
	DNA repair protein RadC [Methylobacillus flagellatus KT]637937211 YP_544427															
MFLA0316		2.621	0.000	2.838	2.621	Y	🟡	🟡	Y		20.924	20.534	21.742	0.390	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937212 YP_544428															
MFLA0317		0.000	0.000				■	■			0.000	0.000				■
	molybdopterin oxidoreductase [Methylobacillus flagellatus KT]637937213 YP_544429															
MFLA0318		0.000	0.000				■	■			0.000	0.000				■
	" Nitrite reductase (NAD(P)H) large subunit, NirD [Methylobacillus flagellatus KT]637937214 YP_544430 """															
MFLA0319		0.000	0.000				■	■			0.000	0.000				■
	" Nitrite reductase (NAD(P)H) large subunit, NirB [Methylobacillus flagellatus KT]637937215 YP_544431 """															
MFLA0320		0.000	0.000				■	■			0.000	0.000				■
	protein serine/threonine phosphatases [Methylobacillus flagellatus KT]637937216 YP_544432															
MFLA0321		0.000	0.000				■	■			0.000	0.000				■
	Nitrate transporter [Methylobacillus flagellatus KT]637937217 YP_544433															
MFLA0322		0.000	0.000				■	■			0.000	0.000				■
	uroporphyrin-III C-methyltransferase [Methylobacillus flagellatus KT]637937218 YP_544434															
MFLA0323			1.000	1.000		Y	🟡	🟡	Y			19.519	19.519		Y	🟡
	putative methyl-accepting chemotaxis sensory transducer [Methylobacillus flagellatus KT]637937219 YP_544435															
MFLA0324		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937220 YP_544436															
MFLA0325		0.000	0.000				■	■			0.000	0.000				■
	nitrate transport ATP-binding subunits C and D [Methylobacillus flagellatus KT]637937221 YP_544437															
MFLA0326		0.000	0.000				■	■			0.000	0.000				■
	nitrate transport permease [Methylobacillus flagellatus KT]637937222 YP_544438															
MFLA0327		0.000	0.000				■	■			0.000	0.000				■
	nitrate transporter periplasmic component [Methylobacillus flagellatus KT]637937223 YP_544439															
MFLA0328		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937224 YP_544440															
MFLA0329		0.000	0.000				■	■			0.000	0.000				■
	response regulator receiver (CheY-like) and ANTAR domain protein [Methylobacillus flagellatus KT]637937225 YP_544441															
MFLA0330		0.000	0.000				■	■			0.000	0.000				■
	protein serine/threonine phosphatases [Methylobacillus flagellatus KT]637937226 YP_544442															

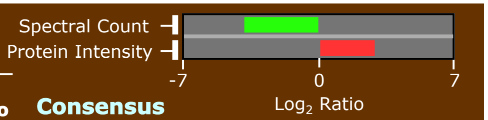
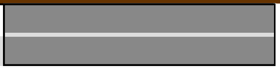
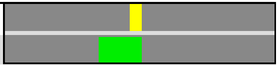
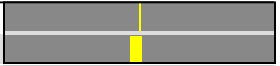
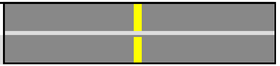
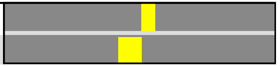
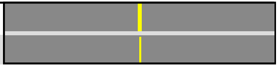
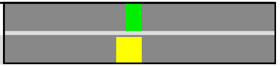
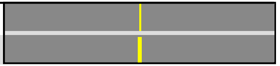
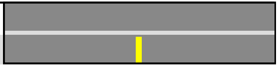
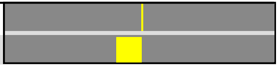
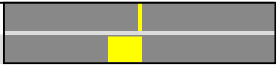


ORF	AM/OH *M Flagellatus* Spectral Count *q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				AM/OH *M Flagellatus* Protein Intensity *q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA0331		0.000	0.000				■	■			0.000	0.000				■
	formate/nitrite transporter [Methylobacillus flagellatus KT]637937227 YP_544443															
MFLA0332		2.521	2.700	3.613	-0.180	Y	●	●	Y		20.557	18.998	20.978	1.559	Y	●
	" ABC transporter, ATP-binding/permease protein [Methylobacillus flagellatus KT]637937228 YP_544444 """															
MFLA0333		3.908	1.668	4.185	1.010	Y	●	●	Y	1.85 E-1	23.217	21.061	23.509	-0.097	Y	●
	hypothetical protein [Methylobacillus flagellatus KT]637937229 YP_544445															
MFLA0334		3.120	2.844	3.989	0.286	Y	●	🟢	G	9.51 E-3	19.716	21.688	22.016	-1.960	Y	●
	carbon starvation protein CstA [Methylobacillus flagellatus KT]637937230 YP_544446															
MFLA0335		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937231 YP_544447															
MFLA0336		1.967	3.140	3.669	-1.167	Y	●	●	Y	1.56 E-1	22.974	22.077	23.594	-0.105	Y	●
	" transcriptional regulator, GntR family [Methylobacillus flagellatus KT]637937232 YP_544448 """															
MFLA0337		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937233 YP_544449															
MFLA0338		5.320	4.719	6.051	0.673	Y	●	●	Y	2.28 E-1	23.886	23.659	24.777	0.061	Y	●
	Oxidoreductase alpha (molybdopterin) subunit [Methylobacillus flagellatus KT]637937234 YP_544450															
MFLA0339		2.106	0.585	2.537	1.521	Y	●	●	Y		21.530	24.177	24.391	-2.647	Y	●
	prolipoprotein diacylglyceryl transferase [Methylobacillus flagellatus KT]637937235 YP_544451															
MFLA0340		7.673	7.733	8.703	-0.105	Y	●	●	Y	2.7 E-2	26.872	27.627	28.298	-0.780	Y	●
	dihydroxy-acid dehydratase [Methylobacillus flagellatus KT]637937236 YP_544452															
MFLA0341	4.16 E-2	6.267	6.341	7.305	-0.121	Y	●	●	Y	1.55 E-1	25.803	25.554	26.684	0.182	Y	●
	Aldose 1-epimerase [Methylobacillus flagellatus KT]637937237 YP_544453															
MFLA0342			0.346	0.346		Y	●	●	Y			22.587	22.587		Y	●
	" cytochrome c, class I [Methylobacillus flagellatus KT]637937238 YP_544454 """															
MFLA0343		0.521		0.521		Y	●	●	Y		17.821		17.821		Y	●
	" sigma54 specific transcriptional regulator with GAF sensor, Fis family [Methylobacillus flagellatus KT]637937239 YP_544455 """															
MFLA0344		3.621	0.346	3.763	3.274	Y	●	●	Y		21.422	16.510	21.469	4.913	Y	●
	Pyrrolo-quinoline quinone [Methylobacillus flagellatus KT]637937240 YP_544456															
MFLA0345		0.521		0.521		Y	●	●	Y		15.366		15.366		Y	●
	amino acid permease-associated region [Methylobacillus flagellatus KT]637937241 YP_544457															
MFLA0346	1.04 E-1	6.144	6.057	7.101	0.069	Y	●	●	Y	1.51 E-1	26.380	26.259	27.321	0.105	Y	●
	Coproporphyrinogen oxidase [Methylobacillus flagellatus KT]637937242 YP_544458															
MFLA0347		3.512	2.505	4.094	0.902	Y	●	●	Y	1.62 E-1	20.770	21.023	21.902	-0.344	Y	●
	SUA5/yciO/yrdC-like protein [Methylobacillus flagellatus KT]637937243 YP_544459															
MFLA0348	3.5 E-7	8.109	7.633	8.890	0.452	Y	●	●	Y	1.46 E-2	26.942	27.454	28.221	-0.515	Y	●
	phosphoribosylamine--glycine ligase [Methylobacillus flagellatus KT]637937244 YP_544460															
MFLA0349	1.28 E-2	8.255	8.156	9.207	0.085	Y	●	●	Y	4.7 E-2	27.667	28.037	28.864	-0.392	Y	●
	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase [Methylobacillus flagellatus KT]637937245 YP_544461															
MFLA0350		4.273	1.915	4.530	3.439	Y	●	●	Y	1.43 E-2	22.995	20.911	23.300	3.095	Y	●
	" helix-turn-helix, Fis-type [Methylobacillus flagellatus KT]637937246 YP_544462 """															
MFLA0351		1.521	1.769	2.650	0.762	Y	●	●	Y	1.19 E-1	20.261	22.483	22.764	-1.102	Y	●
	Dihydrouridine synthase TIM-barrel protein nifR3 [Methylobacillus flagellatus KT]637937247 YP_544463															
MFLA0352		0.000	0.000				■	■			0.000	0.000				■
	methyl-accepting chemotaxis sensory transducer [Methylobacillus flagellatus KT]637937248 YP_544464															

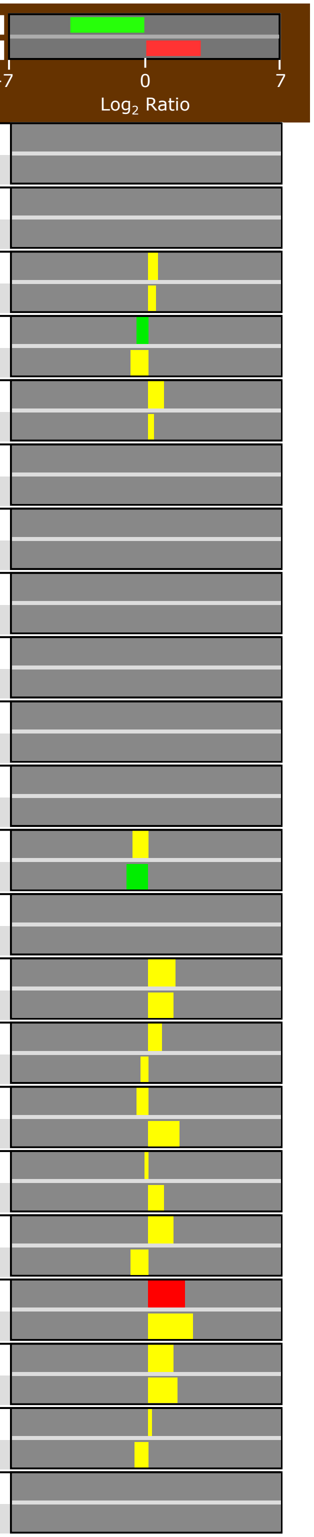


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA0353		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	protein of unknown function DUF72 [Methylobacillus flagellatus KT]637937249 YP_544465															
MFLA0354		4.211	2.749	4.658	1.614	Y	🟡	🟡	Y	9.9 E-2	23.090	21.474	23.497	1.064	Y	🟡
	ThiJ/PfpI [Methylobacillus flagellatus KT]637937250 YP_544466															
MFLA0355		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" transcriptional regulator, TetR family [Methylobacillus flagellatus KT]637937251 YP_544467 """															
MFLA0356		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	protein of unknown function UPF0153 [Methylobacillus flagellatus KT]637937252 YP_544468															
MFLA0357		1.521		1.521		Y	🟡	🟡	Y		20.408		20.408		Y	🟡
	molybdopterin binding domain [Methylobacillus flagellatus KT]637937253 YP_544469															
MFLA0358	8.83 E-2	6.262	6.431	7.349	-0.172	Y	🟡	🟡	Y	7.11 E-2	24.606	25.212	25.940	-0.587	Y	🟡
	DNA polymerase I [Methylobacillus flagellatus KT]637937254 YP_544470															
MFLA0359		5.090	4.635	5.880	0.309	Y	🟡	🟡	Y	2.55 E-1	24.521	24.595	25.558	-0.296	Y	🟡
	conserved hypothetical protein 730 [Methylobacillus flagellatus KT]637937255 YP_544471															
MFLA0360		4.419	5.069	5.780	-0.760	Y	🟡	🟡	Y	1.69 E-1	25.511	25.784	26.654	-0.414	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937256 YP_544472															
MFLA0361		3.952	4.385	5.185	-0.448	Y	🟡	🟢	G	8.9 E-3	22.634	24.527	24.871	-1.897	G	🟢
	homoserine kinase [Methylobacillus flagellatus KT]637937257 YP_544473															
MFLA0362		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937258 YP_544474															
MFLA0363	6.59 E-2	5.458	5.702	6.585	-0.287	Y	🟡	🟡	Y	2.61 E-1	24.497	24.555	25.527	-0.261	Y	🟡
	UvrD/REP helicase [Methylobacillus flagellatus KT]637937259 YP_544475															
MFLA0364		13.061	13.144	14.103	-0.095	Y	🟡	🟡	Y	1.04 E-1	33.607	33.248	34.439	0.312	Y	🟡
	chaperonin GroEL [Methylobacillus flagellatus KT]637937260 YP_544476															
MFLA0365		7.702	7.582	8.643	0.158	Y	🟡	🟡	Y	3.18 E-2	30.280	29.807	31.063	0.466	Y	🟡
	chaperonin Cpn10 [Methylobacillus flagellatus KT]637937261 YP_544477															
MFLA0366		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937262 YP_544478															
MFLA0367		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937263 YP_544479															
MFLA0368		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" transcriptional regulator, TetR family [Methylobacillus flagellatus KT]637937264 YP_544480 """															
MFLA0369		7.794	7.758	8.776	-0.001	Y	🟡	🟡	Y	4.4 E-2	27.675	28.221	28.974	-0.534	Y	🟡
	NADH:flavin oxidoreductase/NADH oxidase [Methylobacillus flagellatus KT]637937265 YP_544481															
MFLA0370		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" transcriptional regulator, ArsR family [Methylobacillus flagellatus KT]637937266 YP_544482 """															
MFLA0371		2.521		2.521		Y	🟡	🟡	Y		20.663		20.663		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937267 YP_544483															
MFLA0372	0	8.125	4.554	8.241	3.591	R	🔴	🔴	R	6.36 E-3	28.283	23.066	28.322	5.225	R	🔴
	" RND efflux system, outer membrane lipoprotein, NodT [Methylobacillus flagellatus KT]637937268 YP_544484 """															
MFLA0373	0	9.340	8.148	9.864	1.167	R	🔴	🟡	Y	4.29 E-2	28.645	27.110	29.073	1.436	R	🔴
	Hydrophobe/amphiphile efflux-1 HAE1 [Methylobacillus flagellatus KT]637937269 YP_544485															
MFLA0374	0	8.925	8.217	9.614	0.679	R	🔴	🟡	Y	2.21 E-2	28.764	27.510	29.269	1.234	R	🔴
	secretion protein HlyD [Methylobacillus flagellatus KT]637937270 YP_544486															

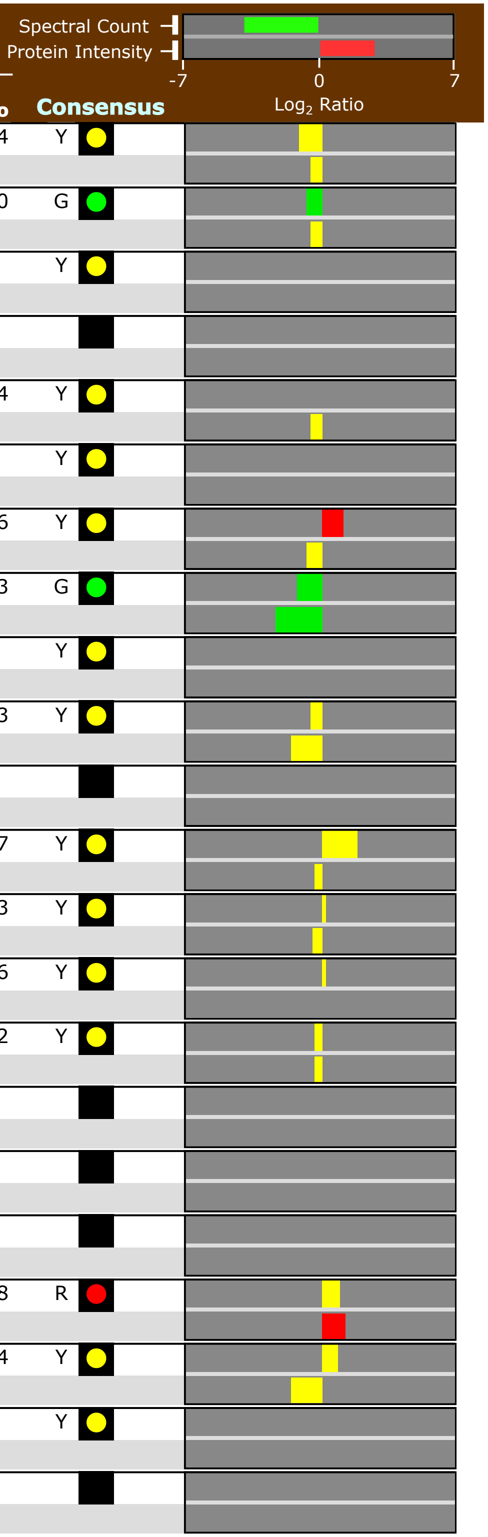


	AM/OH *M Flagellatus* Spectral Count									**AM/OH *M Flagellatus* Protein Intensity**							
ORF	***q*-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**				***q*-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**		
MFLA0375		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637937271 YP_544487																
MFLA0376		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637937272 YP_544488																
MFLA0377		3.221	1.585	3.623	1.636	Y	🟡	🟡	Y		20.676	19.546	21.219	1.130	Y	🟡	
	adenosylmethionine-8-amino-7-oxononanoate aminotransferase [Methylobacillus flagellatus KT]637937273 YP_544489																
MFLA0378		4.247	4.800	5.550	-0.551	Y	🟡	🟢	G	6.36 E-3	21.425	23.471	23.784	-2.170	G	🟢	
	D-alanyl-D-alanine carboxypeptidase/D-alanyl-D-alanine-endopeptidase [Methylobacillus flagellatus KT]637937274 YP_544490																
MFLA0379		8.648	8.109	9.403	-0.086	Y	🟡	🟡	Y	5.87 E-2	26.794	27.327	28.085	-0.589	Y	🟡	
	Peptidylprolyl isomerase [Methylobacillus flagellatus KT]637937275 YP_544491																
MFLA0380		3.514	4.975	5.422	-0.405	Y	🟡	🟡	Y	1.39 E-1	22.625	24.028	24.491	-0.367	Y	🟡	
	OsmC-like protein [Methylobacillus flagellatus KT]637937276 YP_544492																
MFLA0381		2.621		2.621		Y	🟡	🟡	Y		19.851		19.851		Y	🟡	
	Glyoxalase/bleomycin resistance protein/dioxygenase [Methylobacillus flagellatus KT]637937277 YP_544493																
MFLA0382		5.046	4.328	5.731	0.747	Y	🟡	🟡	Y	2.81 E-2	24.170	25.185	25.765	-1.159	Y	🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637937278 YP_544494																
MFLA0383	6.52 E-3	8.051	8.278	9.169	-0.230	Y	🟡	🟡	Y	1.93 E-1	28.059	28.191	29.127	-0.097	Y	🟡	
	carboxyl-terminal protease [Methylobacillus flagellatus KT]637937279 YP_544495																
MFLA0384			2.862	2.862		Y	🟡	🟡	Y			22.717	22.717		Y	🟡	
	SelT/selW/selH selenoprotein [Methylobacillus flagellatus KT]637937280 YP_544496																
MFLA0385			2.585	2.585		Y	🟡	🟡	Y			21.226	21.226		Y	🟡	
	diguanylate phosphodiesterase (EAL domain) [Methylobacillus flagellatus KT]637937281 YP_544497																
MFLA0386	0	9.347	10.155	10.807	-0.810	G	🟢	🟡	Y	1.17 E-2	28.416	29.710	30.204	-1.326	G	🟢	
	Superoxide dismutase [Methylobacillus flagellatus KT]637937282 YP_544498																
MFLA0387		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	zinc/iron permease [Methylobacillus flagellatus KT]637937283 YP_544499																
MFLA0388		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	NLP/P60 [Methylobacillus flagellatus KT]637937284 YP_544500																
MFLA0389		3.224		3.224		Y	🟡	🟡	Y		21.429		21.429		Y	🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637937285 YP_544501																
MFLA0390	1.44 E-1	6.341	6.432	7.387	-0.092	Y	🟡	🟡	Y	1.99 E-2	25.506	25.717	26.615	-0.211	Y	🟡	
	ABC-1 [Methylobacillus flagellatus KT]637937286 YP_544502																
MFLA0391		4.471	4.540	5.506	0.005	Y	🟡	🟡	Y	9.14 E-2	22.638	22.967	23.812	-0.306	Y	🟡	
	protein of unknown function DUF404 [Methylobacillus flagellatus KT]637937287 YP_544503																
MFLA0392		1.813	2.949	3.490	0.055	Y	🟡	🟡	Y	1.34 E-1	18.064	20.647	20.870	-1.298	Y	🟡	
	protein of unknown function DUF403 [Methylobacillus flagellatus KT]637937288 YP_544504																
MFLA0393		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	transglutaminase-like protein [Methylobacillus flagellatus KT]637937289 YP_544505																
MFLA0394	1.21 E-2	5.000	5.293	6.154	-0.202	Y	🟡	🟡	Y	5.44 E-2	22.750	23.917	24.448	-1.737	Y	🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637937290 YP_544506																
MFLA0395		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637937291 YP_544507																
MFLA0396		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	peptidase U32 [Methylobacillus flagellatus KT]637937292 YP_544508																

	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		Consensus
MFLA0397		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" transcriptional regulator, AraC family [Methylobacillus flagellatus KT]637937293 YP_544509 """															
MFLA0398		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937294 YP_544510															
MFLA0399		4.807	4.219	5.543	0.460	Y	🟡	🟡	Y	8.36 E-2	23.809	23.365	24.604	0.404	Y	🟡
	" D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding [Methylobacillus flagellatus KT]637937295 YP_544511 """															
MFLA0400	8.28 E-3	5.364	6.003	6.719	-0.640	G	🟢	🟡	Y	4.79 E-2	24.463	25.401	26.007	-0.890	G	🟢
	aldo/keto reductase [Methylobacillus flagellatus KT]637937296 YP_544512															
MFLA0401		2.521	2.816	3.676	0.762	Y	🟡	🟡	Y	1.75 E-1	20.710	21.448	22.126	0.324	Y	🟡
	" 20S proteasome, A and B subunits [Methylobacillus flagellatus KT]637937297 YP_544513 """															
MFLA0402			0.000	0.000		Y	🟡	🟡	Y			18.214	18.214		Y	🟡
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637937298 YP_544514 """															
MFLA0403		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	transmembrane pair [Methylobacillus flagellatus KT]637937299 YP_544515															
MFLA0404		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	putative ATP-dependent DNA helicase-related protein [Methylobacillus flagellatus KT]637937300 YP_544516															
MFLA0405		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	[Methylobacillus flagellatus KT]639329600															
MFLA0406		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937301 YP_544517															
MFLA0407		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937302 YP_544518															
MFLA0408		4.259	5.034	5.698	-0.778	Y	🟡	🟢	G	4.29 E-3	22.791	23.862	24.424	-1.077	G	🟢
	" Leucine-rich repeat, typical subtype [Methylobacillus flagellatus KT]637937303 YP_544519 """															
MFLA0409		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	cation efflux protein [Methylobacillus flagellatus KT]637937304 YP_544520															
MFLA0410		2.521	2.140	3.343	1.394	Y	🟡	🟡	Y	5.2 E-2	20.743	20.441	21.600	1.345	Y	🟡
	Integron integrase [Methylobacillus flagellatus KT]637937305 YP_544521															
MFLA0411		2.691	2.966	3.835	0.725	Y	🟡	🟡	Y	9.07 E-2	20.731	22.161	22.617	-0.422	Y	🟡
	Helicase c2 [Methylobacillus flagellatus KT]637937306 YP_544522															
MFLA0412		1.521	3.205	3.596	-0.641	Y	🟡	🟡	Y	3.53 E-2	21.767	21.157	22.494	1.632	Y	🟡
	" peptidase M22, glycoprotease [Methylobacillus flagellatus KT]637937307 YP_544523 """															
MFLA0413		0.813	1.000	1.910	-0.187	Y	🟡	🟡	Y		20.398	19.628	21.064	0.770	Y	🟡
	ribosomal-protein-alanine acetyltransferase [Methylobacillus flagellatus KT]637937308 YP_544524															
MFLA0414		3.053	0.585	3.293	1.278	Y	🟡	🟡	Y	1.04 E-1	20.969	20.740	21.859	-0.878	Y	🟡
	phage SPO1 DNA polymerase-related protein [Methylobacillus flagellatus KT]637937309 YP_544525															
MFLA0415	0	7.624	5.644	7.950	1.943	R	🔴	🟡	Y	5.18 E-2	29.221	26.800	29.468	2.337	R	🔴
	LemA [Methylobacillus flagellatus KT]637937310 YP_544526															
MFLA0416		4.430	2.966	4.876	1.286	Y	🟡	🟡	Y	6.9 E-2	24.247	22.545	24.634	1.520	Y	🟡
	protein of unknown function DUF477 [Methylobacillus flagellatus KT]637937311 YP_544527															
MFLA0417	1.48 E-1	5.077	4.924	6.002	0.161	Y	🟡	🟡	Y	1.54 E-1	22.846	23.235	24.053	-0.679	Y	🟡
	protein of unknown function DUF477 [Methylobacillus flagellatus KT]637937312 YP_544528															
MFLA0418			0.585	0.585		Y	🟡	🟡	Y			21.567	21.567		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937313 YP_544529															



	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA0419		5.064	6.452	6.919	-1.187	Y	🟡	🟡	Y	8.15 E-2	25.118	25.634	26.399	-0.604	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937314 YP_544530															
MFLA0420	8.97 E-11	6.757	7.604	8.242	-0.845	G	🟢	🟡	Y	9.62 E-2	26.295	26.770	27.552	-0.610	G	🟢
	prolyl-tRNA synthetase [Methylobacillus flagellatus KT]637937315 YP_544531															
MFLA0421			1.322	1.322		Y	🟡	🟡	Y			19.097	19.097		Y	🟡
	" Lytic transglycosylase, catalytic [Methylobacillus flagellatus KT]637937316 YP_544532 """															
MFLA0422		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937317 YP_544533															
MFLA0423		4.926	4.938	5.932	-0.015	Y	🟡	🟡	Y	1.35 E-1	22.531	22.949	23.755	-0.644	Y	🟡
	S-adenosylmethionine [Methylobacillus flagellatus KT]637937318 YP_544534															
MFLA0424			2.816	2.816		Y	🟡	🟡	Y			20.094	20.094		Y	🟡
	PepSY-associated TM helix [Methylobacillus flagellatus KT]637937320 YP_544535															
MFLA0425	7.35 E-9	6.528	5.424	7.079	1.087	R	🔴	🟡	Y	5.97 E-2	25.034	25.779	26.454	-0.766	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937321 YP_544536															
MFLA0426	8.81 E-17	5.668	7.035	7.508	-1.344	G	🟢	🟢	G	4.1 E-3	25.204	27.649	27.892	-2.443	G	🟢
	hypothetical protein [Methylobacillus flagellatus KT]637937322 YP_544537															
MFLA0427			3.523	3.523		Y	🟡	🟡	Y			22.837	22.837		Y	🟡
	ApbE-like lipoprotein [Methylobacillus flagellatus KT]637937323 YP_544538															
MFLA0428		2.906	3.301	4.117	-0.571	Y	🟡	🟡	Y	2.45 E-2	20.123	21.589	22.035	-1.563	Y	🟡
	flavodoxin/nitric oxide synthase [Methylobacillus flagellatus KT]637937324 YP_544539															
MFLA0429		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	diguanylate cyclase (GGDEF domain) [Methylobacillus flagellatus KT]637937325 YP_544540															
MFLA0430		1.843	0.000	2.197	1.843	Y	🟡	🟡	Y		19.913	20.360	21.154	-0.447	Y	🟡
	multi-sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637937326 YP_544541															
MFLA0431		4.586	4.425	5.508	0.201	Y	🟡	🟡	Y	6.21 E-2	21.382	21.864	22.643	-0.493	Y	🟡
	Peptidoglycan-binding LysM [Methylobacillus flagellatus KT]637937327 YP_544542															
MFLA0432		4.003	3.769	4.890	0.155	Y	🟡	🟡	Y	2.2 E-1	22.510	22.329	23.422	-0.006	Y	🟡
	" two component transcriptional regulator, winged helix family [Methylobacillus flagellatus KT]637937328 YP_544543 """															
MFLA0433	1.49 E-1	4.741	5.061	5.910	-0.365	Y	🟡	🟡	Y	8.15 E-2	26.349	26.668	27.517	-0.352	Y	🟡
	" nitrogen regulatory protein P-II (GlnB, GlnK) [Methylobacillus flagellatus KT]637937329 YP_544544 """															
MFLA0434		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	ammonium transporter [Methylobacillus flagellatus KT]637937330 YP_544545															
MFLA0435		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	acyltransferase 3 [Methylobacillus flagellatus KT]637937331 YP_544546															
MFLA0436		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	GCN5-related N-acetyltransferase [Methylobacillus flagellatus KT]637937332 YP_544547															
MFLA0437		4.757	3.897	5.390	0.852	Y	🟡	🔴	R	4.29 E-3	23.221	21.973	23.728	1.248	R	🔴
	" transcriptional regulator, XRE family with cupin sensor domain [Methylobacillus flagellatus KT]637937333 YP_544548 """															
MFLA0438		3.908	2.871	4.480	0.809	Y	🟡	🟡	Y	3.18 E-2	21.008	22.251	22.759	-1.604	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937334 YP_544549															
MFLA0439		2.923		2.923		Y	🟡	🟡	Y		20.747		20.747		Y	🟡
	Aminomethyltransferase [Methylobacillus flagellatus KT]637937335 YP_544550															
MFLA0440		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937336 YP_544551															



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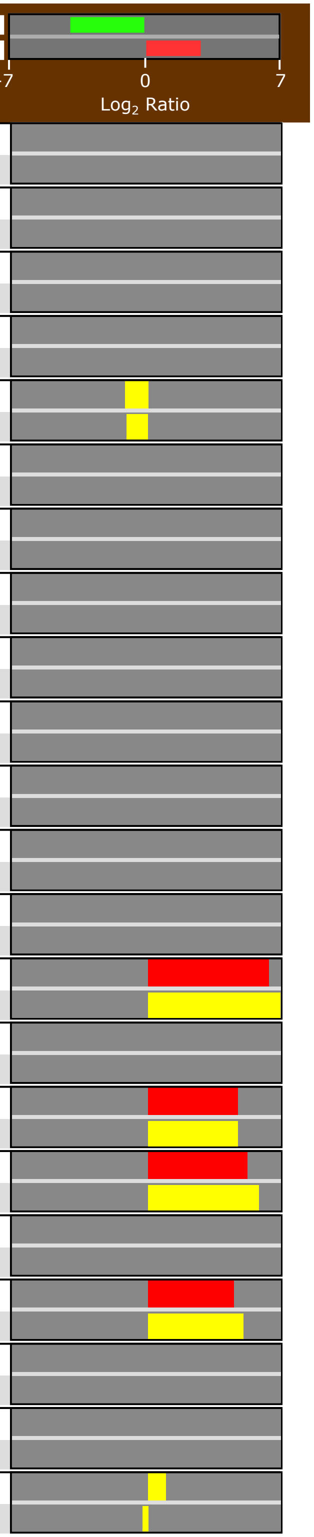
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA0441		0.000	0.000				■	■			0.000	0.000				■
	ferredoxin [Methylobacillus flagellatus KT]637937337 YP_544552															
MFLA0442		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937338 YP_544553															
MFLA0443		0.000	0.000				■	■			0.000	0.000				■
	putative PAS/PAC sensor protein [Methylobacillus flagellatus KT]637937339 YP_544554															
MFLA0444			0.000	0.000		Y	🟡	🟡	Y			19.739	19.739		Y	🟡
	" signal transduction histidine kinase, nitrate/nitrite-specific, NarQ [Methylobacillus flagellatus KT]637937340 YP_544555 """															
MFLA0445		3.828	5.044	5.560	-1.199	Y	🟡	🟡	Y	4.61 E-2	21.327	22.316	22.904	-1.089	Y	🟡
	" two component transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637937341 YP_544556 """															
MFLA0446		0.000	0.000				■	■			0.000	0.000				■
	amino acid permease-associated region [Methylobacillus flagellatus KT]637937342 YP_544557															
MFLA0447			0.585	0.585		Y	🟡	🟡	Y			20.521	20.521		Y	🟡
	" two component transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637937343 YP_544558 """															
MFLA0448		0.000	0.000				■	■			0.000	0.000				■
	putative signal transduction histidine kinase [Methylobacillus flagellatus KT]637937344 YP_544559															
MFLA0449		0.813		0.813		Y	🟡	🟡	Y		21.757		21.757		Y	🟡
	Outer membrane autotransporter barrel [Methylobacillus flagellatus KT]637937345 YP_544560															
MFLA0450		0.000	0.000				■	■			0.000	0.000				■
	multiple antibiotic resistance (MarC)-related proteins [Methylobacillus flagellatus KT]637937346 YP_544561															
MFLA0451		0.000	0.000				■	■			0.000	0.000				■
	Alkaline phosphatase [Methylobacillus flagellatus KT]637937347 YP_544562															
MFLA0452		4.997		4.997		Y	🟡	🟡	Y		24.588		24.588		Y	🟡
	FAD dependent oxidoreductase [Methylobacillus flagellatus KT]637937348 YP_544563															
MFLA0453		3.621		3.621		Y	🟡	🟡	Y		24.478		24.478		Y	🟡
	" Sarcosine oxidase, delta subunit, heterotetrameric [Methylobacillus flagellatus KT]637937349 YP_544564 """															
MFLA0454	0	7.573	0.000	7.581	6.159	R	🔴	🟡	Y	1.16 E-1	25.826	17.406	25.830	7.030	R	🔴
	Aminomethyltransferase [Methylobacillus flagellatus KT]637937350 YP_544565															
MFLA0455		4.302		4.302		Y	🟡	🟡	Y		24.348		24.348		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937351 YP_544566															
MFLA0456	0	7.409	2.334	7.451	4.597	R	🔴	🟡	Y	7.7 E-2	26.528	21.060	26.560	4.645	R	🔴
	Glutamate--ammonia ligase [Methylobacillus flagellatus KT]637937352 YP_544567															
MFLA0457	0	8.410	2.000	8.427	5.132	R	🔴	🟡	Y	9.58 E-2	26.502	19.614	26.515	5.727	R	🔴
	" glutamine amidotransferase, class-II [Methylobacillus flagellatus KT]637937353 YP_544568 """															
MFLA0458		6.812		6.812		Y	🟡	🟡	Y		26.254		26.254		Y	🟡
	" glutamate synthase, alpha subunit-like protein [Methylobacillus flagellatus KT]637937354 YP_544569 """															
MFLA0459	0	8.581	3.754	8.631	4.429	R	🔴	🟡	Y	4.92 E-2	27.760	22.512	27.798	4.930	R	🔴
	ferredoxin-dependent glutamate synthase [Methylobacillus flagellatus KT]637937355 YP_544570															
MFLA0460		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937356 YP_544571															
MFLA0461		0.521		0.521		Y	🟡	🟡	Y		20.414		20.414		Y	🟡
	response regulator receiver (CheY-like) and ANTAR domain protein [Methylobacillus flagellatus KT]637937357 YP_544572															
MFLA0462		3.364	2.505	3.997	0.868	Y	🟡	🟡	Y	2.65 E-1	21.366	21.428	22.397	-0.331	Y	🟡
	" chain B, amide receptor of the amidase operon (Amic) [Methylobacillus flagellatus KT]637937358 YP_544573 """															



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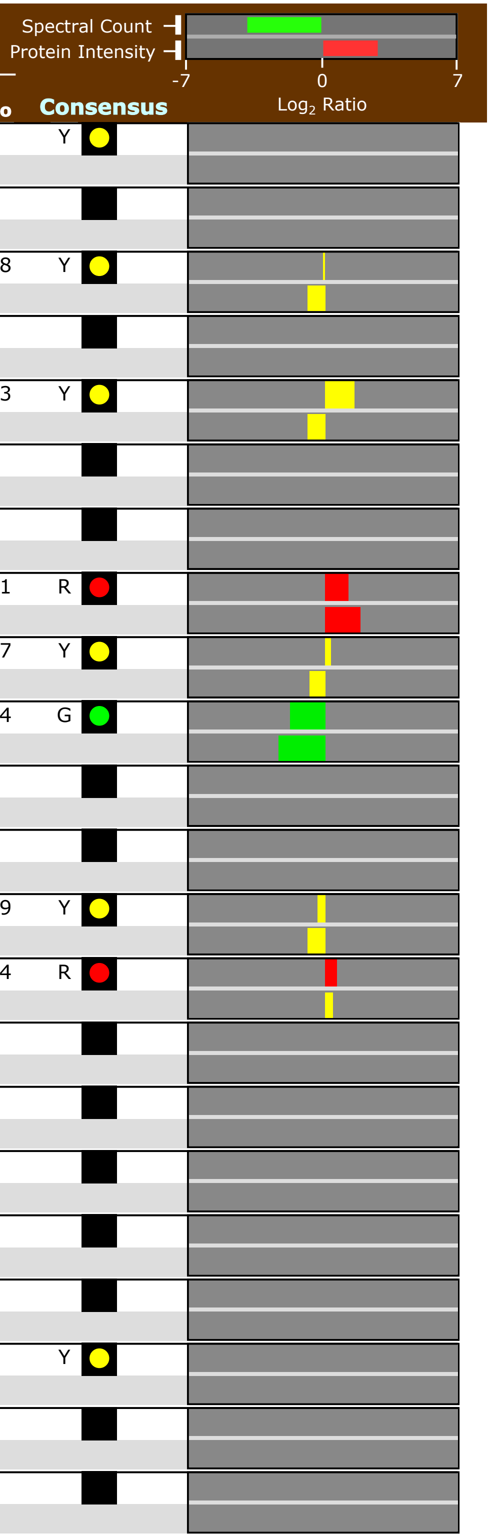
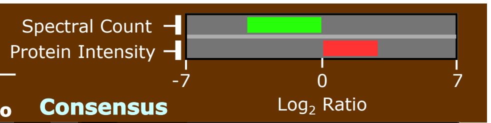
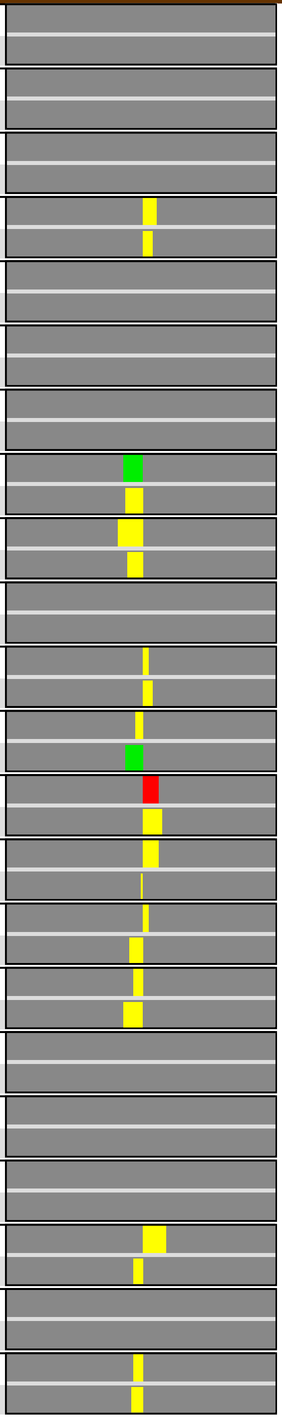
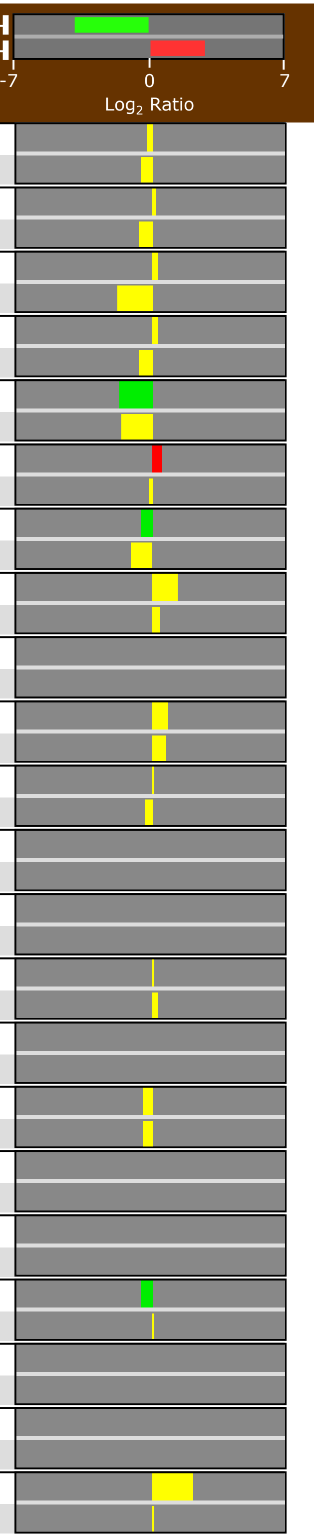
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA0463			0.000	0.000		Y	●	●	Y			18.517	18.517		Y	●
	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase [Methylobacillus flagellatus KT]637937359 YP_544574															
MFLA0464		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937360 YP_544575															
MFLA0465		3.945	3.000	4.549	-0.103	Y	●	●	Y	9.14 E-2	21.906	21.701	22.808	-0.868	Y	●
	hypothetical protein [Methylobacillus flagellatus KT]637937361 YP_544576															
MFLA0466		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937363 YP_544577															
MFLA0467		3.868	2.879	4.456	1.476	Y	●	●	Y	1.15 E-1	21.163	21.715	22.466	-0.873	Y	●
	" bis(5'nucleosyl)-tetraphosphatase, ApaH [Methylobacillus flagellatus KT]637937364 YP_544578 """															
MFLA0468		0.000	0.000				■	■			0.000	0.000				■
	phospholipid/glycerol acyltransferase [Methylobacillus flagellatus KT]637937365 YP_544579															
MFLA0469		0.000	0.000				■	■			0.000	0.000				■
	" conserved hypothetical protein, predicted autoinducer synthesis protein family [Methylobacillus flagellatus KT]637937366 YP_544580 """															
MFLA0470	0	7.406	6.083	7.891	1.215	R	●	●	R	9.49 E-3	26.449	24.629	26.809	1.811	R	●
	17 kDa surface antigen [Methylobacillus flagellatus KT]637937367 YP_544581															
MFLA0471	2 E-2	5.589	5.176	6.397	0.339	Y	●	●	Y	4.54 E-2	24.752	25.482	26.163	-0.817	Y	●
	PfkB [Methylobacillus flagellatus KT]637937368 YP_544582															
MFLA0472	4.41 E-9	4.444	6.028	6.444	-1.781	G	●	●	G	4.46 E-3	22.615	24.994	25.247	-2.424	G	●
	" transcriptional regulator, TetR family [Methylobacillus flagellatus KT]637937369 YP_544583 """															
MFLA0473		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937370 YP_544584															
MFLA0474		0.000	0.000				■	■			0.000	0.000				■
	conserved hypothetical protein 701 [Methylobacillus flagellatus KT]637937371 YP_544585															
MFLA0475		4.222	4.581	5.413	-0.375	Y	●	●	Y	1.46 E-1	23.093	23.753	24.461	-0.889	Y	●
	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen [Methylobacillus flagellatus KT]637937372 YP_544586															
MFLA0476	3.8 E-4	6.684	6.065	7.408	0.636	R	●	●	Y	8.15 E-2	25.116	24.740	25.940	0.414	R	●
	FAD linked oxidase-like protein [Methylobacillus flagellatus KT]637937373 YP_544587															
MFLA0477		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF1568 [Methylobacillus flagellatus KT]637937374 YP_544588															
MFLA0478		0.000	0.000				■	■			0.000	0.000				■
	putative transmembrane protein [Methylobacillus flagellatus KT]637937375 YP_544589															
MFLA0479		0.000	0.000				■	■			0.000	0.000				■
	putative transmembrane protein [Methylobacillus flagellatus KT]637937376 YP_544590															
MFLA0480		0.000	0.000				■	■			0.000	0.000				■
	putative transmembrane protein [Methylobacillus flagellatus KT]637937377 YP_544591															
MFLA0481		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937378 YP_544592															
MFLA0482			0.346	0.346		Y	●	●	Y			21.578	21.578		Y	●
	putative transmembrane protein [Methylobacillus flagellatus KT]637937379 YP_544593															
MFLA0483		0.000	0.000				■	■			0.000	0.000				■
	Adhesin HecA 20-residue repeat x2 [Methylobacillus flagellatus KT]637937380 YP_544594															
MFLA0484		0.000	0.000				■	■			0.000	0.000				■
	Hemolysin activator HlyB [Methylobacillus flagellatus KT]637937381 YP_544595															





ORF	AM/OH *M Flagellatus* Spectral Count					Regulation				AM/OH *M Flagellatus* Protein Intensity					Consensus	
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio					*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		
MFLA0485		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	protein of unknown function UPF0060 [Methylobacillus flagellatus KT]637937382 YP_544596															
MFLA0486		1.813		1.813		Y	🟡	🟡	Y		18.017		18.017		Y	🟡
	" Amylo-alpha-1,6-glucosidase [Methylobacillus flagellatus KT]637937383 YP_544597 """															
MFLA0487		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" glycosyl transferase, group 1 [Methylobacillus flagellatus KT]637937384 YP_544598 """															
MFLA0488		4.179	3.719	4.967	0.712	Y	🟡	🟡	Y	1.3 E-1	22.718	22.160	23.466	0.532	Y	🟡
	multi-sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637937385 YP_544599															
MFLA0489		2.025		2.025		Y	🟡	🟡	Y		23.412		23.412		Y	🟡
	" two component transcriptional regulator, winged helix family [Methylobacillus flagellatus KT]637937386 YP_544600 """															
MFLA0490		2.106		2.106		Y	🟡	🟡	Y		20.440		20.440		Y	🟡
	major facilitator superfamily MFS_1 [Methylobacillus flagellatus KT]637937387 YP_544601															
MFLA0491		0.521		0.521		Y	🟡	🟡	Y		19.342		19.342		Y	🟡
	DNA-3-methyladenine glycosylase I [Methylobacillus flagellatus KT]637937388 YP_544602															
MFLA0492	1.25 E-12	6.380	7.409	7.984	-1.031	G	🟢	🟡	Y	1.29 E-2	25.393	26.307	26.921	-0.908	G	🟢
	Riboflavin synthase [Methylobacillus flagellatus KT]637937389 YP_544603															
MFLA0493		2.521	4.802	5.072	-1.267	Y	🟡	🟡	Y	3.28 E-2	22.409	24.179	24.550	-0.769	Y	🟡
	NusB antitermination factor [Methylobacillus flagellatus KT]637937390 YP_544604															
MFLA0494		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	FHA domain containing protein [Methylobacillus flagellatus KT]637937391 YP_544605															
MFLA0495		3.147	2.897	4.027	0.251	Y	🟡	🟡	Y	1.63 E-1	22.001	21.507	22.775	0.550	Y	🟡
	" UDP-2,3-diacylglucosamine hydrolase [Methylobacillus flagellatus KT]637937392 YP_544606 """															
MFLA0496	4.28 E-5	7.906	8.304	9.118	-0.397	Y	🟡	🟢	G	9.69 E-3	28.377	29.265	29.889	-0.884	G	🟢
	Peptidylprolyl isomerase [Methylobacillus flagellatus KT]637937393 YP_544607															
MFLA0497	5.03 E-4	5.866	5.132	6.545	0.789	R	🔴	🟡	Y	9.74 E-2	26.517	25.624	27.138	0.951	R	🔴
	Peptidylprolyl isomerase [Methylobacillus flagellatus KT]637937394 YP_544608															
MFLA0498		3.038	1.000	3.352	0.752	Y	🟡	🟡	Y	2.16 E-1	20.954	19.459	21.392	-0.141	Y	🟡
	ErfK/YbiS/YcfS/YnhG [Methylobacillus flagellatus KT]637937395 YP_544609															
MFLA0499		7.350	6.881	8.134	0.343	Y	🟡	🟡	Y	2.95 E-2	25.556	26.267	26.955	-0.694	Y	🟡
	Tetratricopeptide TPR_2 [Methylobacillus flagellatus KT]637937396 YP_544610															
MFLA0500		5.561	5.955	6.771	-0.455	Y	🟡	🟡	Y	1.14 E-1	24.605	25.229	25.951	-1.050	Y	🟡
	cysteinyl-tRNA synthetase [Methylobacillus flagellatus KT]637937397 YP_544611															
MFLA0501		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937398 YP_544612															
MFLA0502		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	outer membrane efflux protein [Methylobacillus flagellatus KT]637937399 YP_544613															
MFLA0503		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	secretion protein HlyD [Methylobacillus flagellatus KT]637937400 YP_544614															
MFLA0504		2.996	1.915	3.555	1.155	Y	🟡	🟡	Y	1.89 E-2	19.946	20.448	21.219	-0.507	Y	🟡
	Heavy metal efflux pump CzcA [Methylobacillus flagellatus KT]637937401 YP_544615															
MFLA0505			1.668	1.668		Y	🟡	🟡	Y			19.520	19.520		Y	🟡
	" nitrogen regulatory protein P-II (GlnB, GlnK) [Methylobacillus flagellatus KT]637937402 YP_544616 """															
MFLA0506	1.27 E-2	5.822	6.288	7.074	-0.454	Y	🟡	🟡	Y	2.59 E-2	24.336	24.897	25.644	-0.572	Y	🟡
	Dihydroorotate oxidase [Methylobacillus flagellatus KT]637937403 YP_544617															

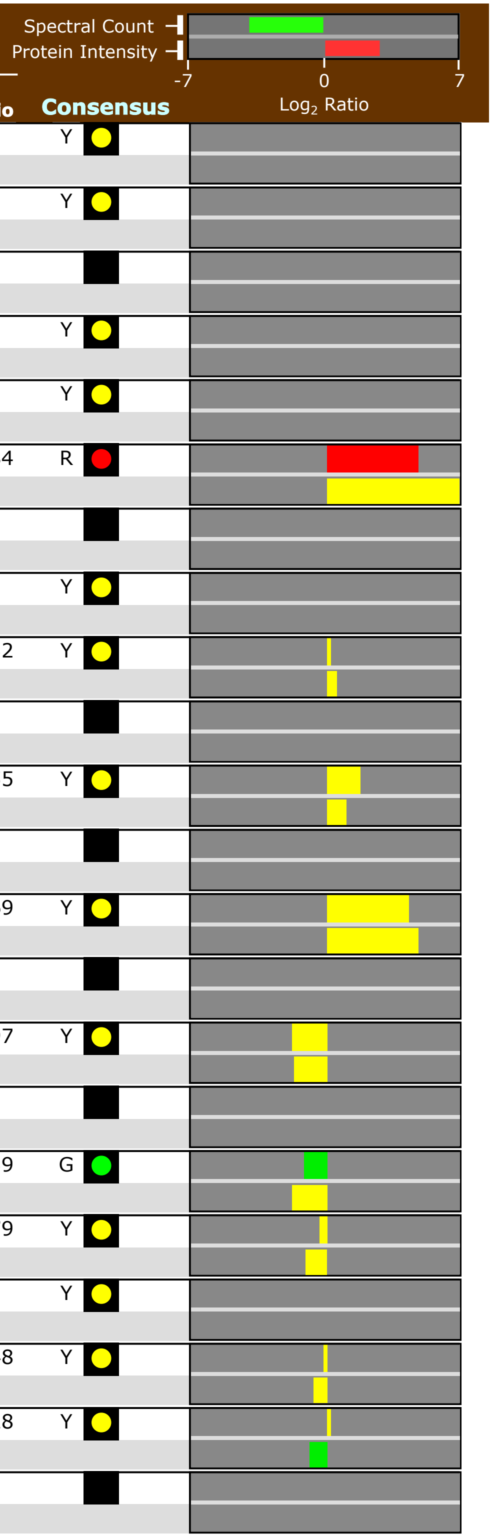




	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	**Consensus**	
MFLA0507		1.843	3.162	3.648	-0.319	Y	🟡	🟡	Y	3.47 E-2	19.090	20.720	21.124	-0.629	Y	🟡
	glutathione S-transferase-like protein [Methylobacillus flagellatus KT]637937404 YP_544618															
MFLA0508		7.083	6.860	7.976	0.185	Y	🟡	🟡	Y	2.79 E-2	26.462	27.213	27.886	-0.750	Y	🟡
	ATPase AAA-2 [Methylobacillus flagellatus KT]637937405 YP_544619															
MFLA0509		4.581	4.407	5.497	0.339	Y	🟡	🟡	Y	2.76 E-2	20.884	22.489	22.899	-1.757	Y	🟡
	ATP-dependent Clp protease adaptor protein ClpS [Methylobacillus flagellatus KT]637937406 YP_544620															
MFLA0510		2.106	2.983	3.610	0.347	Y	🟡	🟡	Y	1.05 E-1	21.069	22.757	23.147	-0.656	Y	🟡
	protein of unknown function DUF21 [Methylobacillus flagellatus KT]637937407 YP_544621															
MFLA0511	0	5.450	7.199	7.575	-1.674	G	🟢	🟡	Y	2.93 E-2	25.757	27.050	27.544	-1.609	G	🟢
	SecF protein [Methylobacillus flagellatus KT]637937408 YP_544622															
MFLA0512	2.38 E-9	8.684	8.171	9.451	0.511	R	🔴	🟡	Y	4.29 E-2	27.423	27.626	28.528	-0.204	Y	🟡
	protein-export membrane protein SecD [Methylobacillus flagellatus KT]637937409 YP_544623															
MFLA0513	0	8.562	9.192	9.911	-0.629	G	🟢	🟡	Y	1.6 E-2	26.807	27.873	28.436	-1.135	G	🟢
	" preprotein translocase, YajC subunit [Methylobacillus flagellatus KT]637937410 YP_544624 """															
MFLA0514		5.286	4.059	5.799	1.258	Y	🟡	🟡	Y	4.22 E-2	22.869	22.512	23.702	0.353	Y	🟡
	queuine tRNA-ribosyltransferase [Methylobacillus flagellatus KT]637937411 YP_544625															
MFLA0515		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	CDP-diacylglycerol--serine O-phosphatidyltransferase [Methylobacillus flagellatus KT]637937412 YP_544626															
MFLA0516		4.253	3.573	4.952	0.786	Y	🟡	🟡	Y	1.12 E-1	21.571	20.766	22.224	0.672	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937413 YP_544627															
MFLA0517	3.62 E-2	6.673	6.557	7.616	0.114	Y	🟡	🟡	Y	2.59 E-2	25.060	25.441	26.263	-0.387	Y	🟡
	2-isopropylmalate synthase [Methylobacillus flagellatus KT]637937414 YP_544628															
MFLA0518		3.812		3.812		Y	🟡	🟡	Y		24.026		24.026		Y	🟡
	GreA/GreB family elongation factor [Methylobacillus flagellatus KT]637937415 YP_544629															
MFLA0519		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	putative integral membrane protein [Methylobacillus flagellatus KT]637937416 YP_544630															
MFLA0520		4.439	4.344	5.392	0.072	Y	🟡	🟡	Y	1.02 E-1	23.298	23.019	24.165	0.257	Y	🟡
	" HAD-superfamily subfamily IB, PSPase-like protein [Methylobacillus flagellatus KT]637937417 YP_544631 """															
MFLA0521		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	cytochrome c assembly protein [Methylobacillus flagellatus KT]637937418 YP_544632															
MFLA0522	5.77 E-5	7.022	7.514	8.289	-0.485	Y	🟡	🟡	Y	8.26 E-2	26.386	26.826	27.623	-0.475	Y	🟡
	signal recognition particle protein [Methylobacillus flagellatus KT]637937419 YP_544633															
MFLA0523		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	Drug resistance transporter EmrB/QacA subfamily [Methylobacillus flagellatus KT]637937421 YP_544634															
MFLA0524		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	GCN5-related N-acetyltransferase [Methylobacillus flagellatus KT]637937422 YP_544635															
MFLA0525	1.45 E-4	6.071	6.566	7.340	-0.595	G	🟢	🟡	Y	2.05 E-1	26.155	25.972	27.066	0.097	Y	🟡
	phospho-2-dehydro-3-deoxyheptonate aldolase [Methylobacillus flagellatus KT]637937423 YP_544636															
MFLA0526		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937424 YP_544637															
MFLA0527		2.328		2.328		Y	🟡	🟡	Y		19.344		19.344		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937425 YP_544638															
MFLA0528		2.135	0.000	2.431	2.135	Y	🟡	🟡	Y		19.274	19.134	20.206	0.139	Y	🟡
	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) [Methylobacillus flagellatus KT]637937426 YP_544639															

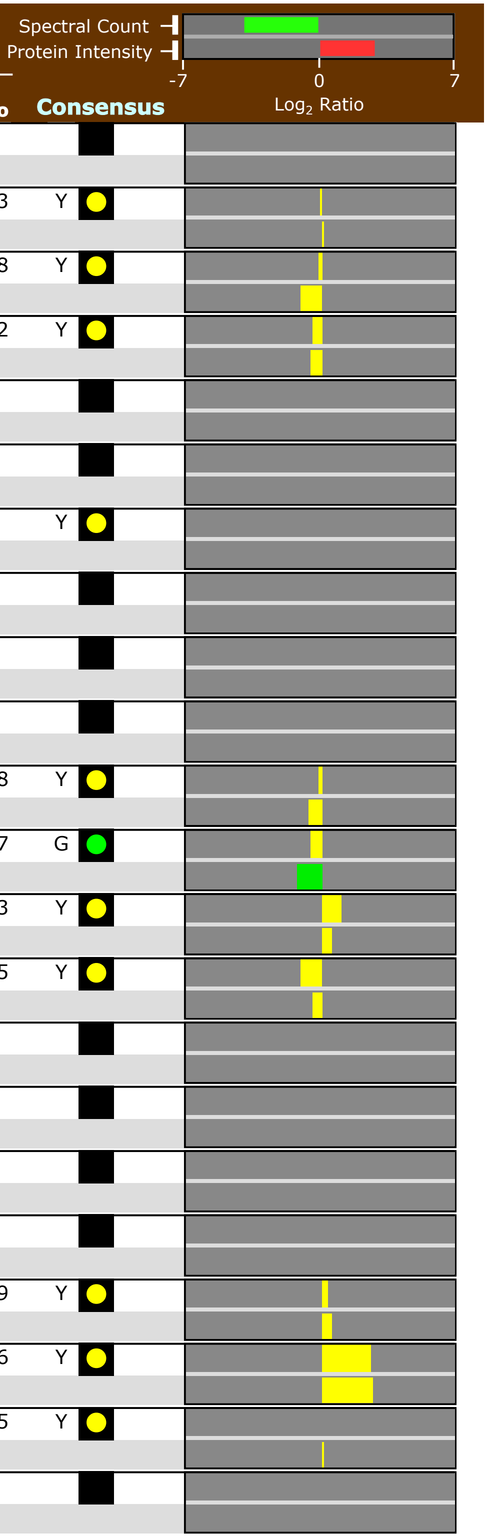
Spectral Count
Protein Intensity
-7 0 7
$\log_2$ Ratio

	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**				**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**	
MFLA0529		3.184	1.915	3.685	1.210	Y	🟡	🟡	Y	1.23 E-1	21.417	22.439	23.017	-0.530	Y	🟡
	diguanylate cyclase (GGDEF domain) [Methylobacillus flagellatus KT]637937427 YP_544640															
MFLA0530	9.92 E-2	6.540	6.543	7.541	-0.015	Y	🟡	🟡	Y	1.65 E-1	25.450	25.539	26.495	-0.077	Y	🟡
	glucose sorbosone dehydrogenase [Methylobacillus flagellatus KT]637937428 YP_544641															
MFLA0531		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" two component transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637937429 YP_544642 """															
MFLA0532		1.813		1.813		Y	🟡	🟡	Y		23.515		23.515		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937430 YP_544643															
MFLA0533		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937431 YP_544644															
MFLA0534		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937432 YP_544645															
MFLA0535	0	11.953	12.675	13.359	-0.721	G	🟢	🟡	Y	1.35 E-2	32.450	33.535	34.092	-1.079	G	🟢
	NHL repeat [Methylobacillus flagellatus KT]637937433 YP_544646															
MFLA0536		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937434 YP_544647															
MFLA0537		4.600	1.000	4.714	2.459	Y	🟡	🟡	Y	1.53 E-1	21.871	19.019	22.058	1.120	Y	🟡
	TonB-dependent siderophore receptor [Methylobacillus flagellatus KT]637937435 YP_544648															
MFLA0538		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937436 YP_544649															
MFLA0539		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	translation initiation factor IF-1 [Methylobacillus flagellatus KT]637937437 YP_544650															
MFLA0540		5.451		5.451		Y	🟡	🟡	Y		25.312		25.312		Y	🟡
	" transcriptional regulator, AraC family [Methylobacillus flagellatus KT]637937438 YP_544651 """															
MFLA0541		2.860		2.860		Y	🟡	🟡	Y		21.468		21.468		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937439 YP_544652															
MFLA0542		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" twin-arginine translocation protein, TatA/E family [Methylobacillus flagellatus KT]637937440 YP_544653 """															
MFLA0543		4.206		4.206		Y	🟡	🟡	Y		19.123		19.123		Y	🟡
	twin-arginine translocation protein TatB [Methylobacillus flagellatus KT]637937441 YP_544654															
MFLA0544		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	Sec-independent protein translocase TatC [Methylobacillus flagellatus KT]637937442 YP_544655															
MFLA0545		5.182		5.182		Y	🟡	🟡	Y		23.776		23.776		Y	🟡
	" transcriptional regulator, AraC family [Methylobacillus flagellatus KT]637937443 YP_544656 """															
MFLA0546		3.521		3.521		Y	🟡	🟡	Y		21.132		21.132		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937444 YP_544657															
MFLA0547		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937445 YP_544658															
MFLA0548	0	12.586	6.092	12.602	6.529	R	🔴	🟡	Y	1.03 E-2	34.229	25.245	34.232	9.035	R	🔴
	Amine dehydrogenase [Methylobacillus flagellatus KT]637937446 YP_544659															
MFLA0549		4.691		4.691		Y	🟡	🟡	Y		25.047		25.047		Y	🟡
	methylamine utilisation MauE [Methylobacillus flagellatus KT]637937447 YP_544660															
MFLA0550	0	10.041	2.322	10.047	6.716	R	🔴	🟡	Y	4.59 E-2	31.402	22.275	31.405	8.115	R	🔴
	hypothetical protein [Methylobacillus flagellatus KT]637937448 YP_544661															

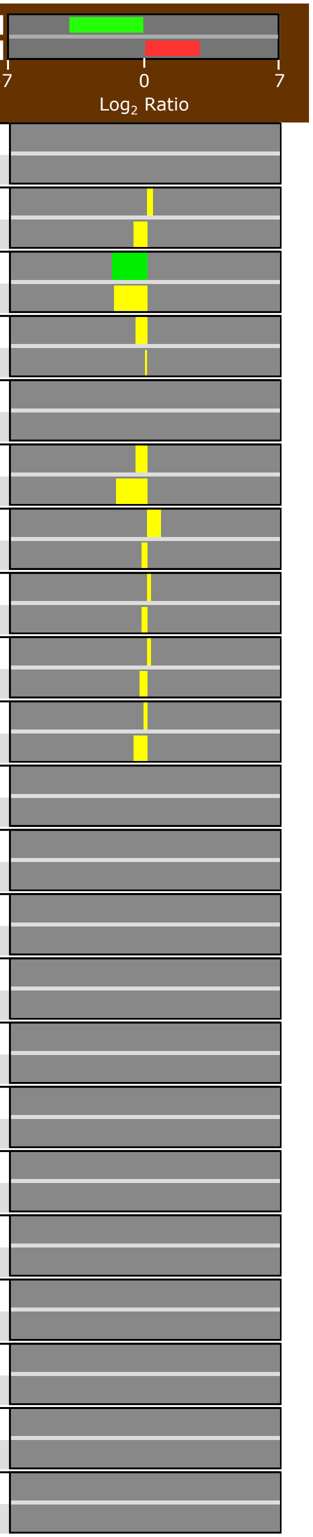


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity							
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	**Consensus**		
MFLA0551		7.785		7.785		Y	🟡	🟡	Y		28.414		28.414		Y	🟡	*Amine dehydrogenase [Methylobacillus flagellatus KT]637937449 YP_544662*
MFLA0552		7.524		7.524		Y	🟡	🟡	Y		27.114		27.114		Y	🟡	*Cytochrome-c peroxidase [Methylobacillus flagellatus KT]637937450 YP_544663*
MFLA0553		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*hypothetical protein [Methylobacillus flagellatus KT]637937451 YP_544664*
MFLA0554		5.720		5.720		Y	🟡	🟡	Y		26.079		26.079		Y	🟡	*MauM/NapG family ferredoxin-type protein [Methylobacillus flagellatus KT]637937452 YP_544665*
MFLA0555		3.720		3.720		Y	🟡	🟡	Y		22.321		22.321		Y	🟡	*" Ferredoxin-type protein, NapH/MauN family [Methylobacillus flagellatus KT]637937453 YP_544666 """*
MFLA0556	0	8.213	2.459	8.239	4.723	R	🔴	🟡	Y	7.03 E-2	30.970	21.533	30.972	8.384	R	🔴	*blue (type 1) copper domain [Methylobacillus flagellatus KT]637937454 YP_544667*
MFLA0557		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*" protein of unknown function DUF6, transmembrane [Methylobacillus flagellatus KT]637937455 YP_544668 """*
MFLA0558		3.199		3.199		Y	🟡	🟡	Y		20.604		20.604		Y	🟡	*" DNA topoisomerase, type I, putative [Methylobacillus flagellatus KT]637937456 YP_544669 """*
MFLA0559	2.39 E-2	5.567	5.273	6.428	0.218	Y	🟡	🟡	Y	1.08 E-1	25.022	24.381	25.737	0.532	Y	🟡	*heat shock protein Hsp20 [Methylobacillus flagellatus KT]637937457 YP_544670*
MFLA0560		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*molybdenum cofactor synthesis-like protein [Methylobacillus flagellatus KT]637937458 YP_544671*
MFLA0561		4.254	2.334	4.592	1.736	Y	🟡	🟡	Y	4.06 E-2	22.114	21.205	22.730	0.955	Y	🟡	*FAD-dependent pyridine nucleotide-disulphide oxidoreductase [Methylobacillus flagellatus KT]637937459 YP_544672*
MFLA0562		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*" 4Fe-4S ferredoxin, iron-sulfur binding [Methylobacillus flagellatus KT]637937460 YP_544673 """*
MFLA0563		6.048	0.585	6.081	4.184	Y	🟡	🟡	Y	7.24 E-2	25.217	19.493	25.245	4.669	Y	🟡	*molybdopterin oxidoreductase [Methylobacillus flagellatus KT]637937461 YP_544674*
MFLA0564		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*hypothetical protein [Methylobacillus flagellatus KT]637937462 YP_544675*
MFLA0565		1.106	3.919	4.111	-1.814	Y	🟡	🟡	Y	2.88 E-2	19.254	21.952	22.159	-1.697	Y	🟡	*" transcriptional regulator, GntR family [Methylobacillus flagellatus KT]637937463 YP_544676 """*
MFLA0566		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*hypothetical protein [Methylobacillus flagellatus KT]637937464 YP_544677*
MFLA0567	6.63 E-13	5.951	6.961	7.543	-1.175	G	🟢	🟡	Y	3.76 E-2	25.177	26.691	27.124	-1.839	G	🟢	*aspartate kinase [Methylobacillus flagellatus KT]637937467 YP_544678*
MFLA0568	3.09 E-5	7.808	8.186	9.010	-0.380	Y	🟡	🟡	Y	1.01 E-2	27.142	28.193	28.761	-1.079	Y	🟡	*alanyl-tRNA synthetase [Methylobacillus flagellatus KT]637937468 YP_544679*
MFLA0569			0.000	0.000		Y	🟡	🟡	Y			18.235	18.235		Y	🟡	*regulatory protein RecX [Methylobacillus flagellatus KT]637937469 YP_544680*
MFLA0570	2.21 E-2	7.588	7.813	8.705	-0.222	Y	🟡	🟡	Y	1.1 E-2	27.324	28.072	28.746	-0.748	Y	🟡	*recA protein [Methylobacillus flagellatus KT]637937470 YP_544681*
MFLA0571		3.591	3.458	4.526	0.168	Y	🟡	🟢	G	8.9 E-3	21.529	22.454	23.065	-0.928	Y	🟡	*CinA-like protein [Methylobacillus flagellatus KT]637937471 YP_544682*
MFLA0572		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*phosphatidylglycerophosphatase A [Methylobacillus flagellatus KT]637937472 YP_544683*

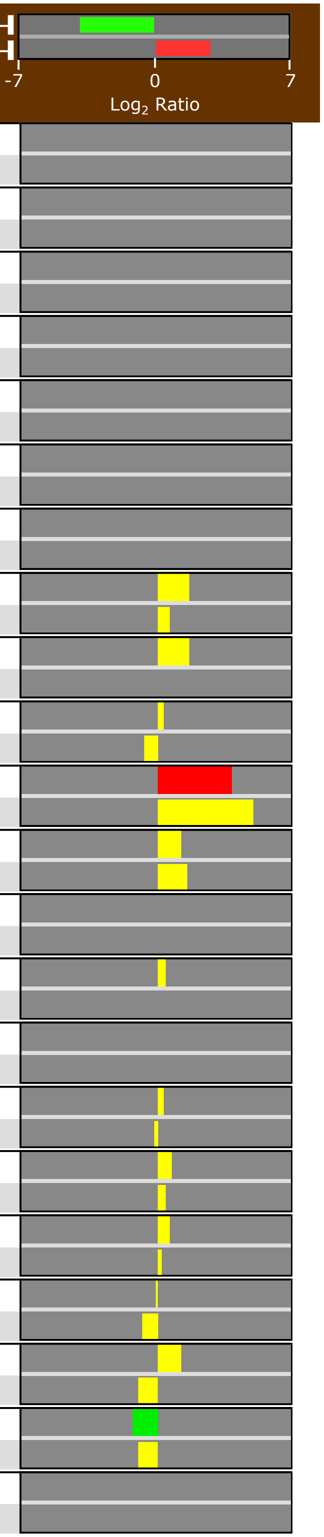
	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA0573		0.000	0.000			■ ■		0.000	0.000			■
	thiamine-monophosphate kinase [Methylobacillus flagellatus KT]637937473 YP_544684											
MFLA0574		3.502	3.616	4.560	-0.064	Y 🟡 🟡 Y	2 E-1	23.807	23.538	24.679	0.073	Y 🟡
	molybdopterin binding domain [Methylobacillus flagellatus KT]637937474 YP_544685											
MFLA0575		3.883	4.129	5.011	-0.236	Y 🟡 🟡 Y	3.04 E-2	21.081	22.196	22.744	-1.098	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937475 YP_544686											
MFLA0576		3.744	3.975	4.864	-0.506	Y 🟡 🟡 Y	1.09 E-1	23.476	24.053	24.793	-0.562	Y 🟡
	" putative site-specific recombinase, prophage insertion [Methylobacillus flagellatus KT]637937476 YP_544687 """											
MFLA0577		0.000	0.000			■ ■		0.000	0.000			■
	Na+/H+ antiporter subunit [Methylobacillus flagellatus KT]637937477 YP_544688											
MFLA0578		0.000	0.000			■ ■		0.000	0.000			■
	multiple resistance and pH regulation protein F [Methylobacillus flagellatus KT]637937478 YP_544689											
MFLA0579			1.931	1.931		Y 🟡 🟡 Y			19.642	19.642		Y 🟡
	cation antiporter [Methylobacillus flagellatus KT]637937479 YP_544690											
MFLA0580		0.000	0.000			■ ■		0.000	0.000			■
	NADH dehydrogenase (quinone) [Methylobacillus flagellatus KT]637937480 YP_544691											
MFLA0581		0.000	0.000			■ ■		0.000	0.000			■
	" NADH-ubiquinone oxidoreductase, chain 4L [Methylobacillus flagellatus KT]637937481 YP_544692 """											
MFLA0582		0.000	0.000			■ ■		0.000	0.000			■
	NADH dehydrogenase (quinone) [Methylobacillus flagellatus KT]637937482 YP_544693											
MFLA0583		6.162	6.413	7.293	-0.200	Y 🟡 🟡 Y	1.19 E-2	24.571	25.272	25.964	-0.698	Y 🟡
	protein of unknown function DUF615 [Methylobacillus flagellatus KT]637937483 YP_544694											
MFLA0584		6.187	6.705	7.469	-0.568	Y 🟡 🟢 G	9.31 E-3	24.481	25.742	26.245	-1.277	G 🟢
	" peptidase U62, modulator of DNA gyrase [Methylobacillus flagellatus KT]637937484 YP_544695 """											
MFLA0585		8.035	6.642	8.500	1.010	Y 🟡 🟡 Y	1.25 E-1	27.009	25.981	27.585	0.513	Y 🟡
	VacJ-like lipoprotein [Methylobacillus flagellatus KT]637937485 YP_544696											
MFLA0586	1.52 E-2	5.339	5.605	6.478	-1.080	Y 🟡 🟡 Y	1.51 E-1	23.665	23.984	24.833	-0.475	Y 🟡
	" Inositol phosphatase/fructose-1,6-bisphosphatase [Methylobacillus flagellatus KT]637937486 YP_544697 """											
MFLA0587		0.000	0.000			■ ■		0.000	0.000			■
	" transcriptional regulator, AraC family [Methylobacillus flagellatus KT]637937487 YP_544698 """											
MFLA0588		0.000	0.000			■ ■		0.000	0.000			■
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637937488 YP_544699											
MFLA0589		0.000	0.000			■ ■		0.000	0.000			■
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637937489 YP_544700											
MFLA0590		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937490 YP_544701											
MFLA0591		1.843	1.585	2.719	0.258	Y 🟡 🟡 Y		20.531	20.012	21.294	0.519	Y 🟡
	Deoxyribodipyrimidine photolyase [Methylobacillus flagellatus KT]637937491 YP_544702											
MFLA0592		2.843	0.346	3.078	2.496	Y 🟡 🟡 Y		20.588	17.992	20.809	2.596	Y 🟡
	protein of unknown function DUF163 [Methylobacillus flagellatus KT]637937492 YP_544703											
MFLA0593		5.653	5.445	6.553	0.001	Y 🟡 🟡 Y	2.68 E-1	25.122	25.100	26.111	0.055	Y 🟡
	Iojap-related protein [Methylobacillus flagellatus KT]637937493 YP_544704											
MFLA0594		0.000	0.000			■ ■		0.000	0.000			■
	aspartate 1-decarboxylase [Methylobacillus flagellatus KT]637937494 YP_544705											

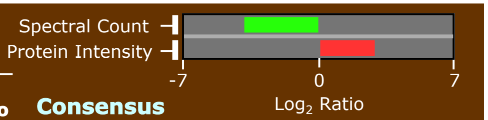


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**				**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**	
MFLA0595		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937495 YP_544706															
MFLA0596	1.01 E-1	5.448	5.194	6.327	0.276	Y	🟡	🟡	Y	7.27 E-2	23.701	24.292	25.027	-0.729	Y	🟡
	pantoate--beta-alanine ligase [Methylobacillus flagellatus KT]637937496 YP_544707															
MFLA0597	4.23 E-15	4.908	6.460	6.883	-1.779	G	🟢	🟡	Y	2.42 E-2	23.353	24.738	25.206	-1.701	G	🟢
	3-methyl-2-oxobutanoate hydroxymethyltransferase [Methylobacillus flagellatus KT]637937497 YP_544708															
MFLA0598	1 E-2	4.521	6.129	6.538	-0.578	Y	🟡	🟡	Y	2.18 E-1	22.930	24.028	24.581	-0.075	Y	🟡
	deoxynucleoside kinase [Methylobacillus flagellatus KT]637937498 YP_544709															
MFLA0599		0.000	0.000				■	■			0.000	0.000				■
	2-amino-4-hydroxy-6- hydroxymethyldihydropteridine pyrophosphokinase [Methylobacillus flagellatus KT]637937499 YP_544710															
MFLA0600		5.191	5.676	6.454	-0.576	Y	🟡	🟡	Y	3.02 E-2	23.655	25.079	25.536	-1.608	Y	🟡
	poly(A) polymerase [Methylobacillus flagellatus KT]637937500 YP_544711															
MFLA0601		3.804	3.095	4.493	0.723	Y	🟡	🟡	Y	2.55 E-2	22.040	22.362	23.210	-0.329	Y	🟡
	metal dependent phosphohydrolase [Methylobacillus flagellatus KT]637937501 YP_544712															
MFLA0602	9.43 E-2	5.097	5.014	6.056	0.163	Y	🟡	🟡	Y	2.02 E-1	23.255	23.512	24.389	-0.300	Y	🟡
	" CRISPR-associated protein, CT1134 [Methylobacillus flagellatus KT]637937502 YP_544713 """															
MFLA0603		6.259	6.216	7.238	0.200	Y	🟡	🟡	Y	9.48 E-2	25.444	25.823	26.646	-0.419	Y	🟡
	" CRISPR-associated protein, CT1133 [Methylobacillus flagellatus KT]637937503 YP_544714 """															
MFLA0604	2.97 E-2	6.702	6.867	7.787	-0.199	Y	🟡	🟡	Y	1.99 E-2	26.419	27.147	27.829	-0.745	Y	🟡
	CRISPR-associated protein TM1801 [Methylobacillus flagellatus KT]637937504 YP_544715															
MFLA0605		0.000	0.000				■	■			0.000	0.000				■
	CRISPR-associated protein Cas4 [Methylobacillus flagellatus KT]637937505 YP_544716															
MFLA0606		3.883		3.883		Y	🟡	🟡	Y		19.785		19.785		Y	🟡
	CRISPR-associated protein Cas1 [Methylobacillus flagellatus KT]637937506 YP_544717															
MFLA0607		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF196 [Methylobacillus flagellatus KT]637937507 YP_544718															
MFLA0608		0.000	0.000				■	■			0.000	0.000				■
	putative signaling membrane protein [Methylobacillus flagellatus KT]637937508 YP_544719															
MFLA0609		3.915		3.915		Y	🟡	🟡	Y		22.982		22.982		Y	🟡
	Sulphate transport system permease protein 1 [Methylobacillus flagellatus KT]637937509 YP_544720															
MFLA0610		0.000	0.000				■	■			0.000	0.000				■
	" Sulfate ABC transporter, permease protein CysW [Methylobacillus flagellatus KT]637937510 YP_544721 """															
MFLA0611		0.000	0.000				■	■			0.000	0.000				■
	" Sulfate ABC transporter, permease protein CysT [Methylobacillus flagellatus KT]637937511 YP_544722 """															
MFLA0612		0.000	0.000				■	■			0.000	0.000				■
	diguanylate phosphodiesterase (EAL domain) [Methylobacillus flagellatus KT]637937512 YP_544723															
MFLA0613		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937513 YP_544724															
MFLA0614		3.532		3.532		Y	🟡	🟡	Y		22.321		22.321		Y	🟡
	Thiosulphate-binding protein [Methylobacillus flagellatus KT]637937514 YP_544725															
MFLA0615		0.000	0.000				■	■			0.000	0.000				■
	Serine O-acetyltransferase [Methylobacillus flagellatus KT]637937515 YP_544726															
MFLA0616		0.000	0.000				■	■			0.000	0.000				■
	major membrane protein I [Methylobacillus flagellatus KT]637937516 YP_544727															

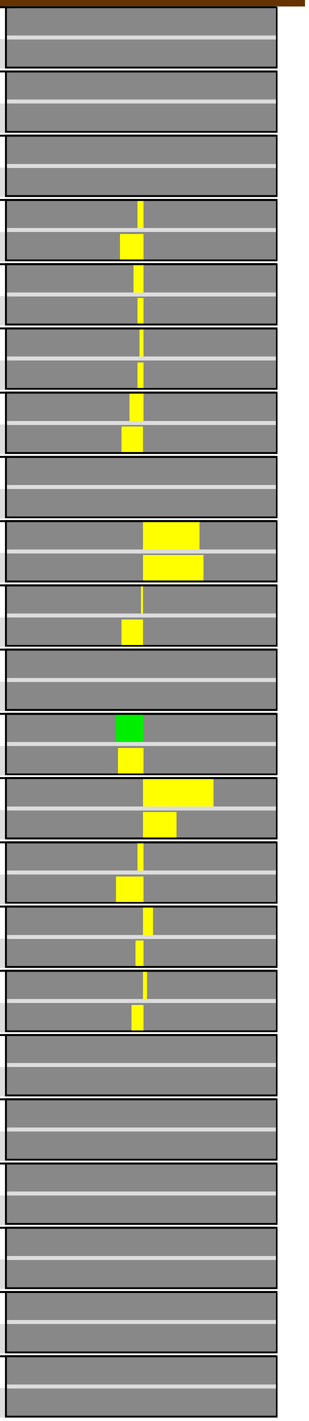


	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	q-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation	q-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA0617 *" cysteine desulfurases, SufS subfamily [Methylobacillus flagellatus KT]637937517 YP_544728 """*		0.000	0.000			■ ■		0.000	0.000			■
MFLA0618 *molybdenum-pterin binding domain [Methylobacillus flagellatus KT]637937518 YP_544729*		0.000	0.000			■ ■		0.000	0.000			■
MFLA0619 *hypothetical protein [Methylobacillus flagellatus KT]637937519 YP_544730*		0.000	0.000			■ ■		0.000	0.000			■
MFLA0620 *Thiosulphate-binding protein [Methylobacillus flagellatus KT]637937520 YP_544731*		4.128		4.128		Y 🟡 🟡 Y		21.802		21.802		Y 🟡
MFLA0621 *hypothetical protein [Methylobacillus flagellatus KT]637937521 YP_544732*		0.000	0.000			■ ■		0.000	0.000			■
MFLA0622 *hypothetical protein [Methylobacillus flagellatus KT]637937522 YP_544733*		3.318		3.318		Y 🟡 🟡 Y		20.700		20.700		Y 🟡
MFLA0623 *hypothetical protein [Methylobacillus flagellatus KT]637937523 YP_544734*		0.000	0.000			■ ■		0.000	0.000			■
MFLA0624 *Glutamate racemase [Methylobacillus flagellatus KT]637937524 YP_544735*		2.135	0.585	2.559	1.550	Y 🟡 🟡 Y		19.678	19.064	20.403	0.614	Y 🟡
MFLA0625 *hypothetical protein [Methylobacillus flagellatus KT]637937525 YP_544736*		3.398	2.844	4.147	1.564	Y 🟡 🟡 Y	2.75 E-1	21.173	22.170	22.756	0.006	Y 🟡
MFLA0626 *branched-chain amino acid aminotransferase [Methylobacillus flagellatus KT]637937526 YP_544737*	7.36 E-4	7.993	7.678	8.844	0.304	Y 🟡 🟡 Y	1.44 E-1	27.001	27.461	28.249	-0.720	Y 🟡
MFLA0627 *OmpW [Methylobacillus flagellatus KT]637937527 YP_544738*	0	8.542	4.746	8.642	3.824	R 🔴 🟡 Y	3.17 E-2	27.138	22.267	27.187	4.861	R 🔴
MFLA0628 *electron transport protein SCO1/SenC [Methylobacillus flagellatus KT]637937528 YP_544739*		2.521	1.322	3.042	1.199	Y 🟡 🟡 Y		20.123	18.616	20.558	1.507	Y 🟡
MFLA0629 *" cytochrome c oxidase, cbb3-type, subunit I [Methylobacillus flagellatus KT]637937529 YP_544740 """*		4.328		4.328		Y 🟡 🟡 Y		23.464		23.464		Y 🟡
MFLA0630 *" cytochrome c oxidase, cbb3-type, subunit II [Methylobacillus flagellatus KT]637937530 YP_544741 """*		7.930	7.518	8.739	0.440	Y 🟡 🟡 Y	2.02 E-1	28.382	28.376	29.379	0.006	Y 🟡
MFLA0631 *hypothetical protein [Methylobacillus flagellatus KT]637937531 YP_544742*		0.000	0.000			■ ■		0.000	0.000			■
MFLA0632 *" cytochrome c oxidase, cbb3-type, subunit III [Methylobacillus flagellatus KT]637937532 YP_544743 """*		8.503	8.289	9.400	0.266	Y 🟡 🟡 Y	7.24 E-2	28.005	28.258	29.137	-0.241	Y 🟡
MFLA0633 *" 4Fe-4S ferredoxin, iron-sulfur binding [Methylobacillus flagellatus KT]637937533 YP_544744 """*		5.233	4.251	5.824	0.731	Y 🟡 🟡 Y	2.39 E-2	23.902	23.510	24.719	0.398	Y 🟡
MFLA0634 *hypothetical protein [Methylobacillus flagellatus KT]637937534 YP_544745*		4.678	4.036	5.393	0.625	Y 🟡 🟡 Y	8.3 E-2	24.399	24.225	25.314	0.176	Y 🟡
MFLA0635 *Heavy metal translocating P-type ATPase [Methylobacillus flagellatus KT]637937535 YP_544746*		3.210	3.410	4.313	-0.091	Y 🟡 🟡 Y	3.54 E-2	21.999	22.863	23.495	-0.850	Y 🟡
MFLA0636 *bacterioferritin [Methylobacillus flagellatus KT]637937536 YP_544747*		2.980	1.807	3.510	1.173	Y 🟡 🟡 Y		22.941	23.929	24.518	-0.988	Y 🟡
MFLA0637 *bacterioferritin [Methylobacillus flagellatus KT]637937537 YP_544748*	3.97 E-8	4.581	5.960	6.429	-1.325	G 🟢 🟡 Y	4.79 E-2	24.010	24.809	25.464	-0.960	G 🟢
MFLA0638 *BFD-like (2Fe-2S)-binding region [Methylobacillus flagellatus KT]637937538 YP_544749*		0.000	0.000			■ ■		0.000	0.000			■

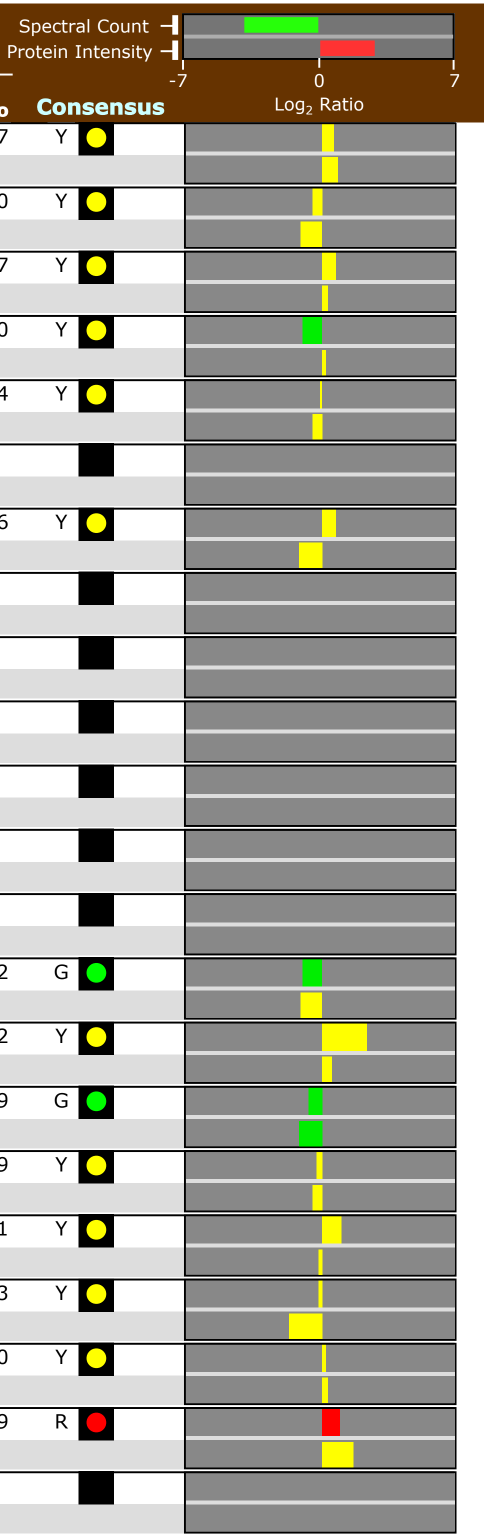




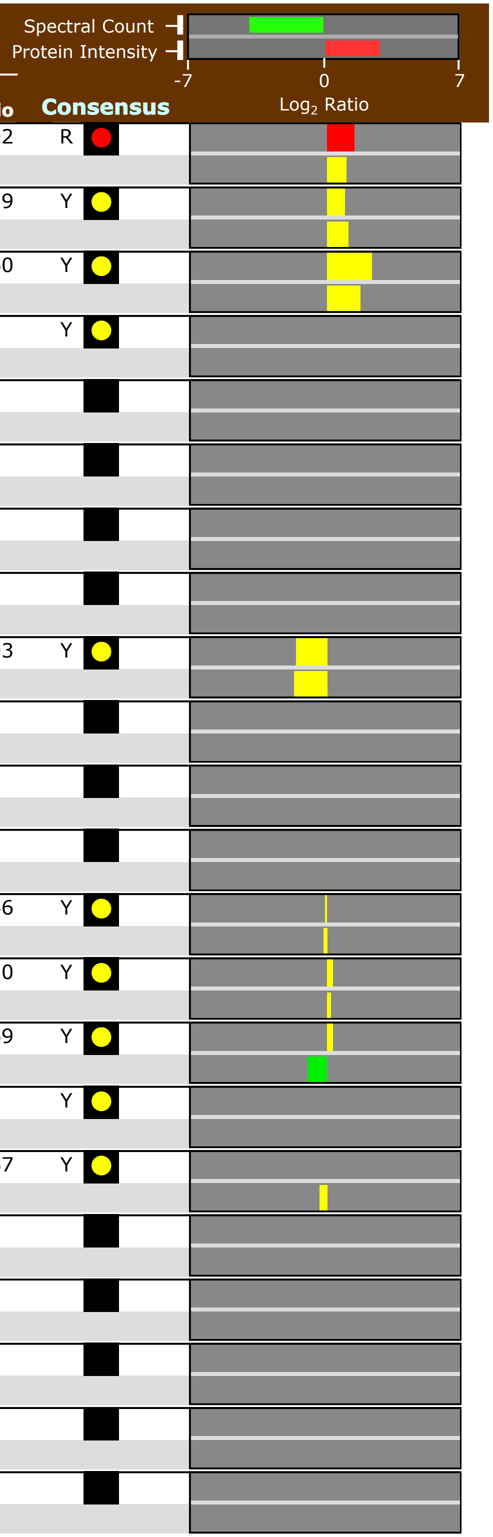
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	***q*-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**				***q*-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**	
MFLA0639			1.668	1.668		Y	🟡	🟡	Y			21.156	21.156		Y	🟡
	globin [Methylobacillus flagellatus KTJ637937539 YP_544750															
MFLA0640		1.843		1.843		Y	🟡	🟡	Y		17.928		17.928		Y	🟡
	" transcriptional regulator, BadM/Rrf2 family [Methylobacillus flagellatus KTJ637937540 YP_544751 """															
MFLA0641		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	protein of unknown function DUF45 [Methylobacillus flagellatus KTJ637937541 YP_544752															
MFLA0642		3.943	3.974	4.959	-0.336	Y	🟡	🟡	Y	2.48 E-1	22.435	22.634	23.538	-1.242	Y	🟡
	phospholipid/glycerol acyltransferase [Methylobacillus flagellatus KTJ637937542 YP_544753															
MFLA0643	1.38 E-1	5.039	5.379	6.219	-0.457	Y	🟡	🟡	Y	8.61 E-2	23.602	23.855	24.734	-0.276	Y	🟡
	Histidinol-phosphate phosphatase [Methylobacillus flagellatus KTJ637937543 YP_544754															
MFLA0644	5.1 E-2	7.603	7.816	8.713	-0.213	Y	🟡	🟡	Y	1.04 E-1	26.877	27.106	27.996	-0.255	Y	🟡
	Glycine--tRNA ligase [Methylobacillus flagellatus KTJ637937544 YP_544755															
MFLA0645		3.996	4.745	5.418	-0.728	Y	🟡	🟡	Y	6.17 E-2	23.408	24.549	25.088	-1.082	Y	🟡
	Glycine--tRNA ligase [Methylobacillus flagellatus KTJ637937545 YP_544756															
MFLA0646		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	apolipoprotein N-acyltransferase [Methylobacillus flagellatus KTJ637937546 YP_544757															
MFLA0647		3.221	0.346	3.405	2.875	Y	🟡	🟡	Y		23.863	20.801	24.026	3.062	Y	🟡
	large conductance mechanosensitive channel protein [Methylobacillus flagellatus KTJ637937547 YP_544758															
MFLA0648	5.41 E-2	6.014	6.059	7.037	-0.098	Y	🟡	🟡	Y	3.18 E-2	24.680	25.624	26.228	-1.081	Y	🟡
	CBS [Methylobacillus flagellatus KTJ637937548 YP_544759															
MFLA0649		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	protein of unknown function UPF0054 [Methylobacillus flagellatus KTJ637937549 YP_544760															
MFLA0650	1.36 E-11	5.210	6.564	7.040	-1.389	G	🟢	🟡	Y	3.17 E-2	24.827	26.237	26.698	-1.349	G	🟢
	PhoH-like protein [Methylobacillus flagellatus KTJ637937550 YP_544761															
MFLA0651		5.357	0.585	5.409	3.647	Y	🟡	🟡	Y	1.33 E-1	23.656	20.550	23.815	1.718	Y	🟡
	tRNA-i(6)A37 modification enzyme MiaB [Methylobacillus flagellatus KTJ637937551 YP_544762															
MFLA0652		3.960	4.219	5.096	-0.332	Y	🟡	🟡	Y	1.2 E-2	21.695	23.026	23.509	-1.363	Y	🟡
	uroporphyrin-III C-methyltransferase [Methylobacillus flagellatus KTJ637937552 YP_544763															
MFLA0653		3.835	3.198	4.552	0.494	Y	🟡	🟡	Y	9.18 E-2	22.973	23.333	24.164	-0.355	Y	🟡
	histidine kinase [Methylobacillus flagellatus KTJ637937553 YP_544764															
MFLA0654	8.61 E-2	6.325	6.095	7.215	0.240	Y	🟡	🟡	Y	5.91 E-2	25.645	26.286	27.000	-0.633	Y	🟡
	" two component transcriptional regulator, winged helix family [Methylobacillus flagellatus KTJ637937554 YP_544765 """															
MFLA0655		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	putative signal transduction protein with EFhand domain [Methylobacillus flagellatus KTJ637937555 YP_544766															
MFLA0656		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	osmotically inducible lipoprotein [Methylobacillus flagellatus KTJ637937556 YP_544767															
MFLA0657		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	protein of unknown function DUF482 [Methylobacillus flagellatus KTJ637937557 YP_544768															
MFLA0658		4.259		4.259		Y	🟡	🟡	Y		21.098		21.098		Y	🟡
	Potassium efflux system protein [Methylobacillus flagellatus KTJ637937558 YP_544769															
MFLA0659		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	cyclase/dehydrase [Methylobacillus flagellatus KTJ637937559 YP_544770															
MFLA0660		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KTJ637937560 YP_544771															



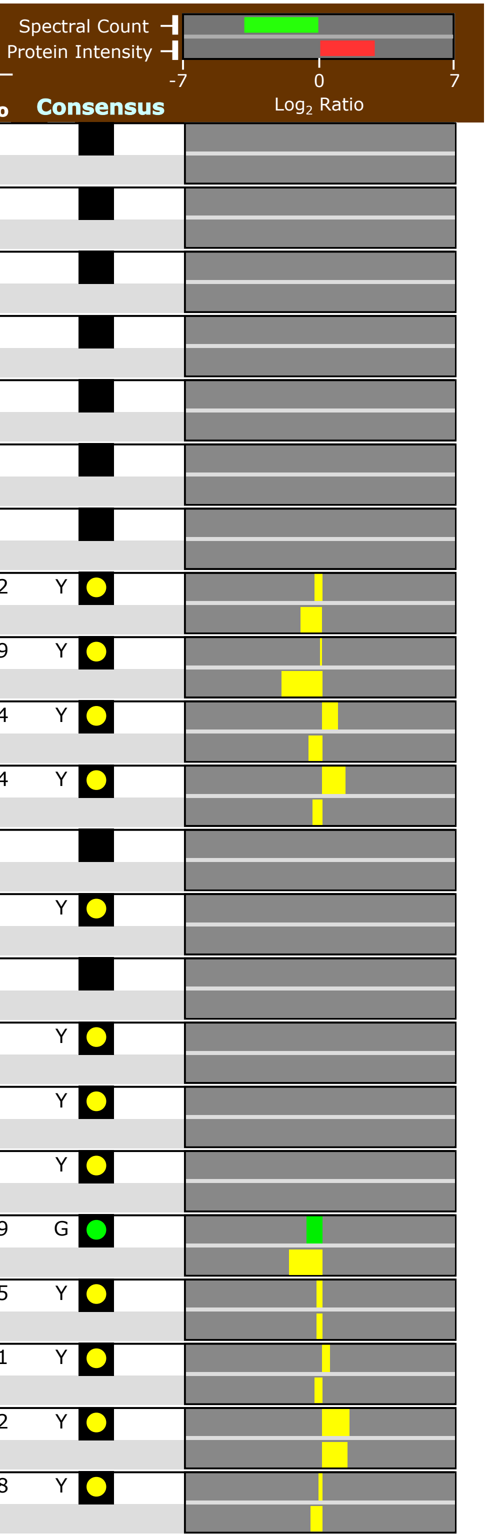
	AM/OH *M Flagellatus* Spectral Count					Regulation				AM/OH *M Flagellatus* Protein Intensity					Consensus	
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio					*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		
MFLA0661		2.521	1.931	3.256	0.589	Y	🟡	🟡	Y		22.472	21.625	23.110	0.847	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937561 YP_544772															
MFLA0662		2.983	4.562	4.979	-0.537	Y	🟡	🟡	Y	2.59 E-2	19.395	21.526	21.822	-1.130	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937562 YP_544773															
MFLA0663		2.674	0.931	3.051	0.736	Y	🟡	🟡	Y	1.4 E-1	20.826	19.516	21.315	0.287	Y	🟡
	phospholipase D/Transphosphatidylase [Methylobacillus flagellatus KT]637937563 YP_544774															
MFLA0664	0	7.415	8.463	9.032	-1.027	G	🟢	🟡	Y	1.17 E-1	28.414	28.185	29.304	0.220	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937564 YP_544775															
MFLA0665		4.277	4.324	5.301	-0.071	Y	🟡	🟡	Y	1.55 E-1	22.593	22.923	23.767	-0.454	Y	🟡
	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC and GAF sensor(s) [Methylobacillus flagellatus KT]637937565 YP_544776															
MFLA0666		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937566 YP_544777															
MFLA0667		2.328	2.659	3.503	0.701	Y	🟡	🟡	Y	5.68 E-2	19.650	21.834	22.121	-1.176	Y	🟡
	GAF sensor hybrid histidine kinase [Methylobacillus flagellatus KT]637937567 YP_544778															
MFLA0668		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937568 YP_544779															
MFLA0669		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	[Methylobacillus flagellatus KT]639329601															
MFLA0671		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937570 YP_544780															
MFLA0672		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937571 YP_544781															
MFLA0673		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937572 YP_544782															
MFLA0674		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937573 YP_544783															
MFLA0675	5.14 E-11	6.331	7.296	7.893	-0.959	G	🟢	🟡	Y	2.52 E-2	25.668	26.786	27.332	-1.112	G	🟢
	hypothetical protein [Methylobacillus flagellatus KT]637937574 YP_544784															
MFLA0676		3.106	1.915	3.630	2.271	Y	🟡	🟡	Y	2.42 E-2	22.042	22.570	23.330	0.472	Y	🟡
	Aminoacyl-tRNA hydrolase [Methylobacillus flagellatus KT]637937575 YP_544785															
MFLA0677	0	9.144	9.773	10.492	-0.700	G	🟢	🟢	G	4.58 E-3	28.364	29.610	30.118	-1.249	G	🟢
	ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5 [Methylobacillus flagellatus KT]637937576 YP_544786															
MFLA0678	1.81 E-2	7.532	7.798	8.671	-0.269	Y	🟡	🟡	Y	7.24 E-2	26.928	27.343	28.150	-0.469	Y	🟡
	ribose-phosphate pyrophosphokinase [Methylobacillus flagellatus KT]637937577 YP_544787															
MFLA0679		3.482	2.471	4.063	1.009	Y	🟡	🟡	Y	6.85 E-2	21.404	21.579	22.494	-0.181	Y	🟡
	4-diphosphocytidyl-2C-methyl-D-erythritol kinase [Methylobacillus flagellatus KT]637937579 YP_544788															
MFLA0680		3.571	3.875	4.731	-0.188	Y	🟡	🟡	Y	1.89 E-2	21.526	23.135	23.544	-1.743	Y	🟡
	outer membrane lipoprotein LolB [Methylobacillus flagellatus KT]637937580 YP_544789															
MFLA0681		8.182	7.911	9.053	0.243	Y	🟡	🟡	Y	1.28 E-1	28.000	27.568	28.800	0.350	Y	🟡
	Tetratricopeptide TPR_2 [Methylobacillus flagellatus KT]637937581 YP_544790															
MFLA0682	6.25 E-11	7.427	6.563	8.059	0.855	R	🔴	🟡	Y	1.75 E-2	26.203	24.641	26.624	1.599	R	🔴
	ABC transporter related [Methylobacillus flagellatus KT]637937582 YP_544791															
MFLA0683		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" ABC transporter, permease protein, putative [Methylobacillus flagellatus KT]637937583 YP_544792 """															



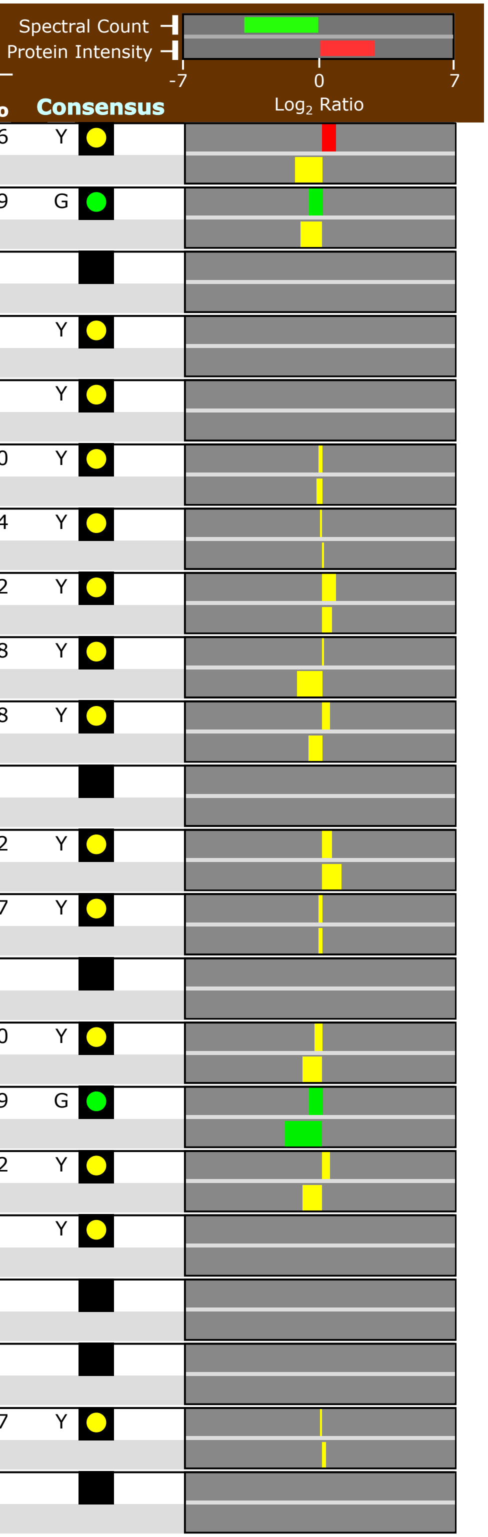
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA0684	8.46 E-11	6.421	5.005	6.880	1.407	R	🔴	🟡	Y	7.8 E-2	26.839	25.973	27.470	1.002	R	🔴
	hypothetical protein [Methylobacillus flagellatus KT]637937584 YP_544793															
MFLA0685		5.153	4.264	5.776	0.936	Y	🟡	🟡	Y	9.44 E-2	24.032	22.593	24.485	1.139	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937585 YP_544794															
MFLA0686		2.328	0.000	2.590	2.328	Y	🟡	🟡	Y		21.006	19.346	21.403	1.660	Y	🟡
	formamidopyrimidine-DNA glycosylase [Methylobacillus flagellatus KT]637937586 YP_544795															
MFLA0687		0.521		0.521		Y	🟡	🟡	Y		18.571		18.571		Y	🟡
	" ATPase associated with various cellular activities, AAA_3 [Methylobacillus flagellatus KT]637937587 YP_544796 """															
MFLA0688		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937588 YP_544797															
MFLA0689		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" MxaA protein, putative [Methylobacillus flagellatus KT]637937589 YP_544798 """															
MFLA0690		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" von Willebrand factor, type A [Methylobacillus flagellatus KT]637937590 YP_544799 """															
MFLA0691		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937591 YP_544800															
MFLA0692		0.521	2.170	2.569	-1.649	Y	🟡	🟡	Y		18.361	20.064	20.451	-1.703	Y	🟡
	" von Willebrand factor, type A [Methylobacillus flagellatus KT]637937592 YP_544801 """															
MFLA0693		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" transcriptional regulator, MerR family [Methylobacillus flagellatus KT]637937593 YP_544802 """															
MFLA0694		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	Co/Zn/Cd efflux system component [Methylobacillus flagellatus KT]637937594 YP_544803															
MFLA0695		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	Na+/solute symporter [Methylobacillus flagellatus KT]637937595 YP_544804															
MFLA0696	1.06 E-1	4.899	4.993	5.947	-0.077	Y	🟡	🟡	Y	2.64 E-1	24.090	24.144	25.117	-0.246	Y	🟡
	2-polyprenylphenol 6-hydroxylase [Methylobacillus flagellatus KT]637937596 YP_544805															
MFLA0697		3.692	3.372	4.541	0.321	Y	🟡	🟡	Y	1.87 E-1	21.608	21.430	22.522	0.150	Y	🟡
	protein of unknown function DUF1243 [Methylobacillus flagellatus KT]637937597 YP_544806															
MFLA0698	8.72 E-2	6.374	6.108	7.247	0.261	Y	🟡	🟢	G	9.51 E-3	24.152	25.104	25.705	-0.969	Y	🟡
	ubiquinone/menaquinone biosynthesis methyltransferases [Methylobacillus flagellatus KT]637937598 YP_544807															
MFLA0699			1.585	1.585		Y	🟡	🟡	Y			20.959	20.959		Y	🟡
	protein of unknown function DUF971 [Methylobacillus flagellatus KT]637937599 YP_544808															
MFLA0700	4.36 E-2	6.568	6.643	7.606	-0.048	Y	🟡	🟡	Y	7.52 E-2	25.646	26.026	26.849	-0.367	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937600 YP_544809															
MFLA0701		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" cytochrome oxidase maturation protein, cbb3-type [Methylobacillus flagellatus KT]637937601 YP_544810 """															
MFLA0702		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	sigma 32 (RpoH) [Methylobacillus flagellatus KT]637937602 YP_544811															
MFLA0703		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937603 YP_544812															
MFLA0704		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	protein of unknown function DUF214 [Methylobacillus flagellatus KT]637937604 YP_544813															
MFLA0705		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	ABC transporter related [Methylobacillus flagellatus KT]637937605 YP_544814															



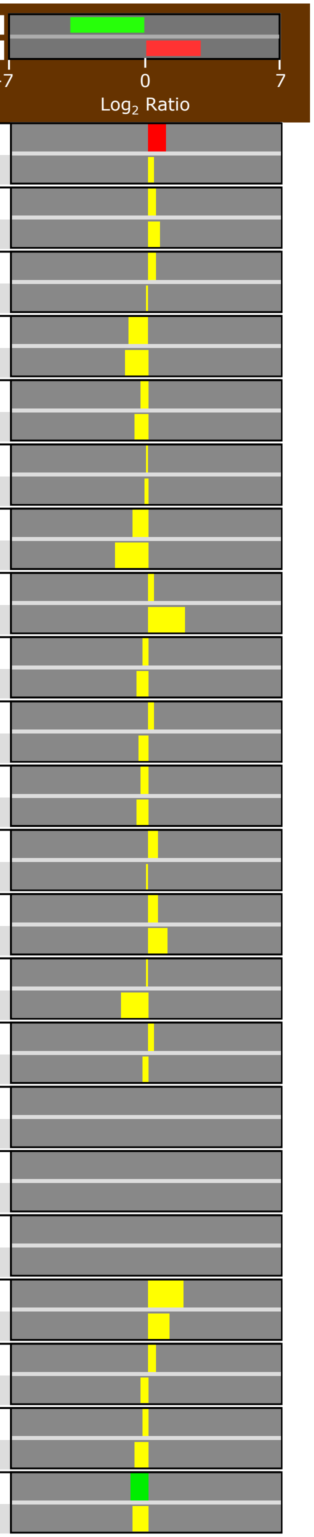
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA0706		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937606 YP_544815															
MFLA0707		0.000	0.000				■	■			0.000	0.000				■
	zinc/iron permease [Methylobacillus flagellatus KT]637937607 YP_544816															
MFLA0708		0.000	0.000				■	■			0.000	0.000				■
	" TonB-dependent receptor, plug [Methylobacillus flagellatus KT]637937608 YP_544817 """															
MFLA0709		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937609 YP_544818															
MFLA0710		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937610 YP_544819															
MFLA0711		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937611 YP_544820															
MFLA0712		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937612 YP_544821															
MFLA0713		2.983	4.385	4.848	-0.386	Y	●	●	Y	1.2 E-1	18.591	20.829	21.106	-1.112	Y	●
	hypothetical protein [Methylobacillus flagellatus KT]637937613 YP_544822															
MFLA0714		2.746	1.585	3.279	-0.126	Y	●	●	Y	1.08 E-2	21.777	22.915	23.456	-2.139	Y	●
	" protein of unknown function DUF861, cupin_3 [Methylobacillus flagellatus KT]637937614 YP_544823 """															
MFLA0715		1.521	1.769	2.650	0.762	Y	●	●	Y	1.26 E-1	19.033	20.790	21.164	-0.684	Y	●
	periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637937615 YP_544824															
MFLA0716		4.306	3.147	4.840	1.199	Y	●	●	Y	2.51 E-2	21.257	21.734	22.515	-0.484	Y	●
	" two component transcriptional regulator, winged helix family [Methylobacillus flagellatus KT]637937616 YP_544825 """															
MFLA0717		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937617 YP_544826															
MFLA0718		2.621		2.621		Y	●	●	Y		21.957		21.957		Y	●
	putative NAD-dependent formate dehydrogenase delta subunit [Methylobacillus flagellatus KT]637937618 YP_544827															
MFLA0719		0.000	0.000				■	■			0.000	0.000				■
	formate dehydrogenase family accessory protein FdhD [Methylobacillus flagellatus KT]637937619 YP_544828															
MFLA0720		6.738		6.738		Y	●	●	Y		25.869		25.869		Y	●
	" formate dehydrogenase, alpha subunit [Methylobacillus flagellatus KT]637937620 YP_544829 """															
MFLA0721		6.692		6.692		Y	●	●	Y		24.631		24.631		Y	●
	NADH dehydrogenase (quinone) [Methylobacillus flagellatus KT]637937621 YP_544830															
MFLA0722		1.398		1.398		Y	●	●	Y		21.744		21.744		Y	●
	" NADH dehydrogenase (ubiquinone), 24 kDa subunit [Methylobacillus flagellatus KT]637937622 YP_544831 """															
MFLA0723	2.82 E-7	6.204	6.942	7.619	-0.785	G	●	●	Y	1.01 E-2	25.001	26.676	27.069	-1.739	G	●
	FAD linked oxidase-like protein [Methylobacillus flagellatus KT]637937623 YP_544832															
MFLA0724	5.76 E-5	8.973	9.236	10.110	-0.259	Y	●	●	Y	2.74 E-2	27.853	28.160	29.015	-0.305	Y	●
	" D-isomer specific 2-hydroxyacid dehydrogenase, NAD-binding [Methylobacillus flagellatus KT]637937624 YP_544833 """															
MFLA0725	5.74 E-2	6.104	5.737	6.932	0.359	Y	●	●	Y	6.15 E-2	24.951	25.354	26.167	-0.391	Y	●
	Electron-transferring-flavoprotein dehydrogenase [Methylobacillus flagellatus KT]637937625 YP_544834															
MFLA0726		3.221	1.807	3.681	1.414	Y	●	●	Y		21.266	19.965	21.758	1.302	Y	●
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637937626 YP_544835 """															
MFLA0727	3.57 E-2	7.477	7.662	8.572	-0.192	Y	●	●	Y	1.53 E-2	27.076	27.707	28.426	-0.648	Y	●
	electron transfer flavoprotein beta-subunit [Methylobacillus flagellatus KT]637937627 YP_544836															



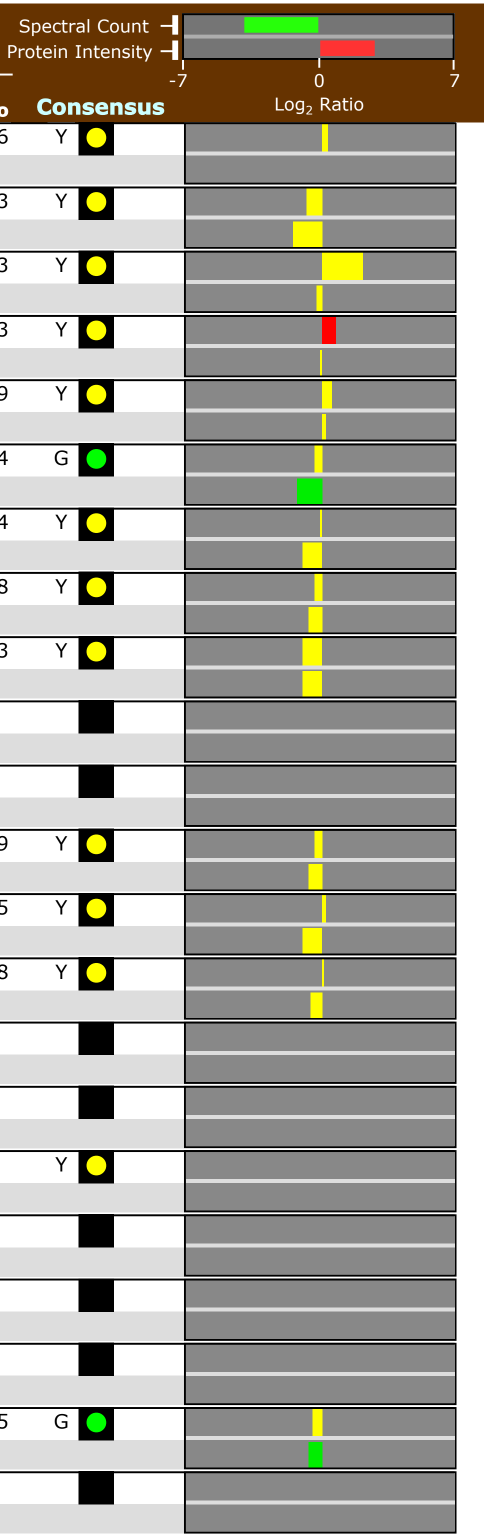
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA0728	7.15 E-8	7.459	6.710	8.133	0.749	R	🔴	🟡	Y	3.47 E-2	25.407	26.615	27.134	-1.436	Y	🟡
	" electron transfer flavoprotein, alpha subunit [Methylobacillus flagellatus KT]637937628 YP_544837 """															
MFLA0729	2.76 E-5	6.381	7.041	7.748	-0.671	G	🟢	🟡	Y	1.1 E-2	26.766	27.815	28.384	-1.059	G	🟢
	Oxidoreductase FAD-binding region [Methylobacillus flagellatus KT]637937629 YP_544838															
MFLA0730		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937630 YP_544839															
MFLA0731		1.843		1.843		Y	🟡	🟡	Y		19.034		19.034		Y	🟡
	protein of unknown function DUF214 [Methylobacillus flagellatus KT]637937631 YP_544840															
MFLA0732			2.505	2.505		Y	🟡	🟡	Y			22.113	22.113		Y	🟡
	ABC transporter related [Methylobacillus flagellatus KT]637937632 YP_544841															
MFLA0733	1.33 E-1	5.801	5.986	6.897	-0.184	Y	🟡	🟡	Y	5.91 E-2	25.166	25.424	26.301	-0.260	Y	🟡
	signal recognition particle-docking protein FtsY [Methylobacillus flagellatus KT]637937633 YP_544842															
MFLA0734	1.14 E-2	7.657	7.757	8.708	-0.099	Y	🟡	🟡	Y	1.98 E-1	27.373	27.199	28.289	0.084	Y	🟡
	peptidase M16-like protein [Methylobacillus flagellatus KT]637937634 YP_544843															
MFLA0735		7.491	6.954	8.247	0.687	Y	🟡	🟡	Y	8.26 E-2	27.164	26.740	27.968	0.452	Y	🟡
	peptidase M16-like protein [Methylobacillus flagellatus KT]637937635 YP_544844															
MFLA0736		2.210	2.254	3.232	0.090	Y	🟡	🟡	Y	2.05 E-2	20.651	21.930	22.428	-1.318	Y	🟡
	conserved hypothetical protein 95 [Methylobacillus flagellatus KT]637937636 YP_544845															
MFLA0737		4.542	4.194	5.378	0.350	Y	🟡	🟡	Y	4.87 E-2	23.310	23.962	24.672	-0.688	Y	🟡
	Coenzyme A biosynthesis protein [Methylobacillus flagellatus KT]637937637 YP_544846															
MFLA0738		0.000	0.000				■	■			0.000	0.000				■
	" 4Fe-4S ferredoxin, iron-sulfur binding [Methylobacillus flagellatus KT]637937638 YP_544847 """															
MFLA0739		2.691	2.154	3.447	0.537	Y	🟡	🟡	Y		22.209	21.167	22.780	1.042	Y	🟡
	Glyoxalase I [Methylobacillus flagellatus KT]637937639 YP_544848															
MFLA0740		5.487	5.459	6.473	-0.166	Y	🟡	🟡	Y	1.43 E-1	24.107	24.314	25.214	-0.247	Y	🟡
	Phosphate acetyltransferase [Methylobacillus flagellatus KT]637937640 YP_544849															
MFLA0741		0.000	0.000				■	■			0.000	0.000				■
	acetate kinase [Methylobacillus flagellatus KT]637937641 YP_544850															
MFLA0742		2.996	3.453	4.243	-0.438	Y	🟡	🟡	Y	1.59 E-2	22.855	23.878	24.455	-1.020	Y	🟡
	secretion protein HlyD [Methylobacillus flagellatus KT]637937642 YP_544851															
MFLA0743		3.259	3.941	4.640	-0.667	G	🟢	🟢	G	4.58 E-3	21.732	23.655	23.993	-1.949	G	🟢
	acriflavin resistance protein [Methylobacillus flagellatus KT]637937643 YP_544852															
MFLA0744		3.307	1.807	3.744	0.360	Y	🟡	🟡	Y	1.25 E-1	20.860	20.605	21.738	-0.952	Y	🟡
	acriflavin resistance protein [Methylobacillus flagellatus KT]637937644 YP_544853															
MFLA0745		3.270		3.270		Y	🟡	🟡	Y		21.077		21.077		Y	🟡
	" RND efflux system, outer membrane lipoprotein, NodT [Methylobacillus flagellatus KT]637937645 YP_544854 """															
MFLA0746		0.000	0.000				■	■			0.000	0.000				■
	Alpha/beta hydrolase fold-3 [Methylobacillus flagellatus KT]637937646 YP_544855															
MFLA0747		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937647 YP_544856															
MFLA0748	1.44 E-1	5.778	5.897	6.839	-0.121	Y	🟡	🟡	Y	7.33 E-2	25.048	24.897	25.975	0.157	Y	🟡
	2-isopropylmalate synthase [Methylobacillus flagellatus KT]637937648 YP_544857															
MFLA0749		0.000	0.000				■	■			0.000	0.000				■
	Drug resistance transporter Bcr/CflA subfamily [Methylobacillus flagellatus KT]637937649 YP_544858															



	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA0750	0	8.092	7.101	8.680	0.863	R 🔴 🟡 Y	1.5 E-1	26.707	26.403	27.563	0.281	R 🔴
	Chaperone DnaJ [Methylobacillus flagellatus KT]637937650 YP_544859											
MFLA0751		12.166	11.762	12.978	0.368	Y 🟡 🟡 Y	3.48 E-2	31.708	31.136	32.450	0.554	Y 🟡
	Chaperone DnaK [Methylobacillus flagellatus KT]637937651 YP_544860											
MFLA0752		9.966	9.466	10.738	0.409	Y 🟡 🟡 Y	2.59 E-1	28.652	28.694	29.673	-0.133	Y 🟡
	GrpE protein [Methylobacillus flagellatus KT]637937652 YP_544861											
MFLA0753		3.259	4.288	4.863	-1.036	Y 🟡 🟡 Y	3.09 E-2	21.650	22.728	23.288	-1.218	Y 🟡
	Lipopolysaccharide heptosyltransferase I [Methylobacillus flagellatus KT]637937653 YP_544862											
MFLA0754		4.113	4.341	5.231	-0.403	Y 🟡 🟡 Y	9.48 E-2	22.663	23.189	23.950	-0.689	Y 🟡
	" glycosyl transferase, group 1 [Methylobacillus flagellatus KT]637937654 YP_544863 """											
MFLA0755		3.571	3.669	4.621	-0.091	Y 🟡 🟡 Y	5.88 E-2	22.900	23.146	24.029	-0.239	Y 🟡
	lipopolysaccharide kinase [Methylobacillus flagellatus KT]637937655 YP_544864											
MFLA0756		3.664	4.132	4.917	-0.764	Y 🟡 🟡 Y	8.56 E-2	21.446	22.368	22.979	-1.743	Y 🟡
	sulfatase [Methylobacillus flagellatus KT]637937656 YP_544865											
MFLA0757		3.945	3.595	4.781	0.320	Y 🟡 🟡 Y	8.72 E-2	25.723	23.167	25.950	1.935	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637937657 YP_544866											
MFLA0758	6.98 E-2	6.201	6.468	7.340	-0.277	Y 🟡 🟡 Y	1.53 E-2	25.557	26.129	26.871	-0.584	Y 🟡
	Carbamoyltransferase [Methylobacillus flagellatus KT]637937658 YP_544867											
MFLA0759	1.59 E-3	7.885	7.605	8.752	0.271	Y 🟡 🟡 Y	3.76 E-2	27.338	27.792	28.583	-0.462	Y 🟡
	6-phosphogluconate dehydratase [Methylobacillus flagellatus KT]637937659 YP_544868											
MFLA0760	2.05 E-3	7.049	7.407	8.239	-0.371	Y 🟡 🟡 Y	1.17 E-2	28.005	28.606	29.337	-0.598	Y 🟡
	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutarate aldolase [Methylobacillus flagellatus KT]637937660 YP_544869											
MFLA0761		1.521	1.000	2.284	0.521	Y 🟡 🟡 Y		19.745	19.867	20.807	-0.122	Y 🟡
	Haloacid dehalogenase-like hydrolase [Methylobacillus flagellatus KT]637937661 YP_544870											
MFLA0762		0.521	0.000	1.284	0.521	Y 🟡 🟡 Y		21.104	20.144	21.702	0.960	Y 🟡
	" toluene tolerance protein, putative [Methylobacillus flagellatus KT]637937662 YP_544871 """											
MFLA0763		3.221	4.367	4.905	-0.095	Y 🟡 🟡 Y	1.17 E-1	21.799	24.344	24.572	-1.388	Y 🟡
	" glycosyl transferase, group 1 [Methylobacillus flagellatus KT]637937663 YP_544872 """											
MFLA0764		4.346	3.871	5.128	0.286	Y 🟡 🟡 Y	1.4 E-1	23.432	23.695	24.570	-0.339	Y 🟡
	Methyltransferase FkbM [Methylobacillus flagellatus KT]637937664 YP_544873											
MFLA0765		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937665 YP_544874											
MFLA0766		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937666 YP_544875											
MFLA0767		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937667 YP_544876											
MFLA0768		3.461	1.710	3.836	1.786	Y 🟡 🟡 Y	4.99 E-2	22.432	21.363	22.994	1.135	Y 🟡
	Lipopolysaccharide heptosyltransferase II [Methylobacillus flagellatus KT]637937668 YP_544877											
MFLA0769		3.901	4.601	5.293	0.377	Y 🟡 🟡 Y	1.8 E-1	23.445	25.107	25.503	-0.384	Y 🟡
	" RfaE bifunctional protein, domain I [Methylobacillus flagellatus KT]637937669 YP_544878 """											
MFLA0770	9.98 E-2	5.405	5.672	6.544	-0.270	Y 🟡 🟡 Y	8.25 E-2	22.765	23.300	24.057	-0.652	Y 🟡
	phosphoheptose isomerase [Methylobacillus flagellatus KT]637937670 YP_544879											
MFLA0771	2.62 E-7	6.054	6.919	7.551	-0.861	G 🟢 🟡 Y	7.11 E-2	25.875	26.568	27.263	-0.837	G 🟢
	ADP-L-glycero-D-manno-heptose-6-epimerase [Methylobacillus flagellatus KT]637937671 YP_544880											



	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA0772		7.255	6.923	8.098	0.313	Y ● ● Y	2.04 E-1	26.274	26.245	27.260	0.026	Y ●
	Ferrochelatase [Methylobacillus flagellatus KT]637937672 YP_544881											
MFLA0773	1.15 E-2	4.921	5.559	6.275	-0.778	Y ● ● Y	4.19 E-2	23.528	24.648	25.194	-1.473	Y ●
	negative regulator of class I heat shock protein [Methylobacillus flagellatus KT]637937673 YP_544882											
MFLA0774		4.120	1.000	4.278	2.120	Y ● ● Y	1.55 E-1	20.817	20.075	21.493	-0.293	Y ●
	NAD(+) kinase [Methylobacillus flagellatus KT]637937674 YP_544883											
MFLA0775	3.1 E-3	5.336	4.606	6.016	0.701	R ● ● Y	2.22 E-1	24.032	24.118	25.075	-0.113	Y ●
	DNA repair protein RecN [Methylobacillus flagellatus KT]637937675 YP_544884											
MFLA0776		4.967	4.431	5.724	0.538	Y ● ● Y	1.98 E-1	24.416	24.155	25.291	0.179	Y ●
	SmpA/OmlA [Methylobacillus flagellatus KT]637937676 YP_544885											
MFLA0777	5.11 E-2	5.791	6.186	7.002	-0.393	Y ● ● G	9.51 E-3	25.005	26.286	26.783	-1.274	G ●
	Dihydrodipicolinate reductase [Methylobacillus flagellatus KT]637937677 YP_544886											
MFLA0778	5.21 E-2	6.622	6.741	7.683	-0.136	Y ● ● Y	3.67 E-2	25.652	26.601	27.203	-1.014	Y ●
	" carbamoyl-phosphate synthase, small subunit [Methylobacillus flagellatus KT]637937678 YP_544887 """											
MFLA0779	1.4 E-5	7.722	8.154	8.954	-0.423	Y ● ● Y	1.01 E-2	26.939	27.628	28.324	-0.698	Y ●
	" carbamoyl-phosphate synthase, large subunit [Methylobacillus flagellatus KT]637937679 YP_544888 """											
MFLA0780		4.359	5.242	5.867	-0.986	Y ● ● Y	2.49 E-2	25.011	26.059	26.628	-1.033	Y ●
	GreA/GreB family elongation factor [Methylobacillus flagellatus KT]637937680 YP_544889											
MFLA0781		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937681 YP_544890											
MFLA0782		0.000	0.000			■ ■		0.000	0.000			■
	ribosomal RNA methyltransferase RrmJ/FtsJ [Methylobacillus flagellatus KT]637937682 YP_544891											
MFLA0783		7.448	7.808	8.639	-0.385	Y ● ● Y	5.48 E-2	26.400	27.101	27.792	-0.699	Y ●
	ATP-dependent metalloprotease FtsH [Methylobacillus flagellatus KT]637937683 YP_544892											
MFLA0784		4.964	4.720	5.847	0.232	Y ● ● Y	1.35 E-2	23.422	24.389	24.985	-0.965	Y ●
	dihydropteroate synthase [Methylobacillus flagellatus KT]637937684 YP_544893											
MFLA0785		4.875	4.747	5.813	0.092	Y ● ● Y	2.16 E-1	23.481	23.759	24.627	-0.638	Y ●
	phosphoglucosamine mutase [Methylobacillus flagellatus KT]637937685 YP_544894											
MFLA0786		0.000	0.000			■ ■		0.000	0.000			■
	" phosphoesterase, PA-phosphatase related [Methylobacillus flagellatus KT]637937686 YP_544895 """											
MFLA0787		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937687 YP_544896											
MFLA0788		3.221		3.221		Y ● ● Y		18.994		18.994		Y ●
	diacylglycerol kinase [Methylobacillus flagellatus KT]637937688 YP_544897											
MFLA0789		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637937689 YP_544898											
MFLA0790		0.000	0.000			■ ■		0.000	0.000			■
	" glycosyl transferase, group 1 [Methylobacillus flagellatus KT]637937690 YP_544899 """											
MFLA0791		0.000	0.000			■ ■		0.000	0.000			■
	D-amino-acid dehydrogenase [Methylobacillus flagellatus KT]637937691 YP_544900											
MFLA0792	1.26 E-2	5.783	6.193	7.002	-0.453	Y ● ● G	9.03 E-6	25.637	26.353	27.039	-0.715	G ●
	Phosphate transport system permease protein 1 [Methylobacillus flagellatus KT]637937692 YP_544901											
MFLA0793		0.000	0.000			■ ■		0.000	0.000			■
	Phosphate transport system permease protein 2 [Methylobacillus flagellatus KT]637937693 YP_544902											



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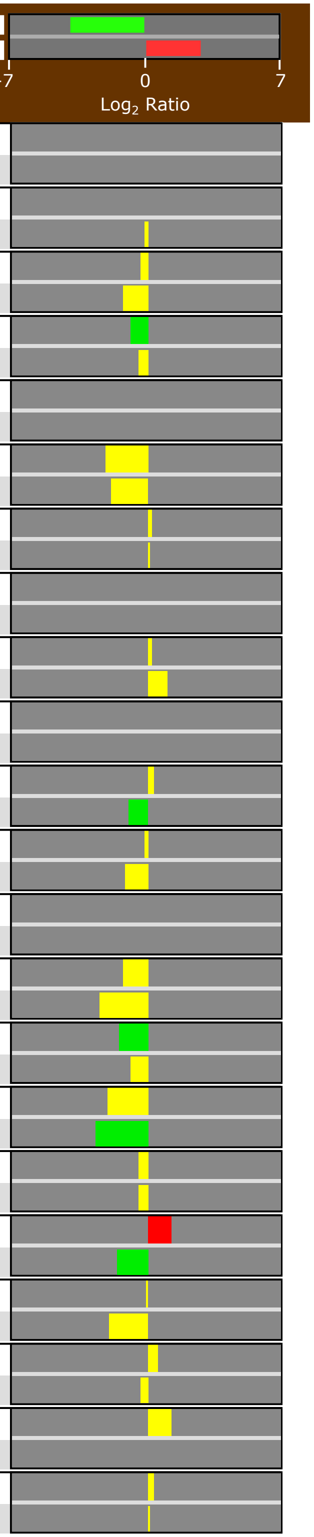
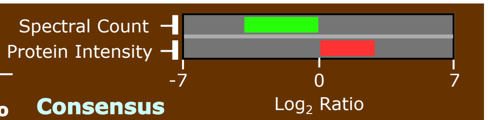
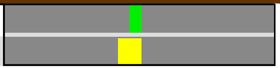
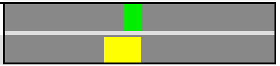
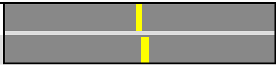
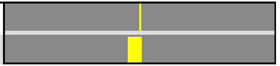
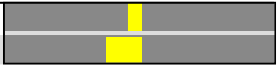
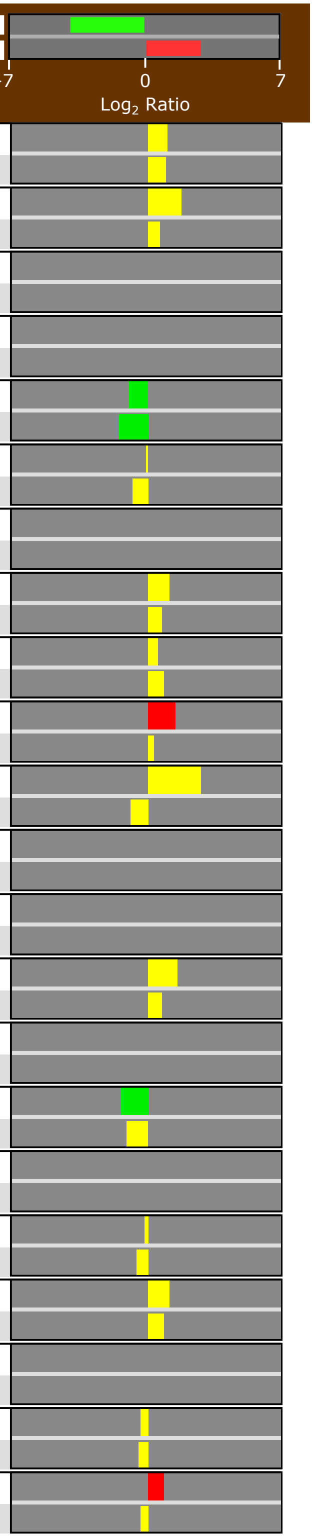
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio					*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		
MFLA0794		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" Phosphate ABC transporter, permease protein PstC [Methylobacillus flagellatus KT]637937694 YP_544903 """															
MFLA0795	1.16 E-1	7.068	7.029	8.049	0.050	Y	🟡	🟡	Y	4.09 E-2	26.367	26.585	27.480	-0.217	Y	🟡
	Phosphate binding protein [Methylobacillus flagellatus KT]637937695 YP_544904															
MFLA0796	1.65 E-2	5.828	6.164	7.006	-0.386	Y	🟡	🟡	Y	1.66 E-2	24.698	26.020	26.505	-1.299	Y	🟡
	peptide chain release factor 2 [Methylobacillus flagellatus KT]637937696 YP_544905															
MFLA0797	8.36 E-9	5.474	6.489	7.069	-0.908	G	🟢	🟡	Y	7.77 E-2	26.046	26.549	27.319	-0.454	G	🟢
	lysyl-tRNA synthetase [Methylobacillus flagellatus KT]637937697 YP_544906															
MFLA0798		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637937698 YP_544907															
MFLA0799		2.828	4.000	4.530	-2.172	Y	🟡	🟡	Y	8.26 E-2	22.556	23.056	23.827	-1.902	Y	🟡
	sulphate transporter [Methylobacillus flagellatus KT]637937699 YP_544908															
MFLA0800		8.939	8.750	9.848	0.169	Y	🟡	🟡	Y	2.17 E-1	29.094	28.967	30.032	0.150	Y	🟡
	carbonic anhydrase [Methylobacillus flagellatus KT]637937700 YP_544909															
MFLA0801		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	phosphate-selective porin O and P [Methylobacillus flagellatus KT]637937701 YP_544910															
MFLA0802		1.521	1.346	2.436	0.174	Y	🟡	🟡	Y		18.855	17.874	19.447	0.981	Y	🟡
	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) [Methylobacillus flagellatus KT]637937702 YP_544911															
MFLA0803		1.398		1.398		Y	🟡	🟡	Y		21.510		21.510		Y	🟡
	" Ferredoxin, 2Fe-2S type [Methylobacillus flagellatus KT]637937703 YP_544912 """															
MFLA0804	6.75 E-2	6.924	6.650	7.794	0.274	Y	🟡	🟢	G	9.69 E-3	24.834	25.842	26.424	-1.022	Y	🟡
	Fe-S protein assembly chaperone HscA [Methylobacillus flagellatus KT]637937704 YP_544913															
MFLA0805		4.222	4.370	5.298	-0.164	Y	🟡	🟡	Y	1.1 E-2	23.149	24.327	24.855	-1.211	Y	🟡
	co-chaperone Hsc20 [Methylobacillus flagellatus KT]637937705 YP_544914															
MFLA0806		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	iron-sulfur cluster assembly protein IscA [Methylobacillus flagellatus KT]637937706 YP_544915															
MFLA0807		2.813	5.151	5.411	-1.334	Y	🟡	🟡	Y	3.26 E-2	22.252	25.709	25.834	-2.454	Y	🟡
	FeS cluster assembly scaffold IscU [Methylobacillus flagellatus KT]637937707 YP_544916															
MFLA0808	0	6.766	8.203	8.656	-1.454	G	🟢	🟡	Y	4.51 E-2	26.234	27.064	27.708	-0.889	G	🟢
	cysteine desulfurase IscS [Methylobacillus flagellatus KT]637937708 YP_544917															
MFLA0809		3.330	5.119	5.486	-2.064	Y	🟡	🟢	G	9.69 E-3	21.717	24.122	24.371	-2.693	G	🟢
	" aminotransferase, class V [Methylobacillus flagellatus KT]637937709 YP_544918 """															
MFLA0810		3.106	4.559	5.008	-0.453	Y	🟡	🟡	Y	6.98 E-2	20.708	22.245	22.673	-0.532	Y	🟡
	" transcriptional regulator, BadM/Rrf2 family [Methylobacillus flagellatus KT]637937710 YP_544919 """															
MFLA0811	5.1 E-5	5.658	4.450	6.177	1.225	R	🔴	🟢	G	5.17 E-3	22.776	24.340	24.760	-1.562	Y	🟡
	serine O-acetyltransferase [Methylobacillus flagellatus KT]637937711 YP_544920															
MFLA0812		3.996	4.117	5.058	-0.075	Y	🟡	🟡	Y	1.37 E-2	20.440	22.458	22.777	-2.034	Y	🟡
	" RNA methyltransferase TrmH, group 1 [Methylobacillus flagellatus KT]637937712 YP_544921 """															
MFLA0813		5.687	5.065	6.409	0.530	Y	🟡	🟡	Y	7.57 E-2	25.294	25.644	26.480	-0.362	Y	🟡
	inositol monophosphatase [Methylobacillus flagellatus KT]637937713 YP_544922															
MFLA0814		3.600	2.295	4.090	1.201	Y	🟡	🟡	Y	2.59 E-1	21.659	21.620	22.639	-0.037	Y	🟡
	" signal transduction histidine kinase, glucose-6-phosphate specific [Methylobacillus flagellatus KT]637937714 YP_544923 """															
MFLA0815		3.753	3.453	4.611	0.325	Y	🟡	🟡	Y	2.08 E-1	23.501	23.402	24.452	0.099	Y	🟡
	" two component transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637937715 YP_544924 """															

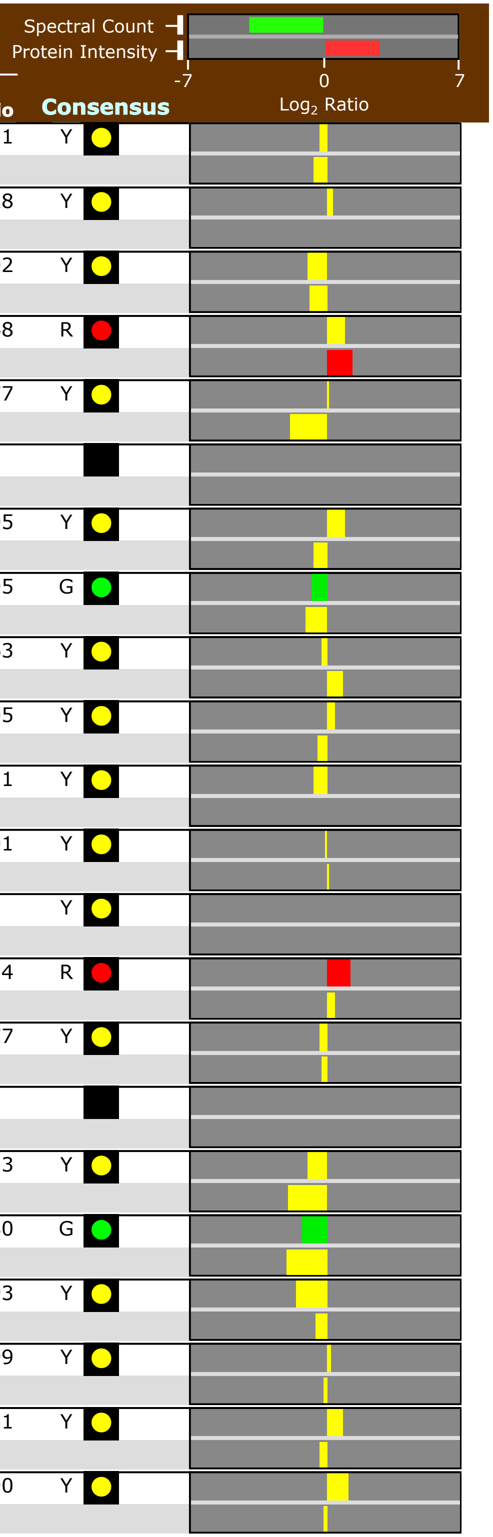


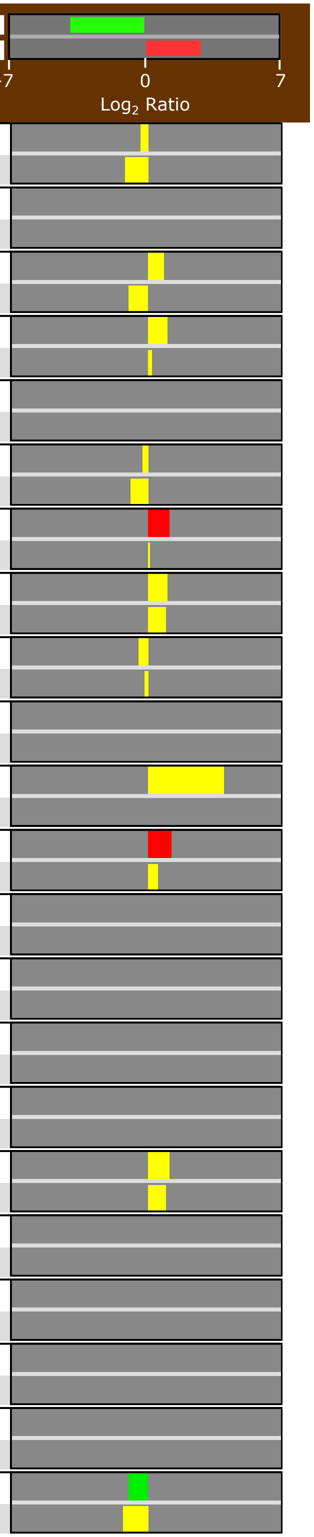
	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	Log$_2$ Ratio
MFLA0816	1.31 E-6	6.810	7.423	8.149	-0.641	G 🟢 🟡 Y	3.67 E-2	26.339	27.324	27.914	-1.168	G 🟢	
	" two component transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637937716 YP_544925 """												
MFLA0817	1.34 E-6	5.590	6.305	6.992	-0.909	G 🟢 🟡 Y	7.67 E-2	24.820	25.809	26.398	-1.867	G 🟢	
	" signal transduction histidine kinase, glucose-6-phosphate specific [Methylobacillus flagellatus KT]637937717 YP_544926 """												
MFLA0818		3.930		3.930		Y 🟡 🟡 Y		21.641		21.641		Y 🟡	
	" TonB-dependent receptor, plug [Methylobacillus flagellatus KT]637937718 YP_544927 """												
MFLA0819		6.700	6.938	7.824	-0.306	Y 🟡 🟡 Y	1.2 E-1	27.101	26.613	27.877	0.384	Y 🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637937719 YP_544928												
MFLA0820		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0964	*hypothetical protein [Methylobacillus flagellatus KT]637937720 YP_544929*												
MFLA0821		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0965	*" glycoside hydrolase, family 24 [Methylobacillus flagellatus KT]637937721 YP_544930 """*												
MFLA0822		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0966	*hypothetical protein [Methylobacillus flagellatus KT]637937722 YP_544931*												
MFLA0823		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0967	*hypothetical protein [Methylobacillus flagellatus KT]637937723 YP_544932*												
MFLA0824		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0968	*hypothetical protein [Methylobacillus flagellatus KT]637937724 YP_544933*												
MFLA0825		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0969	*hypothetical protein [Methylobacillus flagellatus KT]637937725 YP_544934*												
MFLA0826		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0970	*hypothetical protein [Methylobacillus flagellatus KT]637937726 YP_544935*												
MFLA0827		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0971	*hypothetical protein [Methylobacillus flagellatus KT]637937727 YP_544936*												
MFLA0828		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0972	*hypothetical protein [Methylobacillus flagellatus KT]637937728 YP_544937*												
MFLA0829		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0973	*hypothetical protein [Methylobacillus flagellatus KT]637937729 YP_544938*												
MFLA0830		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0974	*hypothetical protein [Methylobacillus flagellatus KT]637937730 YP_544939*												
MFLA0831		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0975	*bacteriophage replication gene A [Methylobacillus flagellatus KT]637937731 YP_544940*												
MFLA0832		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0976	*hypothetical protein [Methylobacillus flagellatus KT]637937732 YP_544941*												
MFLA0833		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0977	*TonB-dependent receptor [Methylobacillus flagellatus KT]637937733 YP_544942*												
MFLA0834		5.358	5.672	6.523	-0.150	Y 🟡 🟡 Y	1.06 E-1	22.981	23.887	24.504	-0.722	Y 🟡	
MFLA0978	*DNA mismatch repair protein MutS [Methylobacillus flagellatus KT]637937734 YP_544943*												
MFLA0835		0.000	0.000			■ ■		0.000	0.000			■	
MFLA0979	*hypothetical protein [Methylobacillus flagellatus KT]637937735 YP_544944*												
MFLA0836		7.008	7.649	8.364	-0.765	Y 🟡 🟡 Y	2.87 E-2	25.999	27.407	27.868	-1.905	Y 🟡	
MFLA0980	*fkbp-type peptidyl-prolyl cis-trans isomerase [Methylobacillus flagellatus KT]637937736 YP_544945*												
MFLA0837		4.295	4.877	5.615	-0.667	Y 🟡 🟡 Y	4.29 E-2	22.209	24.089	24.436	-1.756	Y 🟡	
MFLA0981	*alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen [Methylobacillus flagellatus KT]637937737 YP_544946*												

	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA0838		2.843	3.429	4.165	1.045	Y	🟡	🟡	Y	1.93 E-1	21.678	22.212	22.970	0.948	Y	🟡
MFLA0982	*Cupin 4 [Methylobacillus flagellatus KT]637937738 YP_544947*															
MFLA0839		3.364	1.710	3.762	1.690	Y	🟡	🟡	Y	8.99 E-2	20.701	19.954	21.376	0.650	Y	🟡
MFLA0983	*NolW-like protein [Methylobacillus flagellatus KT]637937739 YP_544948*															
MFLA0840		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA0984	*Lip [Methylobacillus flagellatus KT]637937740 YP_544949*															
MFLA0841		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA0985	*beta-lactamase-like protein [Methylobacillus flagellatus KT]637937741 YP_544950*															
MFLA0842	5.96 E-9	5.838	6.759	7.371	-1.010	G	🟢	🟢	G	1.69 E-3	25.834	27.318	27.759	-1.484	G	🟢
MFLA0986	*uncharacterized lipoprotein [Methylobacillus flagellatus KT]637937742 YP_544951*															
MFLA0843		7.384	7.427	8.405	-0.133	Y	🟡	🟡	Y	1.82 E-2	26.731	27.531	28.185	-0.788	Y	🟡
MFLA0987	*dihydrodipicolinate synthase [Methylobacillus flagellatus KT]637937743 YP_544952*															
MFLA0844		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA0988	*hypothetical protein [Methylobacillus flagellatus KT]637937744 YP_544953*															
MFLA0845		3.960	1.807	4.253	1.056	Y	🟡	🟡	Y	9.62 E-2	22.202	20.442	22.575	0.733	Y	🟡
MFLA0989	*protein of unknown function UPF0227 [Methylobacillus flagellatus KT]637937745 YP_544954*															
MFLA0846		4.754	3.957	5.410	0.473	Y	🟡	🟡	Y	1.32 E-1	23.378	22.416	23.976	0.849	Y	🟡
MFLA0990	*" HAD-superfamily subfamily IIA hydrolase, hypothetical 2 [Methylobacillus flagellatus KT]637937746 YP_544955 """*															
MFLA0847	1.04 E-5	5.567	4.212	6.043	1.355	R	🔴	🟡	Y	2.16 E-1	23.492	23.332	24.414	0.304	R	🔴
MFLA0991	*hypothetical protein [Methylobacillus flagellatus KT]637937747 YP_544956*															
MFLA0848		2.843	1.184	3.239	2.669	Y	🟡	🟡	Y	1.48 E-1	19.754	21.935	22.222	-0.894	Y	🟡
MFLA0992	*hypothetical protein [Methylobacillus flagellatus KT]637937748 YP_544957*															
MFLA0849		6.517		6.517		Y	🟡	🟡	Y		23.788		23.788		Y	🟡
MFLA0993	*hypothetical protein [Methylobacillus flagellatus KT]637937749 YP_544958*															
MFLA0850		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA0994	*" electron transport complex, RnfABCDGE type, B subunit [Methylobacillus flagellatus KT]637937750 YP_544959 """*															
MFLA0851		3.093	0.585	3.327	1.486	Y	🟡	🟡	Y	1.58 E-1	20.478	18.388	20.782	0.733	Y	🟡
MFLA0995	*endonuclease III [Methylobacillus flagellatus KT]637937751 YP_544960*															
MFLA0852		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA0996	*hypothetical protein [Methylobacillus flagellatus KT]637937752 YP_544961*															
MFLA0853	1.26 E-10	4.993	6.355	6.829	-1.435	G	🟢	🟡	Y	1.13 E-2	24.011	25.144	25.686	-1.145	G	🟢
MFLA0997	*Phosphomethylpyrimidine kinase [Methylobacillus flagellatus KT]637937753 YP_544962*															
MFLA0854		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA0998	*hypothetical protein [Methylobacillus flagellatus KT]637937754 YP_544963*															
MFLA0855		4.324	4.511	5.421	-0.200	Y	🟡	🟡	Y	6.58 E-2	22.536	23.065	23.824	-0.615	Y	🟡
MFLA0999	*L-aspartate oxidase [Methylobacillus flagellatus KT]637937755 YP_544964*															
MFLA0856		4.736	3.710	5.312	1.058	Y	🟡	🟡	Y	1.08 E-1	23.667	22.888	24.330	0.783	Y	🟡
MFLA1000	*sigma-24 (FecI-like) [Methylobacillus flagellatus KT]637937756 YP_544965*															
MFLA0857		1.813		1.813		Y	🟡	🟡	Y		21.206		21.206		Y	🟡
MFLA1001	*hypothetical protein [Methylobacillus flagellatus KT]637937757 YP_544966*															
MFLA0858		4.557	4.895	5.736	-0.391	Y	🟡	🟡	Y	8.38 E-2	22.610	23.019	23.829	-0.480	Y	🟡
MFLA1002	*" sigma E regulatory protein, MucB/RseB [Methylobacillus flagellatus KT]637937758 YP_544967 """*															
MFLA0859	0	9.864	9.089	10.528	0.780	R	🔴	🟡	Y	6.37 E-2	28.280	28.628	29.464	-0.373	Y	🟡
MFLA1003	*" Peptidase S1C, Do [Methylobacillus flagellatus KT]637937759 YP_544968 """*															



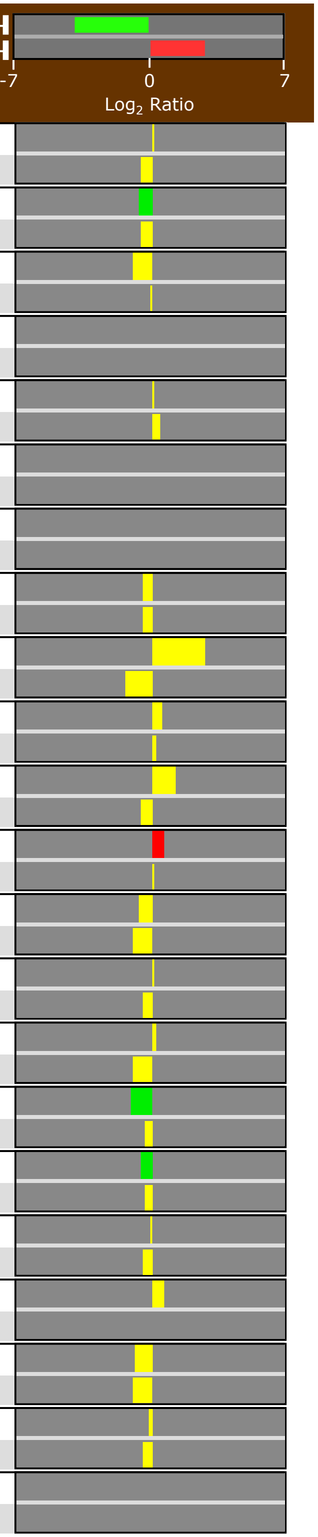
ORF	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
	q-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA0860		6.234	6.589	7.423	-0.410	Y	🟡	🟡	Y	1.35 E-1	25.126	25.600	26.382	-0.731	Y	🟡
MFLA1004	*Small GTP-binding protein domain [Methylobacillus flagellatus KT]637937760 YP_544969*															
MFLA0861		5.276	4.648	5.996	0.318	Y	🟡	🟡	Y	1.95 E-1	24.837	24.449	25.656	-0.028	Y	🟡
MFLA1005	*" Peptidase S26A, signal peptidase I [Methylobacillus flagellatus KT]637937761 YP_544970 """*															
MFLA0862		3.648	4.395	5.069	-0.992	Y	🟡	🟡	Y	9.6 E-2	22.752	23.391	24.107	-0.902	Y	🟡
MFLA1006	*putative transmembrane protein [Methylobacillus flagellatus KT]637937762 YP_544971*															
MFLA0863		3.915	2.966	4.517	0.947	Y	🟡	🔴	R	9.95 E-3	23.135	21.780	23.611	1.348	R	🔴
MFLA1007	*Ribonuclease III [Methylobacillus flagellatus KT]637937763 YP_544972*															
MFLA0864		5.352	5.117	6.239	0.132	Y	🟡	🟡	Y	1.89 E-1	23.402	23.864	24.651	-1.877	Y	🟡
MFLA1008	*GTP-binding protein Era [Methylobacillus flagellatus KT]637937764 YP_544973*															
MFLA0865		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1009	*putative lipoprotein [Methylobacillus flagellatus KT]637937765 YP_544974*															
MFLA0866		1.843	2.095	2.974	0.877	Y	🟡	🟡	Y	1.53 E-1	20.354	22.292	22.627	-0.705	Y	🟡
MFLA1010	*DNA repair protein RecO [Methylobacillus flagellatus KT]637937766 YP_544975*															
MFLA0867	1.77 E-5	5.926	6.699	7.364	-0.776	G	🟢	🟡	Y	1.77 E-2	25.985	27.090	27.641	-1.095	G	🟢
MFLA1011	*pyridoxal phosphate biosynthetic protein PdxJ [Methylobacillus flagellatus KT]637937767 YP_544976*															
MFLA0868		2.543	1.668	3.171	-0.340	Y	🟡	🟡	Y	3.76 E-2	21.173	19.409	21.545	0.763	Y	🟡
MFLA1012	*phosphopantethiene--protein transferase domain [Methylobacillus flagellatus KT]637937768 YP_544977*															
MFLA0869		4.046	3.729	4.896	0.360	Y	🟡	🟡	Y	1.15 E-1	21.764	22.174	22.984	-0.505	Y	🟡
MFLA1013	*hypothetical protein [Methylobacillus flagellatus KT]637937769 YP_544978*															
MFLA0870		0.813	2.505	2.894	-0.682	Y	🟡	🟡	Y	2.39 E-1	19.387	20.550	21.083	0.011	Y	🟡
MFLA1014	*UBA/THIF-type NAD/FAD binding fold [Methylobacillus flagellatus KT]637937770 YP_544979*															
MFLA0871	8.51 E-2	5.554	5.568	6.561	-0.057	Y	🟡	🟡	Y	2.09 E-1	24.745	24.579	25.664	0.101	Y	🟡
MFLA1015	*hypothetical protein [Methylobacillus flagellatus KT]637937771 YP_544980*															
MFLA0872		3.580		3.580		Y	🟡	🟡	Y		23.886		23.886		Y	🟡
MFLA1016	*TonB-dependent receptor [Methylobacillus flagellatus KT]637937772 YP_544981*															
MFLA0873	0	9.000	7.778	9.515	1.218	R	🔴	🟡	Y	4.58 E-3	28.596	28.163	29.396	0.434	R	🔴
MFLA1017	*heat shock protein Hsp90 [Methylobacillus flagellatus KT]637937773 YP_544982*															
MFLA0874	0	9.314	9.739	10.542	-0.424	Y	🟡	🟡	Y	1.7 E-1	30.028	30.236	31.136	-0.277	Y	🟡
MFLA1018	*ribosomal protein S4 [Methylobacillus flagellatus KT]637937774 YP_544983*															
MFLA0875		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1019	*hypothetical protein [Methylobacillus flagellatus KT]637937775 YP_544984*															
MFLA0876		2.328	4.305	4.631	-0.957	Y	🟡	🟡	Y	2.09 E-2	21.895	24.929	25.095	-2.033	Y	🟡
MFLA1020	*TonB-like protein [Methylobacillus flagellatus KT]637937776 YP_544985*															
MFLA0877	1.83 E-13	5.703	6.972	7.473	-1.278	G	🟢	🟡	Y	1.06 E-2	24.619	26.508	26.852	-2.080	G	🟢
MFLA1021	*MotA/TolQ/ExbB proton channel [Methylobacillus flagellatus KT]637937777 YP_544986*															
MFLA0878		4.199	4.594	5.410	-1.635	Y	🟡	🟡	Y	2.6 E-2	24.043	23.635	24.853	-0.593	Y	🟡
MFLA1022	*Biopolymer transport protein ExbD/TolR [Methylobacillus flagellatus KT]637937778 YP_544987*															
MFLA0879		7.340	7.108	8.229	0.152	Y	🟡	🟡	Y	2.24 E-1	25.989	26.097	27.044	-0.199	Y	🟡
MFLA1023	*Glycogen/starch/alpha-glucan phosphorylase [Methylobacillus flagellatus KT]637937779 YP_544988*															
MFLA0880		5.050	4.223	5.695	0.797	Y	🟡	🟡	Y	2.38 E-1	25.208	25.340	26.276	-0.351	Y	🟡
MFLA1024	*hypothetical protein [Methylobacillus flagellatus KT]637937780 YP_544989*															
MFLA0881		4.253	3.102	4.789	1.079	Y	🟡	🟡	Y	2.63 E-1	22.053	21.997	23.026	-0.190	Y	🟡
MFLA1025	*protein of unknown function DUF1234 [Methylobacillus flagellatus KT]637937781 YP_544990*															



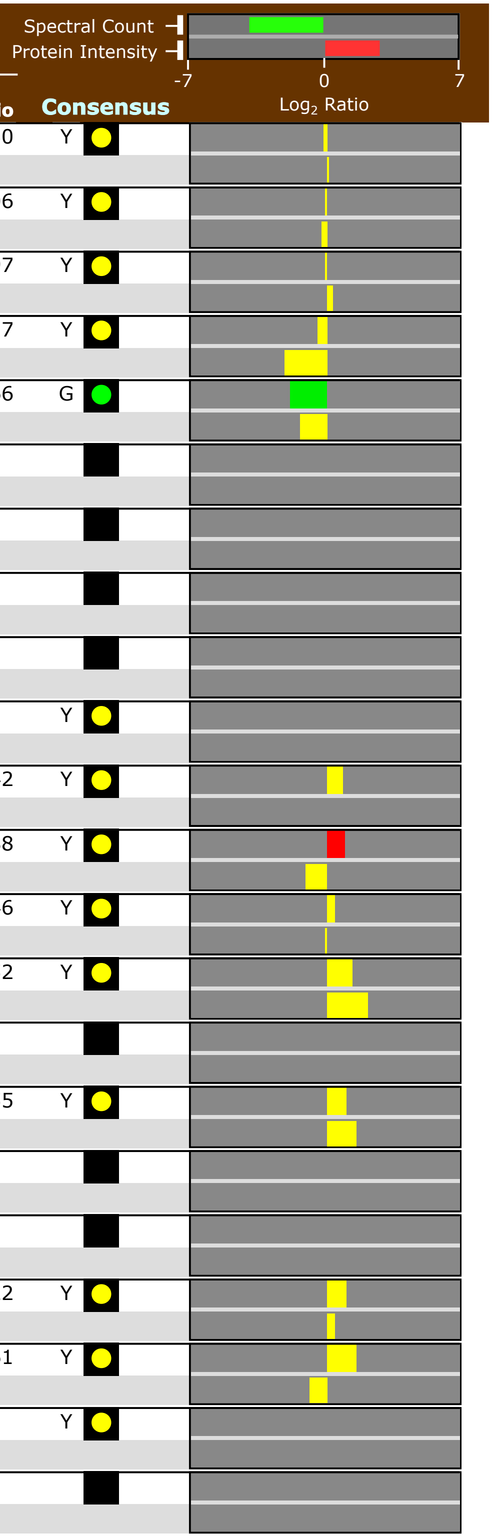


ORF	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio		Regulation			*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA0882		4.397	4.732	5.574	-0.376	Y	🟡	🟡	Y	1 E-1	21.488	22.507	23.086	-1.205	Y	🟡
MFLA1026	*Glyoxalase/bleomycin resistance protein/dioxygenase [Methylobacillus flagellatus KT]637937782 YP_544991*															
MFLA0883		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1027	*small multidrug resistance protein [Methylobacillus flagellatus KT]637937783 YP_544992*															
MFLA0884		3.819	2.627	4.343	0.833	Y	🟡	🟡	Y	7.7 E-2	21.568	22.304	22.982	-1.027	Y	🟡
MFLA1028	*hypothetical protein [Methylobacillus flagellatus KT]637937784 YP_544993*															
MFLA0885		3.988	2.897	4.543	0.959	Y	🟡	🟡	Y	1.68 E-1	21.635	21.411	22.527	0.172	Y	🟡
MFLA1029	*Endonuclease/exonuclease/phosphatase [Methylobacillus flagellatus KT]637937785 YP_544994*															
MFLA0886			1.322	1.322		Y	🟡	🟡	Y			20.114	20.114		Y	🟡
MFLA1030	*diguanylate cyclase (GGDEF domain) [Methylobacillus flagellatus KT]637937786 YP_544995*															
MFLA0887	1.03 E-4	8.393	8.729	9.571	-0.336	Y	🟡	🟡	Y	1.05 E-2	27.136	28.024	28.647	-0.882	Y	🟡
MFLA1031	*phosphoribosylformylglycinamidine synthase [Methylobacillus flagellatus KT]637937787 YP_544996*															
MFLA0888	8.21 E-5	5.316	4.194	5.861	1.087	R	🔴	🟡	Y	1.96 E-1	23.557	23.430	24.495	0.144	R	🔴
MFLA1032	*Ankyrin [Methylobacillus flagellatus KT]637937788 YP_544997*															
MFLA0889		4.845	3.441	5.307	1.029	Y	🟡	🟡	Y	8.26 E-2	24.024	23.007	24.603	0.910	Y	🟡
MFLA1033	*" L-sorbosone dehydrogenase, putative [Methylobacillus flagellatus KT]637937789 YP_544998 """*															
MFLA0890		6.029	6.466	7.264	-0.513	Y	🟡	🟡	Y	1.88 E-1	25.657	25.855	26.759	-0.231	Y	🟡
MFLA1034	*hypothetical protein [Methylobacillus flagellatus KT]637937790 YP_544999*															
MFLA0891		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1035	*Twin-arginine translocation pathway signal [Methylobacillus flagellatus KT]637937791 YP_545000*															
MFLA0892		5.081	1.184	5.174	3.880	Y	🟡	🟡	Y	2.76 E-1	22.666	22.678	23.672	-0.048	Y	🟡
MFLA1036	*hypothetical protein [Methylobacillus flagellatus KT]637937792 YP_545001*															
MFLA0893	2.23 E-8	6.169	4.993	6.697	1.158	R	🔴	🟡	Y	1.04 E-1	24.125	23.704	24.930	0.517	R	🔴
MFLA1037	*Fructose-6-phosphate phosphoketolase [Methylobacillus flagellatus KT]637937793 YP_545002*															
MFLA0894		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1038	*hypothetical protein [Methylobacillus flagellatus KT]637937794 YP_545003*															
MFLA0895		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1039	*hypothetical protein [Methylobacillus flagellatus KT]637937795 YP_545004*															
MFLA0896		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1040	*Rhs element Vgr protein [Methylobacillus flagellatus KT]637937796 YP_545005*															
MFLA0897		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1041	*hypothetical protein [Methylobacillus flagellatus KT]637937797 YP_545006*															
MFLA0898		2.691	2.659	3.675	1.064	Y	🟡	🟡	Y	4.7 E-2	21.428	21.551	22.491	0.887	Y	🟡
MFLA1042	*protein of unknown function DUF455 [Methylobacillus flagellatus KT]637937798 YP_545007*															
MFLA0899		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1043	*" sigma54 specific transcriptional regulator with GAF sensor, Fis family [Methylobacillus flagellatus KT]637937799 YP_545008 """*															
MFLA0900		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1044	*metallophosphoesterase [Methylobacillus flagellatus KT]637937800 YP_545009*															
MFLA0901		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1045	*" 4Fe-4S ferredoxin, iron-sulfur binding [Methylobacillus flagellatus KT]637937801 YP_545010 """*															
MFLA0902		0.000	0.000				⬛	⬛			0.000	0.000				⬛
MFLA1046	*protein of unknown function DUF498 [Methylobacillus flagellatus KT]637937802 YP_545011*															
MFLA0903	5.79 E-12	6.326	7.171	7.810	-0.988	G	🟢	🟡	Y	1.33 E-1	25.439	26.040	26.771	-1.308	G	🟢
MFLA1047	*" aminotransferase, class I and II [Methylobacillus flagellatus KT]637937803 YP_545012 """*															

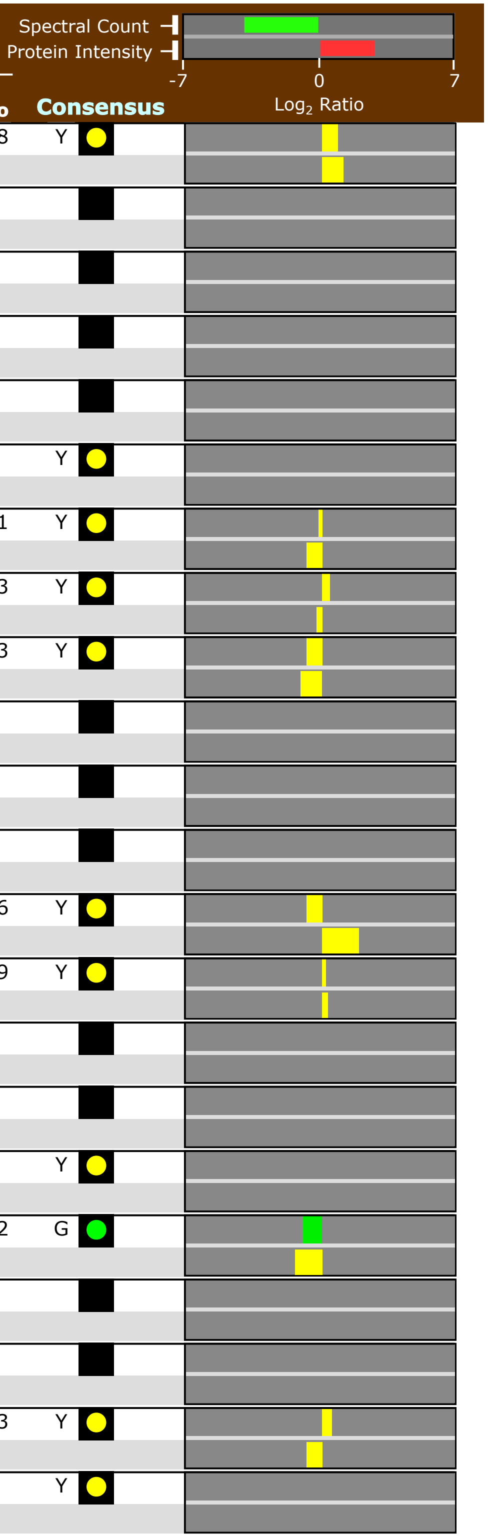
	AM/OH *M Flagellatus* Spectral Count							AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation		*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA0904	1.15 E-2	7.439	7.335	8.388	0.139	Y 🟡	🟡 Y	2.13 E-2	26.378	26.968	27.703	-0.583	Y 🟡
MFLA1048	*Homoserine dehydrogenase [Methylobacillus flagellatus KT]637937804 YP_545013*												
MFLA0905	8.35 E-9	6.731	7.420	8.116	-0.723	G 🟢	🟡 Y	7.33 E-2	26.819	27.356	28.112	-0.603	G 🟢
MFLA1049	*threonine synthase [Methylobacillus flagellatus KT]637937805 YP_545014*												
MFLA0906		4.258	4.783	5.544	-1.032	Y 🟡	🟡 Y	1.45 E-1	24.639	23.584	25.206	-0.101	Y 🟡
MFLA1050	*Thymidylate synthase [Methylobacillus flagellatus KT]637937806 YP_545015*												
MFLA0907			2.844	2.844		Y 🟡	🟡 Y			20.737	20.737		Y 🟡
MFLA1051	*diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) [Methylobacillus flagellatus KT]637937807 YP_545016*												
MFLA0908		3.692	3.826	4.761	0.092	Y 🟡	🟡 Y	1.06 E-1	22.330	21.986	23.168	0.413	Y 🟡
MFLA1052	*" Propeptide, PepSY amd peptidase M4 [Methylobacillus flagellatus KT]637937808 YP_545017 """*												
MFLA0909		0.000	0.000			■	■		0.000	0.000			■
MFLA1053	*hypothetical protein [Methylobacillus flagellatus KT]637937809 YP_545018*												
MFLA0910		1.843		1.843		Y 🟡	🟡 Y		19.059		19.059		Y 🟡
MFLA1054	*hypothetical protein [Methylobacillus flagellatus KT]637937810 YP_545019*												
MFLA0911	5.77 E-2	5.100	5.547	6.341	-0.457	Y 🟡	🟡 Y	1.92 E-1	23.797	24.052	24.930	-0.477	Y 🟡
MFLA1055	*" two component, sigma54 specific, transcriptional regulator, Fis family [Methylobacillus flagellatus KT]637937811 YP_545020 """*												
MFLA0912		2.691	0.000	2.898	2.691	Y 🟡	🟡 Y		19.522	20.961	21.414	-1.439	Y 🟡
MFLA1056	*hypothetical protein [Methylobacillus flagellatus KT]637937812 YP_545021*												
MFLA0913		4.456	3.962	5.230	0.527	Y 🟡	🟡 Y	2.18 E-1	22.461	22.315	23.389	0.216	Y 🟡
MFLA1057	*periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637937813 YP_545022*												
MFLA0914		1.521	0.346	2.050	1.174	Y 🟡	🟡 Y		18.997	19.551	20.300	-0.554	Y 🟡
MFLA1058	*Dihydrofolate reductase [Methylobacillus flagellatus KT]637937814 YP_545023*												
MFLA0915	4.51 E-6	7.631	7.053	8.371	0.578	R 🔴	🟡 Y	2.17 E-1	26.444	26.357	27.401	0.107	R 🔴
MFLA1059	*Lysine decarboxylase [Methylobacillus flagellatus KT]637937815 YP_545024*												
MFLA0916		4.039	4.661	5.384	-0.725	Y 🟡	🟡 Y	4.87 E-2	23.840	24.949	25.498	-1.027	Y 🟡
MFLA1060	*Deoxycytidine triphosphate deaminase [Methylobacillus flagellatus KT]637937816 YP_545025*												
MFLA0917		9.070	8.922	9.998	0.106	Y 🟡	🟡 Y	1.29 E-2	28.648	29.189	29.944	-0.537	Y 🟡
MFLA1061	*glucose-6-phosphate 1-dehydrogenase [Methylobacillus flagellatus KT]637937817 YP_545026*												
MFLA0918		9.861	9.496	10.690	0.173	Y 🟡	🟡 Y	6.21 E-2	28.765	29.539	30.203	-0.979	Y 🟡
MFLA1062	*6-phosphogluconate dehydrogenase related protein [Methylobacillus flagellatus KT]637937818 YP_545027*												
MFLA0919	2.96 E-7	5.280	6.391	6.940	-1.109	G 🟢	🟡 Y	9.7 E-2	25.779	26.204	27.007	-0.387	G 🟢
MFLA1063	*6-phosphogluconolactonase [Methylobacillus flagellatus KT]637937819 YP_545028*												
MFLA0920	6.62 E-3	4.552	5.214	5.921	-0.636	G 🟢	🟡 Y	7.99 E-2	24.099	24.475	25.299	-0.365	G 🟢
MFLA1064	*protein of unknown function DUF59 [Methylobacillus flagellatus KT]637937820 YP_545029*												
MFLA0921		6.742	6.719	7.731	-0.058	Y 🟡	🟡 Y	4.62 E-2	25.730	26.246	27.011	-0.494	Y 🟡
MFLA1065	*methionyl-tRNA synthetase [Methylobacillus flagellatus KT]637937821 YP_545030*												
MFLA0922		6.621	5.715	7.238	0.583	Y 🟡	🟡 Y	2.22 E-1	25.765	25.851	26.809	-0.050	Y 🟡
MFLA1066	*Competence protein ComEA helix-hairpin-helix region [Methylobacillus flagellatus KT]637937822 YP_545031*												
MFLA0923		3.876	4.790	5.405	-0.937	Y 🟡	🟡 Y	1.66 E-2	23.537	24.487	25.088	-0.979	Y 🟡
MFLA1067	*orotidine 5'-phosphate decarboxylase [Methylobacillus flagellatus KT]637937823 YP_545032*												
MFLA0924	9.98 E-2	6.351	6.597	7.479	-0.247	Y 🟡	🟡 Y	5.72 E-2	24.636	25.110	25.892	-0.490	Y 🟡
MFLA1068	*Tetratricopeptide region [Methylobacillus flagellatus KT]637937824 YP_545033*												
MFLA0925		0.000	0.000			■	■		0.000	0.000			■
MFLA1069	*hypothetical protein [Methylobacillus flagellatus KT]637937825 YP_545034*												



ORF	AM/OH *M Flagellatus* Spectral Count					Regulation				AM/OH *M Flagellatus* Protein Intensity					Consensus	
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio					*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		
MFLA0926		1.813	3.015	3.536	-0.152	Y	🟡	🟡	Y	2.72 E-1	22.494	23.470	24.063	0.130	Y	🟡
MFLA1070	*" integration host factor, beta subunit [Methylobacillus flagellatus KT]637937826 YP_545035 """*															
MFLA0927		10.718	10.805	11.762	-0.094	Y	🟡	🟡	Y	6.35 E-2	30.593	30.888	31.748	-0.306	Y	🟡
MFLA1071	*ribosomal protein S1 [Methylobacillus flagellatus KT]637937827 YP_545036*															
MFLA0928		4.915	4.972	5.944	-0.059	Y	🟡	🟡	Y	6.87 E-2	22.759	22.446	23.611	0.297	Y	🟡
MFLA1072	*cytidylate kinase [Methylobacillus flagellatus KT]637937828 YP_545037*															
MFLA0929		4.184	4.548	5.378	-0.461	Y	🟡	🟡	Y	2.7 E-2	21.214	23.169	23.500	-2.217	Y	🟡
MFLA1073	*3-phosphoshikimate 1-carboxyvinyltransferase [Methylobacillus flagellatus KT]637937829 YP_545038*															
MFLA0930	1.43 E-9	4.330	5.992	6.388	-1.918	G	🟢	🟡	Y	1.66 E-2	23.122	24.510	24.976	-1.366	G	🟢
MFLA1074	*Prephenate dehydrogenase [Methylobacillus flagellatus KT]637937830 YP_545039*															
MFLA0931		0.000	0.000				■	■			0.000	0.000				■
MFLA1075	*Arginyltransferase [Methylobacillus flagellatus KT]637937831 YP_545040*															
MFLA0932		0.000	0.000				■	■			0.000	0.000				■
MFLA1076	*Leucyltransferase [Methylobacillus flagellatus KT]637937832 YP_545041*															
MFLA0933		0.000	0.000				■	■			0.000	0.000				■
MFLA1077	*hypothetical protein [Methylobacillus flagellatus KT]637937833 YP_545042*															
MFLA0934		0.000	0.000				■	■			0.000	0.000				■
MFLA1078	*hypothetical protein [Methylobacillus flagellatus KT]637937834 YP_545043*															
MFLA0935		1.843		1.843		Y	🟡	🟡	Y		19.767		19.767		Y	🟡
MFLA1079	*outer membrane efflux protein [Methylobacillus flagellatus KT]637937835 YP_545044*															
MFLA0936		2.843	3.056	3.953	0.792	Y	🟡	🟡	Y	2.7 E-1	21.559	22.544	23.134	0.042	Y	🟡
MFLA1080	*Twin-arginine translocation pathway signal [Methylobacillus flagellatus KT]637937836 YP_545045*															
MFLA0937	3.18 E-9	7.135	6.243	7.757	0.887	R	🔴	🟡	Y	6.09 E-2	27.047	27.884	28.525	-1.088	Y	🟡
MFLA1081	*Heavy metal transport/detoxification protein [Methylobacillus flagellatus KT]637937837 YP_545046*															
MFLA0938	1.98 E-2	5.397	4.938	6.186	0.422	Y	🟡	🟡	Y	2.05 E-1	23.922	24.067	24.997	-0.146	Y	🟡
MFLA1082	*Heavy metal translocating P-type ATPase [Methylobacillus flagellatus KT]637937838 YP_545047*															
MFLA0939		1.521	1.184	2.362	1.347	Y	🟡	🟡	Y	5.5 E-2	19.004	18.135	19.634	2.052	Y	🟡
MFLA1083	*Radical SAM [Methylobacillus flagellatus KT]637937839 YP_545048*															
MFLA0940		0.000	0.000				■	■			0.000	0.000				■
MFLA1084	*hypothetical protein [Methylobacillus flagellatus KT]637937840 YP_545049*															
MFLA0941		2.691	1.668	3.268	1.022	Y	🟡	🟡	Y		20.664	19.209	21.113	1.455	Y	🟡
MFLA1085	*GCN5-related N-acetyltransferase [Methylobacillus flagellatus KT]637937841 YP_545050*															
MFLA0942		0.000	0.000				■	■			0.000	0.000				■
MFLA1086	*" cytochrome d ubiquinol oxidase, subunit II [Methylobacillus flagellatus KT]637937842 YP_545051 """*															
MFLA0943		0.000	0.000				■	■			0.000	0.000				■
MFLA1087	*" cytochrome bd ubiquinol oxidase, subunit I [Methylobacillus flagellatus KT]637937843 YP_545052 """*															
MFLA0944		2.328	1.322	2.911	1.006	Y	🟡	🟡	Y		21.059	20.637	21.863	0.422	Y	🟡
MFLA1088	*response regulator receiver domain protein (CheY-like) [Methylobacillus flagellatus KT]637937844 YP_545053*															
MFLA0945		2.328	1.915	3.136	1.494	Y	🟡	🟡	Y	1.49 E-1	20.161	22.306	22.600	-0.861	Y	🟡
MFLA1089	*" two component transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637937845 YP_545054 """*															
MFLA0946		2.621		2.621		Y	🟡	🟡	Y		18.956		18.956		Y	🟡
MFLA1090	*hypothetical protein [Methylobacillus flagellatus KT]637937846 YP_545055*															
MFLA0947		0.000	0.000				■	■			0.000	0.000				■
MFLA1091	*protein of unknown function DUF1328 [Methylobacillus flagellatus KT]637937847 YP_545056*															

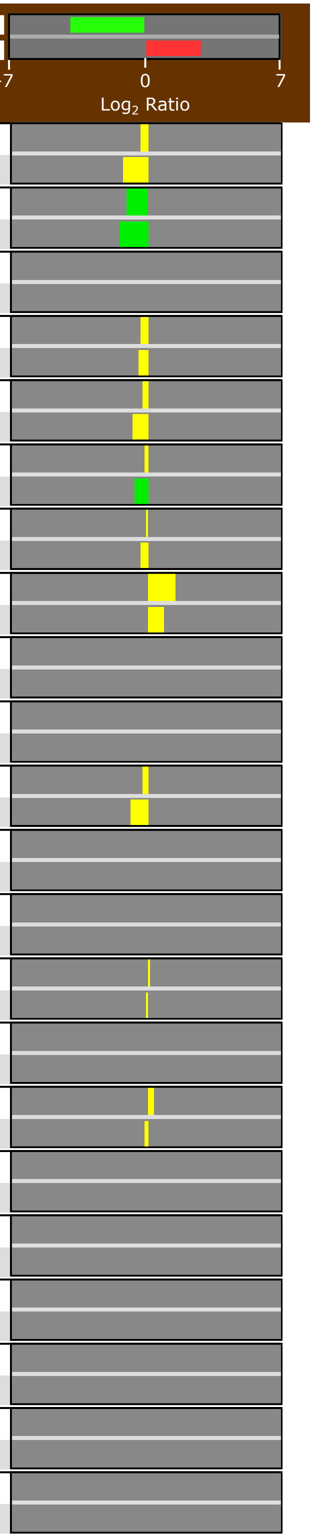


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**				**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**	
MFLA0948 MFLA1092		3.106	3.281	4.196	0.847	Y	●	●	Y	6.2 E-2	21.795	21.756	22.776	1.078	Y	●
	periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637937848 YP_545057															
MFLA0949 MFLA1093		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937849 YP_545058															
MFLA0950 MFLA1094		0.000	0.000				■	■			0.000	0.000				■
	transport-associated [Methylobacillus flagellatus KT]637937850 YP_545059															
MFLA0951 MFLA1095		0.000	0.000				■	■			0.000	0.000				■
	Lipocalin-like protein [Methylobacillus flagellatus KT]637937851 YP_545060															
MFLA0952 MFLA1096		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF188 [Methylobacillus flagellatus KT]637937852 YP_545061															
MFLA0953 MFLA1097			0.000	0.000		Y	●	●	Y			18.572	18.572		Y	●
	ATP-dependent DNA helicase RecQ [Methylobacillus flagellatus KT]637937853 YP_545062															
MFLA0954 MFLA1098		5.611	5.656	6.634	-0.249	Y	●	●	Y	2.11 E-1	24.002	24.274	25.144	-0.831	Y	●
	DEAD/DEAH box helicase-like protein [Methylobacillus flagellatus KT]637937854 YP_545063															
MFLA0955 MFLA1099		4.586	4.321	5.459	0.362	Y	●	●	Y	2.22 E-1	22.899	23.045	23.974	-0.283	Y	●
	" Pseudouridine synthase, Rsu [Methylobacillus flagellatus KT]637937855 YP_545064 """															
MFLA0956 MFLA1100		4.081	4.540	5.329	-0.810	Y	●	●	Y	6.15 E-2	23.021	23.827	24.479	-1.053	Y	●
	hypothetical protein [Methylobacillus flagellatus KT]637937856 YP_545065															
MFLA0957 MFLA1101		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637937857 YP_545066															
MFLA0958 MFLA1102		0.000	0.000				■	■			0.000	0.000				■
	alkylphosphonate utilization operon protein PhnA [Methylobacillus flagellatus KT]637937858 YP_545067															
MFLA0959 MFLA1103		0.000	0.000				■	■			0.000	0.000				■
	Secretion chaperone CsaA [Methylobacillus flagellatus KT]637937859 YP_545068															
MFLA0960 MFLA1104		0.813	1.585	2.250	-0.772	Y	●	●	Y		21.930	20.064	22.280	1.866	Y	●
	" Dihydroxyacetone kinase DhaK, subunit 1 [Methylobacillus flagellatus KT]637937860 YP_545069 """															
MFLA0961 MFLA1105	1.05 E-1	5.104	4.917	6.014	0.194	Y	●	●	Y	1.33 E-1	24.250	23.911	25.090	0.339	Y	●
	" Dihydroxyacetone kinase, subunit L [Methylobacillus flagellatus KT]637937861 YP_545070 """															
MFLA0962 MFLA1106		0.000	0.000				■	■			0.000	0.000				■
	ribose 5-phosphate isomerase [Methylobacillus flagellatus KT]637937862 YP_545071															
MFLA0963		0.000	0.000				■	■			0.000	0.000				■
	tRNA/rRNA methyltransferase (SpoU) [Methylobacillus flagellatus KT]637937863 YP_545072															
MFLA1107		1.521		1.521		Y	●	●	Y		19.697		19.697		Y	●
	tRNA/rRNA methyltransferase (SpoU) [Methylobacillus flagellatus KT]637938007 YP_545216															
MFLA1108	7.77 E-5	4.450	5.479	6.054	-0.979	G	●	●	Y	1.53 E-2	22.412	23.824	24.284	-1.392	G	●
	Hsp33 protein [Methylobacillus flagellatus KT]637938008 YP_545217															
MFLA1109		0.000	0.000				■	■			0.000	0.000				■
	Glutamate--tRNA ligase [Methylobacillus flagellatus KT]637938009 YP_545218															
MFLA1110		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938010 YP_545219															
MFLA1111		4.696	4.202	5.470	0.494	Y	●	●	Y	1.43 E-1	22.707	23.489	24.151	-0.773	Y	●
	twitching motility protein [Methylobacillus flagellatus KT]637938011 YP_545220															
MFLA1112		0.521		0.521		Y	●	●	Y		18.071		18.071		Y	●
	hypothetical protein [Methylobacillus flagellatus KT]637938012 YP_545221															

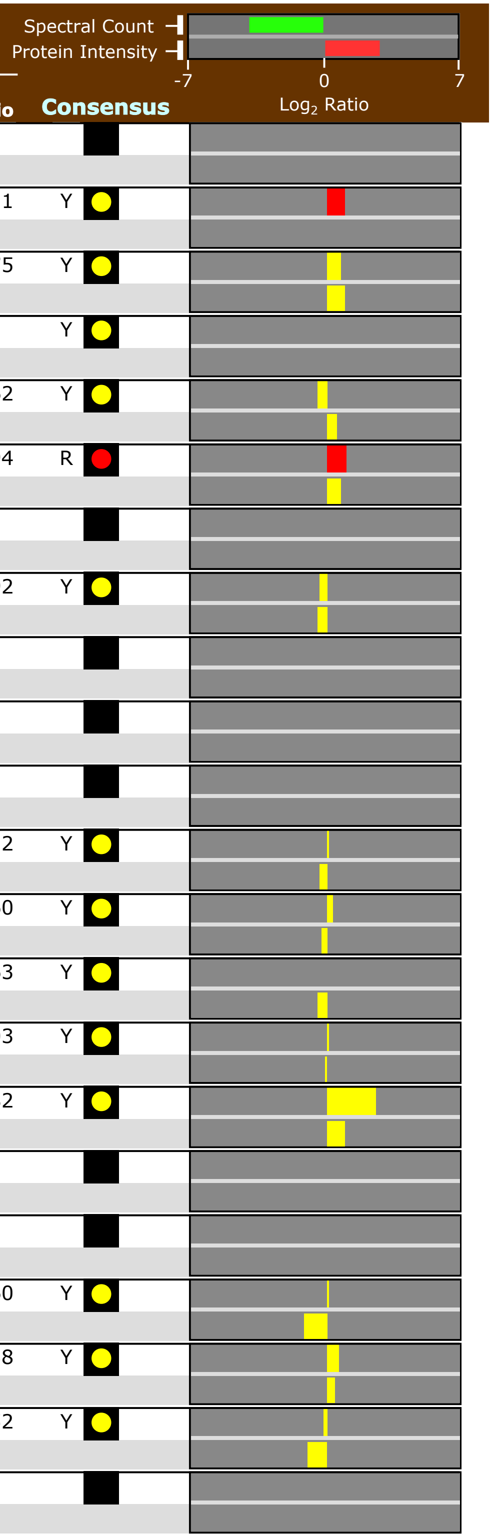


ORF	AM/OH *M Flagellatus* Spectral Count					Regulation				AM/OH *M Flagellatus* Protein Intensity					Consensus		
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio					*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio			
MFLA1113		5.046	5.060	6.053	-0.136	Y	🟡	🟡	Y	4.99 E-2	23.192	22.573	23.916	0.628	Y	🟡	*protein of unknown function DUF344 [Methylobacillus flagellatus KT]637938013 YP_545222*
MFLA1114			2.862	2.862		Y	🟡	🟡	Y			21.743	21.743		Y	🟡	*diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) [Methylobacillus flagellatus KT]637938014 YP_545223*
MFLA1115		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*protein of unknown function DUF454 [Methylobacillus flagellatus KT]637938015 YP_545224*
MFLA1116		4.492	4.710	5.605	-0.203	Y	🟡	🟡	Y	8.99 E-2	22.558	23.467	24.083	-0.781	Y	🟡	*2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Methylobacillus flagellatus KT]637938016 YP_545225*
MFLA1117		3.514	4.257	4.933	0.494	Y	🟡	🟡	Y	1.29 E-1	20.128	23.163	23.329	-1.721	Y	🟡	*" 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Methylobacillus flagellatus KT]637938017 YP_545226 """*
MFLA1118		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*Smr protein/MutS2 [Methylobacillus flagellatus KT]637938018 YP_545227*
MFLA1119		7.882	8.103	8.997	-0.246	Y	🟡	🟡	Y	9.55 E-2	27.872	28.013	28.944	-0.146	Y	🟡	*thioredoxin reductase [Methylobacillus flagellatus KT]637938019 YP_545228*
MFLA1120	7.75 E-4	7.156	6.629	7.916	0.527	R	🔴	🟡	Y	1.94 E-1	27.125	27.030	28.078	0.101	R	🔴	*Ferritin and Dps [Methylobacillus flagellatus KT]637938020 YP_545229*
MFLA1121		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*hypothetical protein [Methylobacillus flagellatus KT]637938021 YP_545230*
MFLA1122		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*hypothetical protein [Methylobacillus flagellatus KT]637938022 YP_545231*
MFLA1123		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*hypothetical protein [Methylobacillus flagellatus KT]637938023 YP_545232*
MFLA1124		4.914	4.638	5.782	0.152	Y	🟡	🟡	Y	4.59 E-2	22.928	23.711	24.372	-0.822	Y	🟡	*cell divisionFtsK/SpoIIIE [Methylobacillus flagellatus KT]637938024 YP_545233*
MFLA1125		4.836	4.363	5.619	0.494	Y	🟡	🟡	Y	1.17 E-1	23.881	23.252	24.601	0.455	Y	🟡	*outer membrane lipoprotein carrier protein LolA [Methylobacillus flagellatus KT]637938025 YP_545234*
MFLA1126		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*hypothetical protein [Methylobacillus flagellatus KT]637938026 YP_545235*
MFLA1127		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*hypothetical protein [Methylobacillus flagellatus KT]637938027 YP_545236*
MFLA1128	1.48 E-1	6.099	6.138	7.118	-0.035	Y	🟡	🟡	Y	1.25 E-1	24.126	24.534	25.345	-0.581	Y	🟡	*" AAA ATPase, central region [Methylobacillus flagellatus KT]637938028 YP_545237 """*
MFLA1129	3.43 E-3	7.048	7.425	8.248	-0.378	Y	🟡	🟡	Y	2.13 E-1	26.877	26.672	27.778	0.014	Y	🟡	*seryl-tRNA synthetase [Methylobacillus flagellatus KT]637938029 YP_545238*
MFLA1130		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*sodium/hydrogen exchanger [Methylobacillus flagellatus KT]637938030 YP_545239*
MFLA1131		4.126	3.315	4.777	0.697	Y	🟡	🟡	Y	1.71 E-1	22.560	21.872	23.257	0.236	Y	🟡	*" Lytic transglycosylase, catalytic [Methylobacillus flagellatus KT]637938031 YP_545240 """*
MFLA1132		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637938032 YP_545241*
MFLA1133		0.000	0.000				⬛	⬛			0.000	0.000				⬛	*" protein of unknown function DUF6, transmembrane [Methylobacillus flagellatus KT]637938034 YP_545242 """*
MFLA1134		0.521		0.521		Y	🟡	🟡	Y		15.420		15.420		Y	🟡	*conserved hypothetical chaperone protein [Methylobacillus flagellatus KT]637938035 YP_545243*

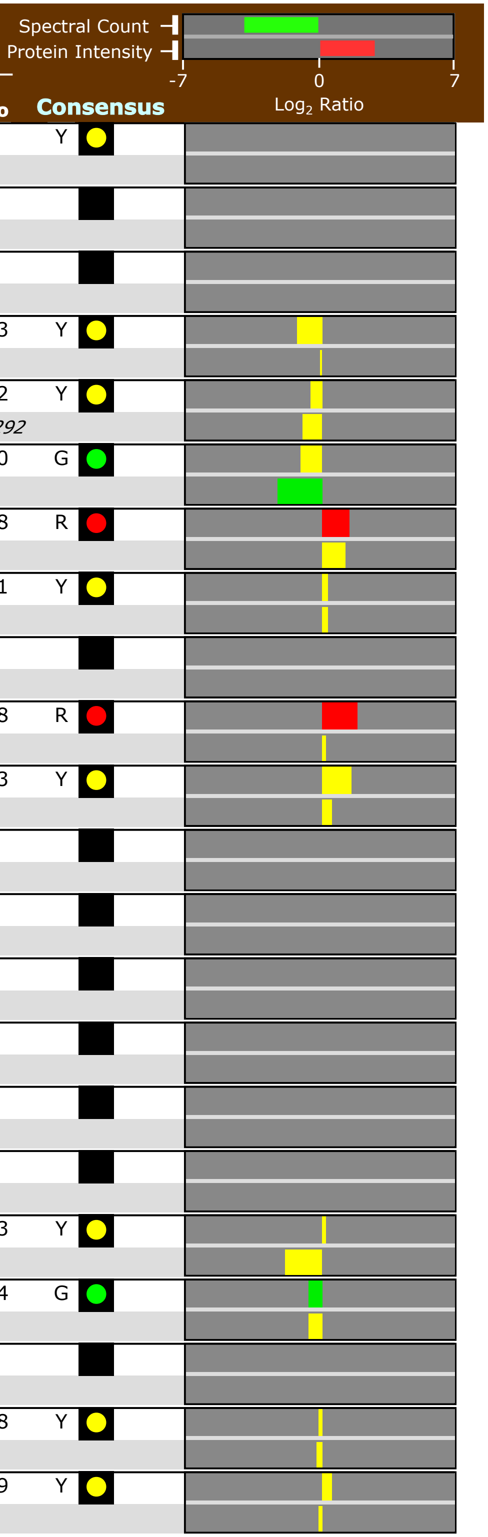
	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	**Consensus**
MFLA1135	2.05 E-5	7.366	7.750	8.570	-0.428	Y 🟡 🟡 Y	1.08 E-2	26.196	27.474	27.972	-1.320	Y 🟡
	ABC transporter related [Methylobacillus flagellatus KT]637938036 YP_545244											
MFLA1136	1.71 E-11	6.032	7.034	7.618	-1.090	G 🟢 🟢 G	4.58 E-3	26.579	28.075	28.513	-1.500	G 🟢
	nitroreductase [Methylobacillus flagellatus KT]637938037 YP_545245											
MFLA1137			2.267	2.267		Y 🟡 🟡 Y			22.383	22.383		Y 🟡
	GreA/GreB family elongation factor [Methylobacillus flagellatus KT]637938038 YP_545246											
MFLA1138	1.53 E-6	7.664	8.078	8.886	-0.381	Y 🟡 🟡 Y	7.57 E-2	26.799	27.331	28.089	-0.544	Y 🟡
	tryptophanyl-tRNA synthetase [Methylobacillus flagellatus KT]637938039 YP_545247											
MFLA1139	2.81 E-3	7.610	7.950	8.790	-0.342	Y 🟡 🟡 Y	2.65 E-2	27.250	27.982	28.662	-0.785	Y 🟡
	GMP synthase-like protein [Methylobacillus flagellatus KT]637938040 YP_545248											
MFLA1140	1.42 E-1	5.567	5.754	6.663	-0.187	Y 🟡 🟢 G	4.29 E-3	25.362	26.044	26.743	-0.682	G 🟢
	protein of unknown function DUF541 [Methylobacillus flagellatus KT]637938041 YP_545249											
MFLA1141	1.18 E-1	9.306	9.370	10.338	-0.064	Y 🟡 🟡 Y	8.99 E-2	29.517	29.849	30.693	-0.373	Y 🟡
	inosine-5'-monophosphate dehydrogenase [Methylobacillus flagellatus KT]637938042 YP_545250											
MFLA1142		4.039	2.852	4.565	1.370	Y 🟡 🟡 Y	1.99 E-2	22.634	21.792	23.274	0.837	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938043 YP_545251											
MFLA1143		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	protein of unknown function UPF0125 [Methylobacillus flagellatus KT]637938044 YP_545252											
MFLA1144			3.528	3.528		Y 🟡 🟡 Y			20.511	20.511		Y 🟡
	cyclase/dehydrase [Methylobacillus flagellatus KT]637938045 YP_545253											
MFLA1145		3.210	3.422	4.320	-0.252	Y 🟡 🟡 Y	2.74 E-2	21.134	22.014	22.640	-0.942	Y 🟡
	SsrA-binding protein [Methylobacillus flagellatus KT]637938046 YP_545254											
MFLA1146		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	Hemerythrin HHE cation binding region [Methylobacillus flagellatus KT]637938047 YP_545255											
MFLA1147			0.000	0.000		Y 🟡 🟡 Y			20.956	20.956		Y 🟡
	nuclease (SNase-like) [Methylobacillus flagellatus KT]637938048 YP_545256											
MFLA1148		2.398	3.417	3.995	0.111	Y 🟡 🟡 Y	1.97 E-1	19.386	20.559	21.088	-0.137	Y 🟡
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637938049 YP_545257											
MFLA1149		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637938050 YP_545258 """											
MFLA1150		0.521	1.184	1.890	0.347	Y 🟡 🟡 Y	1.51 E-1	20.175	21.379	21.899	-0.190	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938051 YP_545259											
MFLA1151		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938052 YP_545260											
MFLA1152		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938053 YP_545261											
MFLA1153		0.813		0.813		Y 🟡 🟡 Y		17.716		17.716		Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938054 YP_545262											
MFLA1154		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	" prophage LambdaMc01, site-specific recombinase, resolvase family [Methylobacillus flagellatus KT]637938055 YP_545263 """											
MFLA1155		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	Recombinase [Methylobacillus flagellatus KT]637938056 YP_545264											
MFLA1156		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938057 YP_545265											



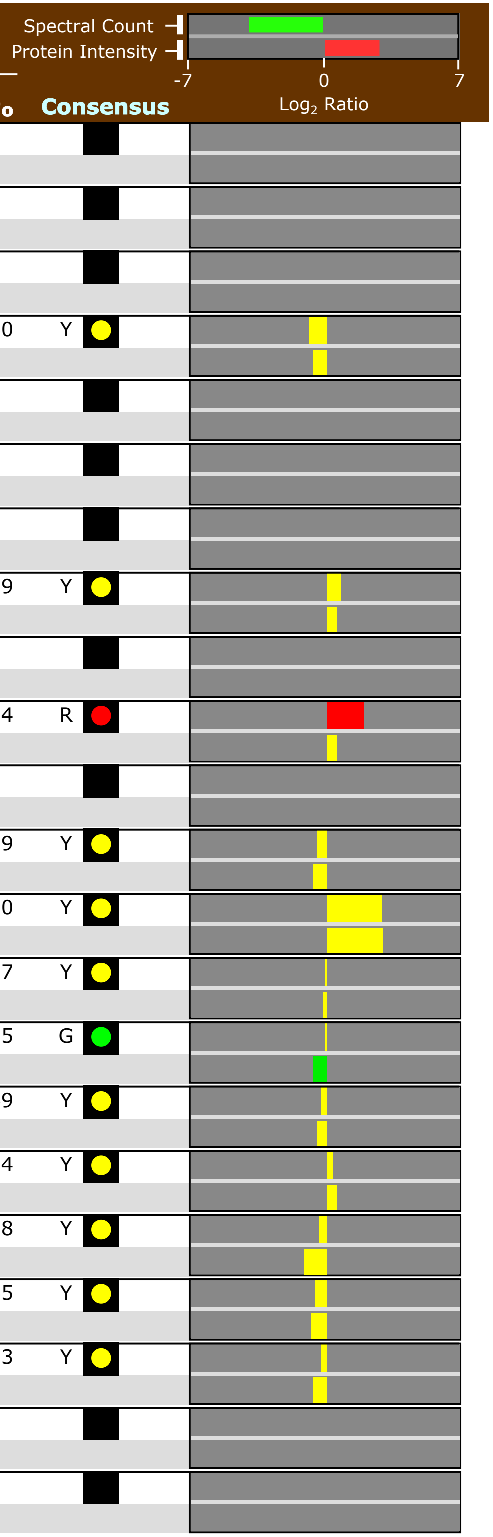
	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**	**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**
MFLA1157		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938058 YP_545266											
MFLA1158	1.92 E-14	7.684	6.744	8.289	0.912	R 🔴 🟡 Y	2.67 E-1	26.508	26.493	27.501	-0.011	Y 🟡
	" peptidase S1 and S6, chymotrypsin/Hap [Methylobacillus flagellatus KT]637938059 YP_545267 """											
MFLA1159		4.470	3.367	5.021	0.701	Y 🟡 🟡 Y	1.1 E-1	22.835	21.325	23.269	0.875	Y 🟡
	" peptidase M48, Ste24p [Methylobacillus flagellatus KT]637938060 YP_545268 """											
MFLA1160		2.398		2.398		Y 🟡 🟡 Y		18.611		18.611		Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938061 YP_545269											
MFLA1161		6.287	6.398	7.344	-0.542	Y 🟡 🟡 Y	8.11 E-2	26.212	25.702	26.979	0.462	Y 🟡
	thioredoxin [Methylobacillus flagellatus KT]637938062 YP_545270											
MFLA1162	3.4 E-16	7.858	6.900	8.457	0.979	R 🔴 🟡 Y	5.13 E-2	27.606	26.880	28.288	0.694	R 🔴
	hypothetical protein [Methylobacillus flagellatus KT]637938063 YP_545271											
MFLA1163		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938064 YP_545272											
MFLA1164	1.8 E-8	8.636	8.990	9.824	-0.375	Y 🟡 🟡 Y	1.66 E-2	29.796	30.278	31.057	-0.492	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938065 YP_545273											
MFLA1165		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938066 YP_545274											
MFLA1166		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	heat shock protein Hsp20 [Methylobacillus flagellatus KT]637938067 YP_545275											
MFLA1167		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938068 YP_545276											
MFLA1168	2.33 E-2	7.679	7.553	8.617	0.122	Y 🟡 🟡 Y	8.09 E-2	26.759	27.136	27.960	-0.412	Y 🟡
	ATP-dependent metalloprotease FtsH [Methylobacillus flagellatus KT]637938069 YP_545277											
MFLA1169	3.63 E-2	6.830	6.484	7.668	0.347	Y 🟡 🟡 Y	2.81 E-2	26.249	26.507	27.384	-0.260	Y 🟡
	phospholipase D/Transphosphatidylase [Methylobacillus flagellatus KT]637938070 YP_545278											
MFLA1170		10.684	10.698	11.691	-0.011	Y 🟡 🟡 Y	1.68 E-2	30.420	30.886	31.672	-0.463	Y 🟡
	ATPase AAA-2 [Methylobacillus flagellatus KT]637938071 YP_545279											
MFLA1171		10.145	10.069	11.108	0.088	Y 🟡 🟡 Y	2.3 E-1	31.704	31.804	32.755	-0.103	Y 🟡
	heat shock protein Hsp20 [Methylobacillus flagellatus KT]637938072 YP_545280											
MFLA1172		4.135	2.659	4.578	2.509	Y 🟡 🟡 Y	5.86 E-2	21.479	21.615	22.549	0.882	Y 🟡
	" phage transcriptional regulator, AlpA [Methylobacillus flagellatus KT]637938073 YP_545281 """											
MFLA1173		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	phospholipase D/Transphosphatidylase [Methylobacillus flagellatus KT]637938074 YP_545282											
MFLA1174		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	protein of unknown function DUF45 [Methylobacillus flagellatus KT]637938075 YP_545283											
MFLA1175		4.769	4.638	5.705	0.053	Y 🟡 🟡 Y	8.26 E-2	22.655	23.581	24.191	-1.160	Y 🟡
	" type I site-specific deoxyribonuclease, HsdR family [Methylobacillus flagellatus KT]637938076 YP_545284 """											
MFLA1176		3.523	2.844	4.223	0.579	Y 🟡 🟡 Y	1.47 E-1	21.495	21.076	22.301	0.438	Y 🟡
	restriction modification system DNA specificity domain [Methylobacillus flagellatus KT]637938077 YP_545285											
MFLA1177		4.774	4.972	5.877	-0.205	Y 🟡 🟡 Y	1.17 E-2	22.654	23.574	24.186	-0.952	Y 🟡
	" transcriptional regulator, XRE family [Methylobacillus flagellatus KT]637938078 YP_545286 """											
MFLA1178		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938079 YP_545287											



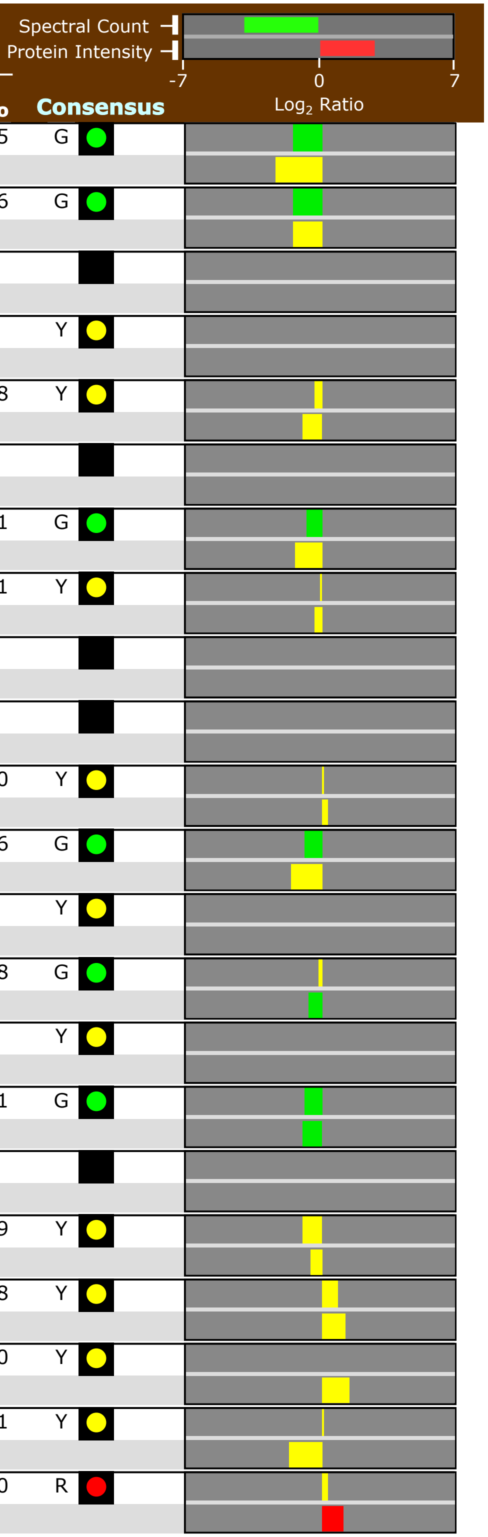
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA1179		2.135		2.135		Y	🟡	🟡	Y		19.117		19.117		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938080 YP_545288															
MFLA1180		0.000	0.000				■	■			0.000	0.000				■
	" transcriptional regulator, AraC family [Methylobacillus flagellatus KT]637938081 YP_545289 """															
MFLA1181		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938082 YP_545290															
MFLA1182		1.674	2.941	3.442	-1.252	Y	🟡	🟡	Y	2.36 E-1	21.300	21.367	22.334	-0.093	Y	🟡
	filamentation induced by cAMP protein Fic [Methylobacillus flagellatus KT]637938083 YP_545291															
MFLA1183		6.012	6.562	7.313	-0.626	Y	🟡	🟡	Y	1.12 E-1	23.605	24.379	25.043	-0.992	Y	🟡
	response regulator receiver modulated diguanylate cyclase/phosphodiesterase with PAS/PAC sensor(s) [Methylobacillus flagellatus KT]637938084 YP_545292															
MFLA1184		3.259	4.353	4.908	-1.091	Y	🟡	🟢	G	6.42 E-3	21.621	23.940	24.204	-2.330	G	🟢
	histidine kinase [Methylobacillus flagellatus KT]637938085 YP_545293															
MFLA1185	6.75 E-9	5.546	3.966	5.962	1.397	R	🔴	🟡	Y	5.13 E-2	24.068	22.758	24.557	1.208	R	🔴
	thioredoxin-related [Methylobacillus flagellatus KT]637938086 YP_545294															
MFLA1186		3.954	2.897	4.520	0.298	Y	🟡	🟡	Y	1.44 E-1	23.305	22.717	24.041	0.321	Y	🟡
	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen [Methylobacillus flagellatus KT]637938087 YP_545295															
MFLA1187		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938090 YP_545296															
MFLA1188	0	7.483	5.675	7.846	1.758	R	🔴	🟡	Y	1.59 E-1	25.457	25.127	26.302	0.228	R	🔴
	cold-shock DNA-binding domain protein [Methylobacillus flagellatus KT]637938091 YP_545297															
MFLA1189		2.746	0.000	2.946	1.459	Y	🟡	🟡	Y	9.14 E-2	20.899	19.363	21.326	0.523	Y	🟡
	Glycogen debranching enzyme GlgX [Methylobacillus flagellatus KT]637938092 YP_545298															
MFLA1190		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938093 YP_545299															
MFLA1191		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938094 YP_545300															
MFLA1192		0.000	0.000				■	■			0.000	0.000				■
	ABC transporter related [Methylobacillus flagellatus KT]637938095 YP_545301															
MFLA1193		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938096 YP_545302															
MFLA1194		0.000	0.000				■	■			0.000	0.000				■
	UDP-galactopyranose mutase [Methylobacillus flagellatus KT]637938097 YP_545303															
MFLA1195		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938098 YP_545304															
MFLA1196	1.25 E-1	5.512	5.328	6.423	0.199	Y	🟡	🟡	Y	2.87 E-2	22.488	24.183	24.572	-1.913	Y	🟡
	FAD-dependent pyridine nucleotide-disulphide oxidoreductase [Methylobacillus flagellatus KT]637938100 YP_545305															
MFLA1197	1.48 E-11	7.450	8.163	8.850	-0.716	G	🟢	🟡	Y	2.81 E-2	26.790	27.487	28.180	-0.714	G	🟢
	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen [Methylobacillus flagellatus KT]637938101 YP_545306															
MFLA1198		0.000	0.000				■	■			0.000	0.000				■
	diguanylate cyclase (GGDEF domain) [Methylobacillus flagellatus KT]637938102 YP_545307															
MFLA1199		4.605	4.754	5.681	-0.151	Y	🟡	🟡	Y	2.39 E-1	23.001	23.128	24.066	-0.268	Y	🟡
	ABC transporter related [Methylobacillus flagellatus KT]637938103 YP_545308															
MFLA1200		4.571	4.154	5.378	0.450	Y	🟡	🟡	Y	1.93 E-1	21.287	21.498	22.397	-0.199	Y	🟡
	AsmA [Methylobacillus flagellatus KT]637938104 YP_545309															



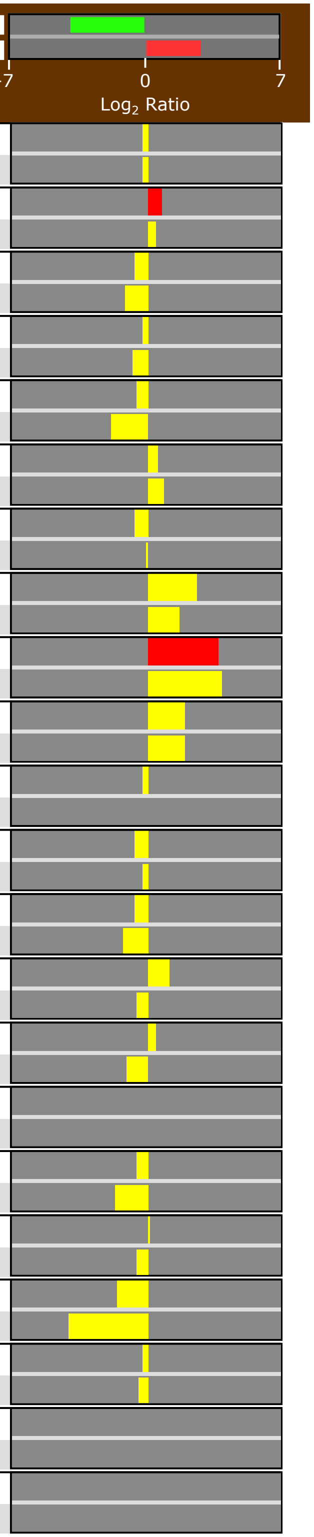
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA1201		0.000	0.000				■	■			0.000	0.000				■
	major facilitator superfamily MFS_1 [Methylobacillus flagellatus KT]637938105 YP_545310															
MFLA1202		0.000	0.000				■	■			0.000	0.000				■
	UvrD/REP helicase [Methylobacillus flagellatus KT]637938106 YP_545311															
MFLA1203		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637938107 YP_545312															
MFLA1204		3.461	4.410	5.012	-0.914	Y	🟡	🟡	Y	4.72 E-2	22.346	23.045	23.737	-0.660	Y	🟡
	GTP-binding [Methylobacillus flagellatus KT]637938108 YP_545313															
MFLA1205		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938109 YP_545314															
MFLA1206		0.000	0.000				■	■			0.000	0.000				■
	Alkaline phosphatase [Methylobacillus flagellatus KT]637938110 YP_545315															
MFLA1207		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938111 YP_545316															
MFLA1208		1.521	1.915	2.731	0.686	Y	🟡	🟡	Y	2.93 E-2	20.471	20.943	21.726	0.529	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938112 YP_545317															
MFLA1209		0.000	0.000				■	■			0.000	0.000				■
	ribonuclease BN [Methylobacillus flagellatus KT]637938113 YP_545318															
MFLA1210	2.62 E-16	6.305	5.458	6.943	1.902	R	🔴	🟡	Y	1.02 E-1	22.132	22.683	23.434	0.474	R	🔴
	protein of unknown function DUF461 [Methylobacillus flagellatus KT]637938114 YP_545319															
MFLA1211		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938115 YP_545320															
MFLA1212	1.65 E-2	5.764	6.271	7.040	-0.505	Y	🟡	🟡	Y	4.58 E-2	24.256	24.912	25.621	-0.709	Y	🟡
	ATP-dependent helicase HrpA [Methylobacillus flagellatus KT]637938116 YP_545321															
MFLA1213		3.427	0.585	3.616	2.843	Y	🟡	🟡	Y		22.137	19.207	22.315	2.930	Y	🟡
	Lytic murein transglycosylase [Methylobacillus flagellatus KT]637938117 YP_545322															
MFLA1214	1.95 E-2	8.031	8.149	9.091	-0.121	Y	🟡	🟡	Y	1.04 E-1	26.051	26.256	27.157	-0.217	Y	🟡
	oxidoreductase-like protein [Methylobacillus flagellatus KT]637938118 YP_545323															
MFLA1215	5.49 E-2	7.056	7.160	8.109	-0.115	Y	🟡	🟢	G	4.29 E-3	25.602	26.316	27.002	-0.715	G	🟢
	" type I site-specific deoxyribonuclease, HsdR family [Methylobacillus flagellatus KT]637938119 YP_545324 """															
MFLA1216	9.72 E-2	5.077	5.261	6.172	-0.310	Y	🟡	🟡	Y	4.93 E-2	23.935	24.438	25.208	-0.549	Y	🟡
	restriction modification system DNA specificity domain [Methylobacillus flagellatus KT]637938120 YP_545325															
MFLA1217		4.160	3.820	5.000	0.286	Y	🟡	🟡	Y	4.5 E-2	21.876	21.366	22.644	0.494	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938121 YP_545326															
MFLA1218	3.82 E-2	5.569	5.965	6.780	-0.404	Y	🟡	🟡	Y	1.13 E-2	23.645	24.814	25.345	-1.208	Y	🟡
	DEAD/DEAH box helicase-like protein [Methylobacillus flagellatus KT]637938122 YP_545327															
MFLA1219		1.521	2.170	2.881	-0.649	Y	🟡	🟡	Y		19.071	19.836	20.504	-0.765	Y	🟡
	anticodon nuclease [Methylobacillus flagellatus KT]637938123 YP_545328															
MFLA1220	6.62 E-2	6.568	6.836	7.708	-0.272	Y	🟡	🟡	Y	1.41 E-2	25.509	26.163	26.873	-0.653	Y	🟡
	" type I restriction-modification system, M subunit [Methylobacillus flagellatus KT]637938124 YP_545329 """															
MFLA1221		0.000	0.000				■	■			0.000	0.000				■
	crcB protein [Methylobacillus flagellatus KT]637938125 YP_545330															
MFLA1222		0.000	0.000				■	■			0.000	0.000				■
	thioredoxin-related [Methylobacillus flagellatus KT]637938126 YP_545331															

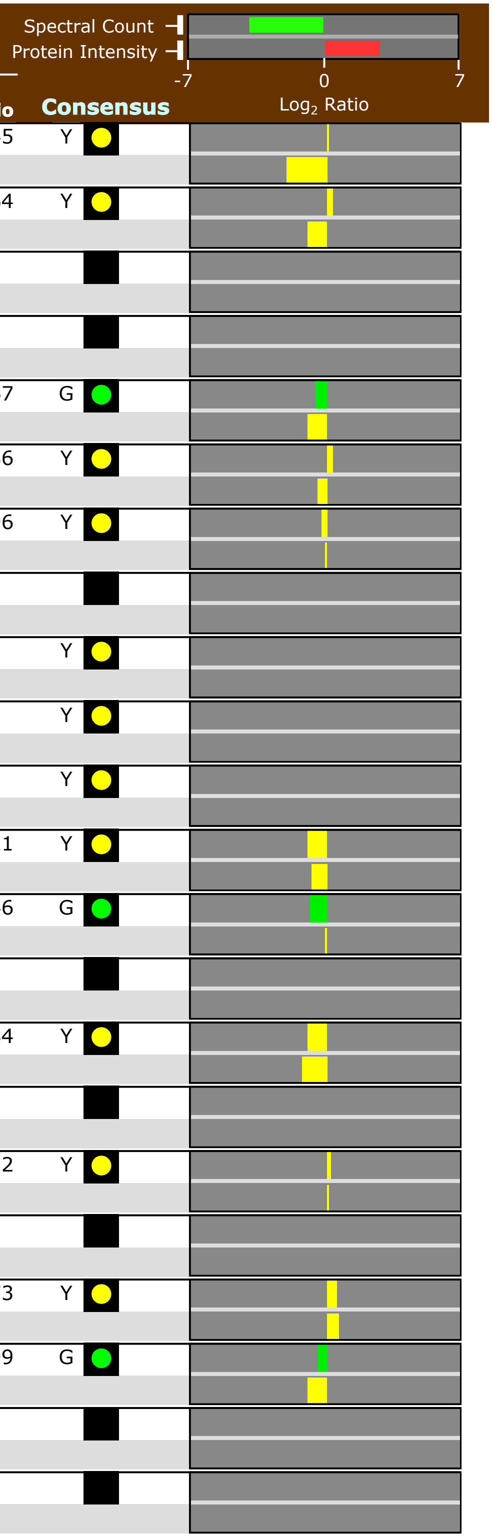


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA1223	0	8.105	9.576	10.021	-1.452	G	🟢	🟡	Y	1.03 E-2	27.460	29.854	30.105	-2.375	G	🟢
	Ribonucleoside-diphosphate reductase [Methylobacillus flagellatus KT]637938127 YP_545332															
MFLA1224	0	5.690	7.178	7.618	-1.455	G	🟢	🟡	Y	1.29 E-2	25.241	26.732	27.171	-1.536	G	🟢
	Ribonucleoside-diphosphate reductase [Methylobacillus flagellatus KT]637938128 YP_545333															
MFLA1225		0.000	0.000				■	■			0.000	0.000				■
	ferredoxin [Methylobacillus flagellatus KT]637938129 YP_545334															
MFLA1226			2.170	2.170		Y	🟡	🟡	Y			21.238	21.238		Y	🟡
	protein of unknown function UPF0118 [Methylobacillus flagellatus KT]637938130 YP_545335															
MFLA1227		4.093	4.511	5.317	-0.439	Y	🟡	🟡	Y	1.56 E-1	22.859	23.496	24.212	-0.998	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938131 YP_545336															
MFLA1228		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938132 YP_545337															
MFLA1229	9.4 E-3	4.624	5.413	6.072	-0.793	G	🟢	🟡	Y	7.05 E-2	21.316	22.232	22.846	-1.381	G	🟢
	" cobalamin synthesis protein, P47K [Methylobacillus flagellatus KT]637938133 YP_545338 """															
MFLA1230	1.33 E-1	5.510	5.650	6.581	-0.147	Y	🟡	🟡	Y	1.06 E-1	24.651	24.988	25.829	-0.401	Y	🟡
	" cobalamin synthesis protein, P47K [Methylobacillus flagellatus KT]637938134 YP_545339 """															
MFLA1231		0.000	0.000				■	■			0.000	0.000				■
	" cobalamin synthesis protein, P47K [Methylobacillus flagellatus KT]637938135 YP_545340 """															
MFLA1232		0.000	0.000				■	■			0.000	0.000				■
	" transcriptional regulators, TraR/DksA family [Methylobacillus flagellatus KT]637938136 YP_545341 """															
MFLA1233		4.294	4.044	5.174	0.094	Y	🟡	🟡	Y	2.17 E-1	23.246	23.064	24.158	0.310	Y	🟡
	" ferric uptake regulator, FUR family [Methylobacillus flagellatus KT]637938137 YP_545342 """															
MFLA1234	4.49 E-4	4.959	5.854	6.475	-0.909	G	🟢	🟡	Y	4.4 E-2	23.167	24.459	24.953	-1.566	G	🟢
	ribonuclease II [Methylobacillus flagellatus KT]637938138 YP_545343															
MFLA1235		2.761		2.761		Y	🟡	🟡	Y		20.972		20.972		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938139 YP_545344															
MFLA1236		3.899	4.087	4.996	-0.167	Y	🟡	🟢	G	9.78 E-3	22.839	23.510	24.213	-0.678	G	🟢
	putative RNA methylase [Methylobacillus flagellatus KT]637938140 YP_545345															
MFLA1237		2.521		2.521		Y	🟡	🟡	Y		20.305		20.305		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938141 YP_545346															
MFLA1238	6.28 E-11	6.762	7.616	8.251	-0.850	G	🟢	🟢	G	6.36 E-3	26.218	27.171	27.772	-0.951	G	🟢
	" Peptidase M1, alanyl aminopeptidase [Methylobacillus flagellatus KT]637938142 YP_545347 """															
MFLA1239		0.000	0.000				■	■			0.000	0.000				■
	Phytanoyl-CoA dioxygenase [Methylobacillus flagellatus KT]637938143 YP_545348															
MFLA1240		9.334	9.745	10.554	-0.958	Y	🟡	🟡	Y	5.71 E-2	29.376	29.943	30.687	-0.649	Y	🟡
	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen [Methylobacillus flagellatus KT]637938144 YP_545349															
MFLA1241		4.647	3.880	5.314	0.798	Y	🟡	🟡	Y	2.7 E-2	24.405	23.284	24.951	1.208	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938145 YP_545350															
MFLA1242		3.081	2.710	3.907	-0.006	Y	🟡	🟡	Y	3.86 E-2	23.773	22.473	24.265	1.370	Y	🟡
	response regulator receiver domain protein (CheY-like) [Methylobacillus flagellatus KT]637938146 YP_545351															
MFLA1243		4.915	4.520	5.731	0.109	Y	🟡	🟡	Y	6.73 E-2	24.573	26.172	26.583	-1.731	Y	🟡
	response regulator receiver domain protein (CheY-like) [Methylobacillus flagellatus KT]637938147 YP_545352															
MFLA1244		3.996	3.700	4.856	0.294	Y	🟡	🔴	R	4.7 E-4	23.058	21.937	23.604	1.120	R	🔴
	CheW protein [Methylobacillus flagellatus KT]637938148 YP_545353															



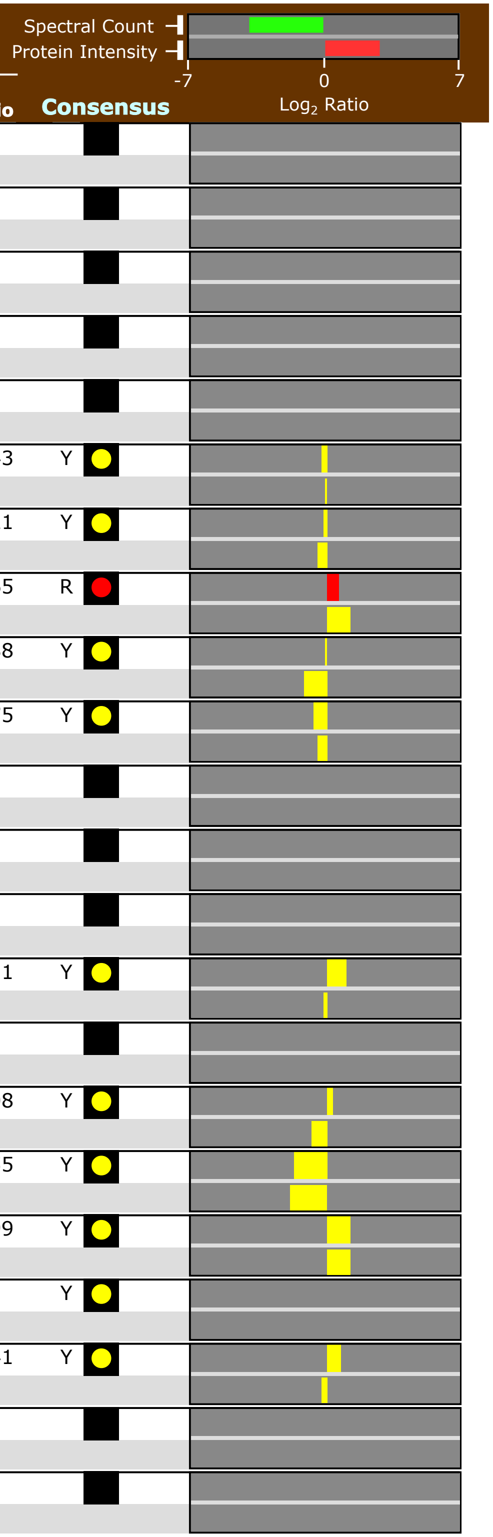
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	***q*-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**				***q*-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**	
MFLA1245		6.559	6.873	7.724	-0.298	Y	🟡	🟡	Y	1.71 E-1	25.500	25.707	26.607	-0.293	Y	🟡
	methyl-accepting chemotaxis sensory transducer [Methylobacillus flagellatus KTJ637938149 YP_545354															
MFLA1246	3.97 E-6	7.173	6.486	7.870	0.702	R	🔴	🟡	Y	4.29 E-2	25.523	25.155	26.351	0.371	R	🔴
	CheA signal transduction histidine kinases [Methylobacillus flagellatus KTJ637938150 YP_545355															
MFLA1247		5.329	6.045	6.731	-0.687	Y	🟡	🟡	Y	1.1 E-1	23.255	24.114	24.748	-1.222	Y	🟡
	" DNA polymerase III, alpha subunit [Methylobacillus flagellatus KTJ637938151 YP_545356 """															
MFLA1248	4.31 E-2	6.287	6.635	7.472	-0.345	Y	🟡	🟡	Y	2.7 E-2	26.196	26.995	27.650	-0.833	Y	🟡
	" acetyl-CoA carboxylase, carboxyl transferase, alpha subunit [Methylobacillus flagellatus KTJ637938152 YP_545357 """															
MFLA1249		1.843	3.523	3.914	-0.645	Y	🟡	🟡	Y	1.17 E-1	19.336	22.437	22.596	-1.880	Y	🟡
	tRNA(Ile)-lysidine synthetase-like protein [Methylobacillus flagellatus KTJ637938153 YP_545358															
MFLA1250		4.353	3.476	4.980	0.459	Y	🟡	🟡	Y	1.14 E-1	23.166	22.399	23.833	0.756	Y	🟡
	Arylesterase [Methylobacillus flagellatus KTJ637938154 YP_545359															
MFLA1251		3.461	4.551	5.107	-0.741	Y	🟡	🟡	Y	2.21 E-1	22.026	22.218	23.125	-0.133	Y	🟡
	ABC transporter related [Methylobacillus flagellatus KTJ637938155 YP_545360															
MFLA1252		4.146	1.184	4.320	2.482	Y	🟡	🟡	Y	6.47 E-2	22.705	21.283	23.162	1.553	Y	🟡
	protein of unknown function DUF214 [Methylobacillus flagellatus KTJ637938156 YP_545361															
MFLA1253	0	6.891	3.301	7.006	3.644	R	🔴	🟡	Y	1.38 E-2	26.020	22.288	26.125	3.751	R	🔴
	TonB-dependent receptor [Methylobacillus flagellatus KTJ637938157 YP_545362															
MFLA1254		5.492	3.584	5.833	1.907	Y	🟡	🟡	Y	1.1 E-2	24.197	22.325	24.545	1.854	Y	🟡
	" two component, sigma54 specific, transcriptional regulator, Fis family [Methylobacillus flagellatus KTJ637938158 YP_545363 """															
MFLA1255	1.06 E-1	5.581	5.838	6.715	-0.261	Y	🟡	🟡	Y	2.58 E-1	25.686	25.643	26.665	-0.014	Y	🟡
	phosphoribosylglycinamide formyltransferase 2 [Methylobacillus flagellatus KTJ637938159 YP_545364															
MFLA1256		1.674	1.322	2.509	-0.655	Y	🟡	🟡	Y	2.18 E-1	21.055	20.250	21.708	-0.318	Y	🟡
	globin [Methylobacillus flagellatus KTJ637938160 YP_545365															
MFLA1257		5.113	5.726	6.452	-0.744	Y	🟡	🟡	Y	1.12 E-1	24.388	25.071	25.769	-1.264	Y	🟡
	DEAD/DEAH box helicase-like protein [Methylobacillus flagellatus KTJ637938161 YP_545366															
MFLA1258		4.642	3.353	5.137	1.146	Y	🟡	🟡	Y	2.13 E-1	23.353	22.960	24.170	-0.633	Y	🟡
	DEAD/DEAH box helicase-like protein [Methylobacillus flagellatus KTJ637938162 YP_545367															
MFLA1259	6.96 E-5	7.762	7.318	8.557	0.427	Y	🟡	🟡	Y	4.29 E-2	25.838	26.855	27.434	-1.123	Y	🟡
	GTP-binding protein TypA [Methylobacillus flagellatus KTJ637938163 YP_545368															
MFLA1260		0.000	0.000				■	■			0.000	0.000				■
	TPR repeat [Methylobacillus flagellatus KTJ637938164 YP_545369															
MFLA1261	3.52 E-2	4.891	5.463	6.205	-0.581	Y	🟡	🟡	Y	1.18 E-2	22.234	23.900	24.295	-1.679	Y	🟡
	protein of unknown function DUF195 [Methylobacillus flagellatus KTJ637938165 YP_545370															
MFLA1262		3.591	2.459	4.133	0.111	Y	🟡	🟡	Y	1.1 E-1	20.977	20.542	21.776	-0.625	Y	🟡
	" molybdopterin converting factor, subunit 1 [Methylobacillus flagellatus KTJ637938166 YP_545371 """															
MFLA1263		0.521	3.162	3.376	-1.641	Y	🟡	🟡	Y	9 E-2	17.504	22.712	22.750	-4.092	Y	🟡
	molybdopterin biosynthesis MoaE [Methylobacillus flagellatus KTJ637938167 YP_545372															
MFLA1264		4.566	4.781	5.677	-0.299	Y	🟡	🟡	Y	1.17 E-1	23.069	23.479	24.288	-0.549	Y	🟡
	ATP-dependent protease-like protein [Methylobacillus flagellatus KTJ637938168 YP_545373															
MFLA1265		0.000	0.000				■	■			0.000	0.000				■
	RNA-binding S4 [Methylobacillus flagellatus KTJ637938169 YP_545374															
MFLA1266		0.000	0.000				■	■			0.000	0.000				■
	Radical SAM [Methylobacillus flagellatus KTJ637938170 YP_545375															



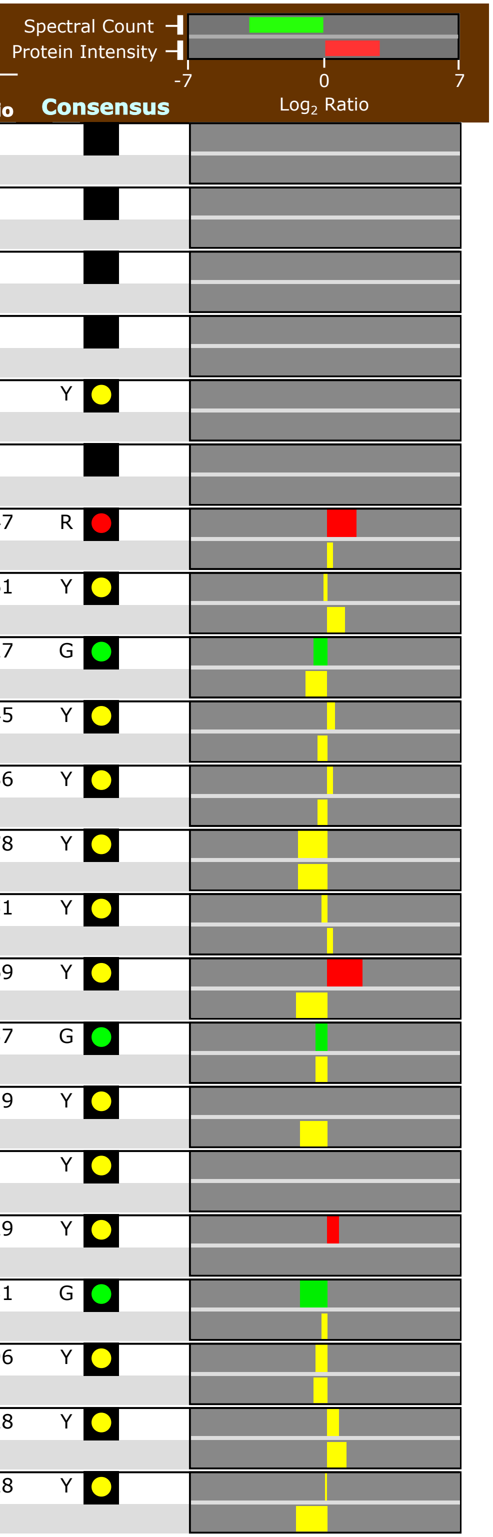


ORF	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA1267		2.843	3.725	4.350	0.131	Y	●	●	Y	5.93 E-2	20.726	23.889	24.042	-2.145	Y	●
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637938171 YP_545376															
MFLA1268		5.237	4.465	5.902	0.342	Y	●	●	Y	1.54 E-1	23.608	24.072	24.859	-0.964	Y	●
	Mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase [Methylobacillus flagellatus KT]637938172 YP_545377															
MFLA1269		0.000	0.000								0.000	0.000				
	ABC-2 [Methylobacillus flagellatus KT]637938173 YP_545378															
MFLA1270		0.000	0.000								0.000	0.000				
	NDP-hexose 3-C-methyltransferase TylCIII [Methylobacillus flagellatus KT]637938174 YP_545379															
MFLA1271	4.42 E-5	5.949	6.605	7.314	-0.591	G	●	●	Y	2.73 E-2	25.738	26.614	27.241	-0.967	G	●
	" GDP-mannose 4,6-dehydratase [Methylobacillus flagellatus KT]637938175 YP_545380 """															
MFLA1272		3.328	4.147	4.795	0.333	Y	●	●	Y	9.42 E-2	21.738	23.236	23.674	-0.486	Y	●
	NAD-dependent epimerase/dehydratase [Methylobacillus flagellatus KT]637938176 YP_545381															
MFLA1273	5.74 E-2	4.967	5.305	6.146	-0.318	Y	●	●	Y	2.41 E-1	24.098	23.980	25.040	-0.096	Y	●
	" glycosyl transferase, group 1 [Methylobacillus flagellatus KT]637938177 YP_545382 """															
MFLA1274		0.000	0.000								0.000	0.000				
	polysaccharide export protein [Methylobacillus flagellatus KT]637938178 YP_545383															
MFLA1275			2.000	2.000		Y	●	●	Y			20.008	20.008		Y	●
	" glycosyl transferase, group 1 [Methylobacillus flagellatus KT]637938179 YP_545384 """															
MFLA1276		1.521		1.521		Y	●	●	Y		19.110		19.110		Y	●
	NAD-dependent epimerase/dehydratase [Methylobacillus flagellatus KT]637938180 YP_545385															
MFLA1277		1.106		1.106		Y	●	●	Y		19.962		19.962		Y	●
	sugar transferase [Methylobacillus flagellatus KT]637938181 YP_545386															
MFLA1278		1.106	3.140	3.455	-1.021	Y	●	●	Y	1.41 E-1	20.240	22.242	22.563	-0.821	Y	●
	polysaccharide biosynthesis protein CapD [Methylobacillus flagellatus KT]637938182 YP_545387															
MFLA1279	8.81 E-17	6.975	7.918	8.523	-0.930	G	●	●	Y	2.25 E-1	27.103	27.193	28.149	-0.146	G	●
	UTP-glucose-1-phosphate uridylyltransferase [Methylobacillus flagellatus KT]637938183 YP_545388															
MFLA1280		0.000	0.000								0.000	0.000				
	phosphoribosyltransferase [Methylobacillus flagellatus KT]637938184 YP_545389															
MFLA1281		4.402	5.379	5.972	-0.981	Y	●	●	Y	1.01 E-2	23.339	24.602	25.104	-1.284	Y	●
	response regulator receiver domain protein (CheY-like) [Methylobacillus flagellatus KT]637938185 YP_545390															
MFLA1282		0.000	0.000								0.000	0.000				
	response regulator receiver domain protein (CheY-like) [Methylobacillus flagellatus KT]637938186 YP_545391															
MFLA1283		4.140	3.975	5.060	0.152	Y	●	●	Y	2.21 E-1	21.824	21.612	22.722	0.132	Y	●
	PAS/PAC sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637938187 YP_545392															
MFLA1284		0.000	0.000								0.000	0.000				
	hypothetical protein [Methylobacillus flagellatus KT]637938188 YP_545393															
MFLA1285		6.893	6.466	7.695	0.473	Y	●	●	Y	6.85 E-2	26.342	25.778	27.087	0.573	Y	●
	hypothetical protein [Methylobacillus flagellatus KT]637938189 YP_545394															
MFLA1286	0	8.905	9.477	10.219	-0.548	G	●	●	Y	2.79 E-2	28.833	29.746	30.361	-0.999	G	●
	Glutamate dehydrogenase (NADP+) [Methylobacillus flagellatus KT]637938190 YP_545395															
MFLA1287		0.000	0.000								0.000	0.000				
	aminoglycoside phosphotransferase [Methylobacillus flagellatus KT]637938191 YP_545396															
MFLA1288		0.000	0.000								0.000	0.000				
	ribosomal protein L36 [Methylobacillus flagellatus KT]637938192 YP_545397															

ORF	AM/OH *M Flagellatus* Spectral Count *q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation	AM/OH *M Flagellatus* Protein Intensity *q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA1289		0.000	0.000			■ ■		0.000	0.000			■
	major facilitator superfamily MFS_1 [Methylobacillus flagellatus KT]637938193 YP_545398											
MFLA1290		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938194 YP_545399											
MFLA1291		0.000	0.000			■ ■		0.000	0.000			■
	protoheme IX farnesyltransferase [Methylobacillus flagellatus KT]637938195 YP_545400											
MFLA1292		0.000	0.000			■ ■		0.000	0.000			■
	cytochrome C oxidase subunit IV [Methylobacillus flagellatus KT]637938196 YP_545401											
MFLA1293		0.000	0.000			■ ■		0.000	0.000			■
	" cytochrome c oxidase, subunit III [Methylobacillus flagellatus KT]637938197 YP_545402 """											
MFLA1294	6.88 E-2	5.826	6.105	6.972	-0.299	Y ● ● Y	1.34 E-1	26.645	26.796	27.723	-0.143	Y ●
	Cytochrome-c oxidase [Methylobacillus flagellatus KT]637938198 YP_545403											
MFLA1295		7.837	8.057	8.951	-0.226	Y ● ● Y	3.12 E-2	28.014	28.539	29.300	-0.521	Y ●
	" ubiquinol oxidase, subunit II [Methylobacillus flagellatus KT]637938199 YP_545404 """											
MFLA1296	1.75 E-3	5.427	4.734	6.122	0.646	R ● ● Y	7.03 E-2	24.859	23.848	25.440	1.165	R ●
	" proteinase inhibitor I11, ecotin [Methylobacillus flagellatus KT]637938200 YP_545405 """											
MFLA1297		7.531	7.251	8.398	-0.105	Y ● ● Y	3.51 E-2	25.750	26.972	27.486	-1.188	Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637938201 YP_545406											
MFLA1298		1.521	3.295	3.665	-0.738	Y ● ● Y	1.16 E-1	19.937	21.439	21.875	-0.475	Y ●
	" (p)ppGpp synthetase I (GTP pyrophosphokinase), SpoT/RelA [Methylobacillus flagellatus KT]637938202 YP_545407 """											
MFLA1299		0.000	0.000			■ ■		0.000	0.000			■
	DNA-3-methyladenine glycosylase II [Methylobacillus flagellatus KT]637938203 YP_545408											
MFLA1300		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938204 YP_545409											
MFLA1301		0.000	0.000			■ ■		0.000	0.000			■
	2OG-Fe(II) oxygenase [Methylobacillus flagellatus KT]637938205 YP_545410											
MFLA1302		5.244	4.194	5.812	1.040	Y ● ● Y	2.33 E-1	23.137	23.237	24.188	-0.211	Y ●
	glutamine amidotransferase class-I [Methylobacillus flagellatus KT]637938206 YP_545411											
MFLA1303		0.000	0.000			■ ■		0.000	0.000			■
	putative GNAT-family acetyltransferase [Methylobacillus flagellatus KT]637938207 YP_545412											
MFLA1304		2.328	2.991	3.697	0.347	Y ● ● Y	9.02 E-2	19.278	21.109	21.467	-0.808	Y ●
	outer membrane efflux protein [Methylobacillus flagellatus KT]637938208 YP_545413											
MFLA1305		3.159	4.571	5.031	-1.673	Y ● ● Y	5.91 E-2	21.950	23.514	23.934	-1.855	Y ●
	Secretion protein HlyD [Methylobacillus flagellatus KT]637938209 YP_545414											
MFLA1306		5.754	4.747	6.337	1.155	Y ● ● Y	7.38 E-2	24.228	23.060	24.759	1.199	Y ●
	Heavy metal efflux pump CzcA [Methylobacillus flagellatus KT]637938210 YP_545415											
MFLA1307		2.106		2.106		Y ● ● Y		19.211		19.211		Y ●
	" two component transcriptional regulator, winged helix family [Methylobacillus flagellatus KT]637938211 YP_545416 """											
MFLA1308		1.674	0.000	2.068	0.667	Y ● ● Y	2.17 E-1	21.296	20.503	21.953	-0.341	Y ●
	periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637938212 YP_545417											
MFLA1309		0.000	0.000			■ ■		0.000	0.000			■
	" Integrase, catalytic region [Methylobacillus flagellatus KT]637938213 YP_545418 """											
MFLA1310		0.000	0.000			■ ■		0.000	0.000			■
	transposase IS3/IS911 [Methylobacillus flagellatus KT]637938214 YP_545419											

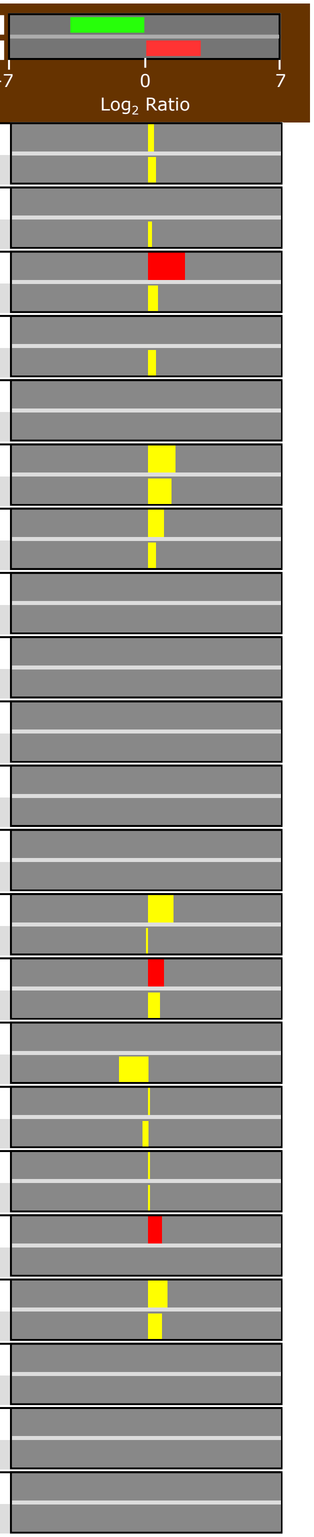


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA1311		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938215 YP_545420															
MFLA1312		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938216 YP_545421															
MFLA1313		0.000	0.000				■	■			0.000	0.000				■
	putative integrase [Methylobacillus flagellatus KT]637938217 YP_545422															
MFLA1314		0.000	0.000				■	■			0.000	0.000				■
	phage integrase [Methylobacillus flagellatus KT]637938218 YP_545423															
MFLA1315		3.235		3.235		Y	🟡	🟡	Y		22.607		22.607		Y	🟡
	MltA-interacting MipA [Methylobacillus flagellatus KT]637938220 YP_545424															
MFLA1316		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938221 YP_545425															
MFLA1317	0	7.805	6.311	8.244	1.459	R	🔴	🟡	Y	8.26 E-2	27.240	26.868	28.066	0.347	R	🔴
	hypothetical protein [Methylobacillus flagellatus KT]637938222 YP_545426															
MFLA1318		0.813	1.000	1.910	-0.187	Y	🟡	🟡	Y		21.254	20.393	21.887	0.861	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938223 YP_545427															
MFLA1319	9.53 E-6	6.314	7.004	7.700	-0.709	G	🟢	🟡	Y	1.1 E-2	26.748	27.833	28.390	-1.127	G	🟢
	" aminotransferase, class I and II [Methylobacillus flagellatus KT]637938224 YP_545428 """															
MFLA1320	9.98 E-2	5.377	5.001	6.201	0.373	Y	🟡	🟡	Y	2.38 E-1	23.540	23.696	24.620	-0.545	Y	🟡
	" excinuclease ABC, B subunit [Methylobacillus flagellatus KT]637938225 YP_545429 """															
MFLA1321		8.648	8.327	9.497	0.295	Y	🟡	🟡	Y	1.02 E-1	27.895	28.364	29.149	-0.486	Y	🟡
	" ribonuclease, Rne/Rng family [Methylobacillus flagellatus KT]637938226 YP_545430 """															
MFLA1322		0.521	3.056	3.285	-1.530	Y	🟡	🟡	Y	7.49 E-2	19.673	22.178	22.412	-1.478	Y	🟡
	" Pseudouridine synthase, RluD [Methylobacillus flagellatus KT]637938227 YP_545431 """															
MFLA1323	1.06 E-1	5.327	5.610	6.475	-0.274	Y	🟡	🟡	Y	1.49 E-1	24.092	23.688	24.904	0.251	Y	🟡
	" HAD-superfamily hydrolase, subfamily IA, variant 1 [Methylobacillus flagellatus KT]637938228 YP_545432 """															
MFLA1324	0	6.796	4.268	7.027	1.824	R	🔴	🟡	Y	6.03 E-2	24.149	25.171	25.749	-1.569	Y	🟡
	peptidase S49 [Methylobacillus flagellatus KT]637938229 YP_545433															
MFLA1325	1.12 E-8	7.279	7.760	8.539	-0.566	G	🟢	🟡	Y	1.66 E-2	26.671	27.217	27.970	-0.557	G	🟢
	Glucose-6-phosphate isomerase [Methylobacillus flagellatus KT]637938230 YP_545434															
MFLA1326		7.900	7.795	8.848	0.002	Y	🟡	🟡	Y	2.51 E-2	26.508	27.717	28.236	-1.419	Y	🟡
	ribosomal protein S6 [Methylobacillus flagellatus KT]637938231 YP_545435															
MFLA1327			0.000	0.000		Y	🟡	🟡	Y			20.943	20.943		Y	🟡
	single-strand binding protein/Primosomal replication protein n [Methylobacillus flagellatus KT]637938232 YP_545436															
MFLA1328	1.63 E-3	6.226	5.580	6.939	0.649	R	🔴	🟡	Y	2.18 E-1	26.469	26.188	27.335	-0.029	Y	🟡
	ribosomal protein S18 [Methylobacillus flagellatus KT]637938233 YP_545437															
MFLA1329	0	7.395	8.778	9.247	-1.379	G	🟢	🟡	Y	3.76 E-2	28.966	29.300	30.143	-0.331	G	🟢
	ribosomal protein L9 [Methylobacillus flagellatus KT]637938234 YP_545438															
MFLA1330	1.13 E-2	5.053	5.686	6.404	-0.608	Y	🟡	🟡	Y	1.53 E-2	24.601	25.289	25.986	-0.696	Y	🟡
	replicative DNA helicase [Methylobacillus flagellatus KT]637938235 YP_545439															
MFLA1331		4.044	4.508	5.295	0.625	Y	🟡	🟡	Y	1.17 E-2	21.936	21.908	22.922	1.028	Y	🟡
	alanine racemase [Methylobacillus flagellatus KT]637938236 YP_545440															
MFLA1332		4.283	4.324	5.304	-0.091	Y	🟡	🟡	Y	1.08 E-2	22.442	24.012	24.431	-1.628	Y	🟡
	DNA repair protein RadA [Methylobacillus flagellatus KT]637938237 YP_545441															

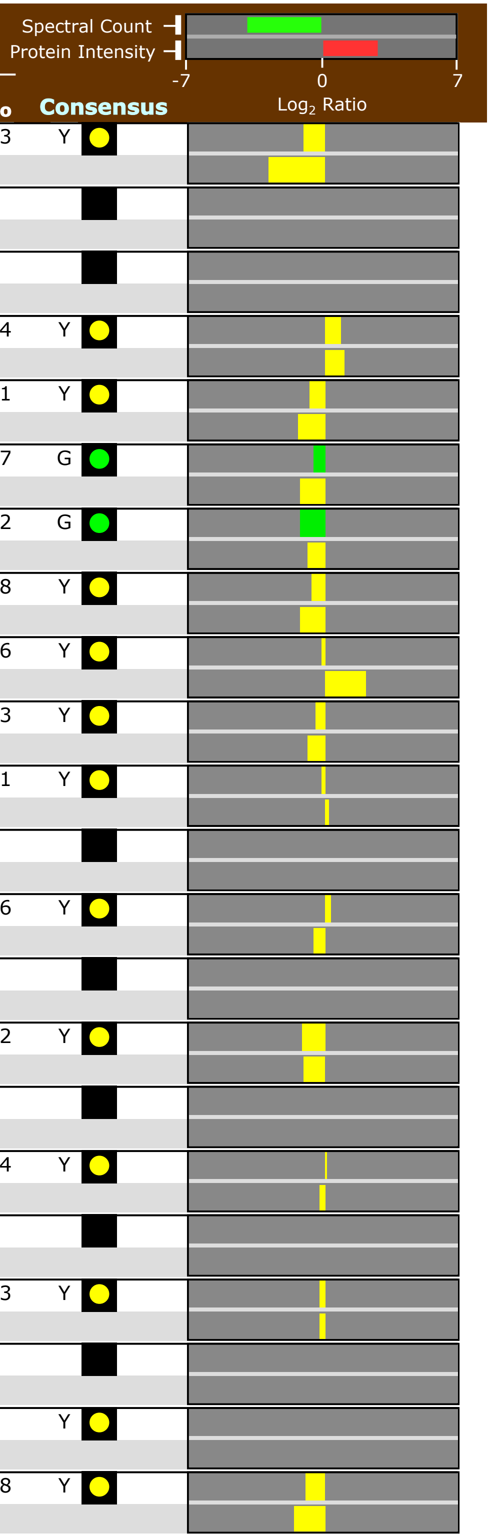


	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity						Spectral Count 🟩 Protein Intensity 🟥 -7 0 7 $\log_2$ Ratio
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA1333		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938239 YP_545442												
MFLA1334		0.000	0.000			■ ■		0.000	0.000			■	
	methylation [Methylobacillus flagellatus KT]637938240 YP_545443												
MFLA1335		0.000	0.000			■ ■		0.000	0.000			■	
	methylation [Methylobacillus flagellatus KT]637938241 YP_545444												
MFLA1336		0.000	0.000			■ ■		0.000	0.000			■	
	type II and III secretion system protein [Methylobacillus flagellatus KT]637938242 YP_545445												
MFLA1337		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938243 YP_545446												
MFLA1338		0.000	0.000			■ ■		0.000	0.000			■	
	putative transmembrane protein [Methylobacillus flagellatus KT]637938244 YP_545447												
MFLA1339		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938245 YP_545448												
MFLA1340		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938246 YP_545449												
MFLA1341		0.000	0.000			■ ■		0.000	0.000			■	
	type II secretion system protein E [Methylobacillus flagellatus KT]637938247 YP_545450												
MFLA1342		0.000	0.000			■ ■		0.000	0.000			■	
	type II secretion system protein [Methylobacillus flagellatus KT]637938248 YP_545451												
MFLA1343		0.000	0.000			■ ■		0.000	0.000			■	
	General secretion pathway protein G [Methylobacillus flagellatus KT]637938249 YP_545452												
MFLA1344		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938250 YP_545453												
MFLA1345		0.000	0.000			■ ■		0.000	0.000			■	
	" Type I secretion outer membrane protein, TolC [Methylobacillus flagellatus KT]637938251 YP_545454 """												
MFLA1346		0.000	0.000			■ ■		0.000	0.000			■	
	" Type I secretion membrane fusion protein, HlyD [Methylobacillus flagellatus KT]637938252 YP_545455 """												
MFLA1347		0.000	0.000			■ ■		0.000	0.000			■	
	" Type I secretion system ATPase, PrtD [Methylobacillus flagellatus KT]637938253 YP_545456 """												
MFLA1348		0.000	0.000			■ ■		0.000	0.000			■	
	" Type I secretion system ATPase, PrtD [Methylobacillus flagellatus KT]637938254 YP_545457 """												
MFLA1349		0.000	0.000			■ ■		0.000	0.000			■	
	Hemolysin-type calcium-binding region [Methylobacillus flagellatus KT]637938255 YP_545458												
MFLA1350		3.648		3.648		Y ● ● Y		23.160		23.160		Y ●	
	hypothetical protein [Methylobacillus flagellatus KT]637938256 YP_545459												
MFLA1351		0.000	0.000			■ ■		0.000	0.000			■	
	TonB-dependent receptor [Methylobacillus flagellatus KT]637938257 YP_545460												
MFLA1352		0.000	0.000			■ ■		0.000	0.000			■	
	putative FecR [Methylobacillus flagellatus KT]637938258 YP_545461												
MFLA1353		0.000	0.000			■ ■		0.000	0.000			■	
	sigma-24 (FecI-like) [Methylobacillus flagellatus KT]637938259 YP_545462												
MFLA1354		0.521	2.372	2.725	-0.814	Y ● ● Y	2.28 E-1	21.346	22.557	23.075	-0.032	Y ●	🟨
	Succinylglutamate desuccinylase/aspartoacylase [Methylobacillus flagellatus KT]637938260 YP_545463												

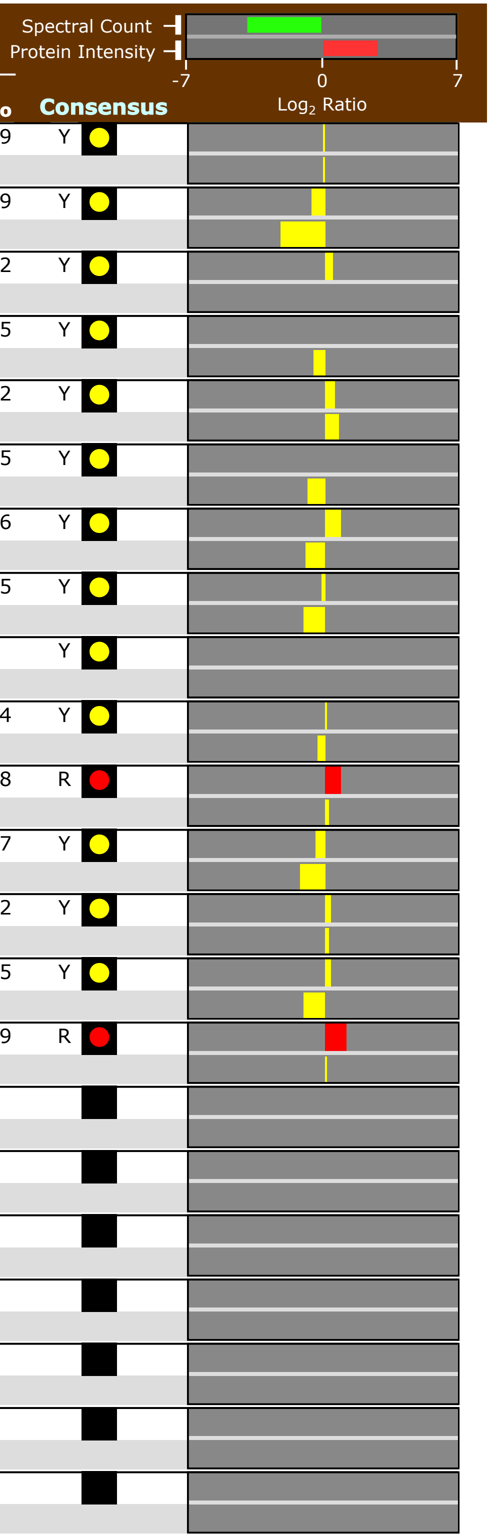
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA1355	8.24 E-2	6.097	5.788	6.951	0.308	Y	🟡	🟡	Y	8.35 E-3	25.518	25.131	26.337	0.389	Y 🟡
	YceI [Methylobacillus flagellatus KT]637938261 YP_545464														
MFLA1356	1.69 E-2	7.606	7.598	8.602	-0.014	Y	🟡	🟡	Y	1.58 E-1	27.077	26.821	27.955	0.195	Y 🟡
	protein of unknown function DUF748 [Methylobacillus flagellatus KT]637938262 YP_545465														
MFLA1357	0	8.645	6.829	9.006	1.852	R	🔴	🟡	Y	1.99 E-2	24.918	24.392	25.679	0.537	R 🔴
	hypothetical protein [Methylobacillus flagellatus KT]637938263 YP_545466														
MFLA1358		4.413	4.438	5.425	-0.022	Y	🟡	🟡	Y	5.12 E-2	23.643	23.249	24.459	0.413	Y 🟡
	GTP cyclohydrolase II [Methylobacillus flagellatus KT]637938264 YP_545467														
MFLA1359		3.461		3.461		Y	🟡	🟡	Y		22.221		22.221		Y 🟡
	" RND efflux system, outer membrane lipoprotein, NodT [Methylobacillus flagellatus KT]637938265 YP_545468 """														
MFLA1360		3.982	1.585	4.232	1.397	Y	🟡	🟡	Y	6.81 E-2	22.201	19.979	22.481	1.207	Y 🟡
	Hydrophobe/amphiphile efflux-1 HAE1 [Methylobacillus flagellatus KT]637938266 YP_545469														
MFLA1361		4.581	3.834	5.256	0.758	Y	🟡	🟡	Y	1.08 E-2	23.757	23.314	24.553	0.441	Y 🟡
	secretion protein HlyD [Methylobacillus flagellatus KT]637938267 YP_545470														
MFLA1362			1.000	1.000		Y	🟡	🟡	Y			20.327	20.327		Y 🟡
	" transcriptional regulator, TetR family [Methylobacillus flagellatus KT]637938268 YP_545471 """														
MFLA1363		0.000	0.000				■	■			0.000	0.000			■
	protein of unknown function DUF204 [Methylobacillus flagellatus KT]637938269 YP_545472														
MFLA1364		1.813		1.813		Y	🟡	🟡	Y		19.262		19.262		Y 🟡
	lipopolysaccharide kinase [Methylobacillus flagellatus KT]637938270 YP_545473														
MFLA1365		0.000	0.000				■	■			0.000	0.000			■
	Lysine exporter protein (LYSE/YGGA) [Methylobacillus flagellatus KT]637938271 YP_545474														
MFLA1366		0.000	0.000				■	■			0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938272 YP_545475														
MFLA1367		4.974	3.725	5.481	1.261	Y	🟡	🟡	Y	1.97 E-1	22.592	22.796	23.698	-0.085	Y 🟡
	" 1,4-alpha-glucan branching enzyme [Methylobacillus flagellatus KT]637938273 YP_545476 """														
MFLA1368	3.18 E-4	6.034	5.252	6.695	0.754	R	🔴	🟡	Y	3.09 E-2	24.904	24.315	25.639	0.573	R 🔴
	Glucose-1-phosphate adenylyltransferase [Methylobacillus flagellatus KT]637938274 YP_545477														
MFLA1369		3.591	3.595	4.593	-0.006	Y	🟡	🟡	Y	5.2 E-2	19.983	21.410	21.866	-1.479	Y 🟡
	" glycoside hydrolase, family 57 [Methylobacillus flagellatus KT]637938275 YP_545478 """														
MFLA1370	2.96 E-2	7.286	7.248	8.267	0.068	Y	🟡	🟡	Y	1.13 E-1	25.991	26.279	27.142	-0.325	Y 🟡
	4-alpha-glucanotransferase [Methylobacillus flagellatus KT]637938276 YP_545479														
MFLA1371		4.128	3.807	4.976	0.106	Y	🟡	🟡	Y	1.93 E-1	23.171	22.885	24.035	0.100	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938277 YP_545480														
MFLA1372	3.23 E-4	6.420	5.693	7.102	0.736	R	🔴	🟡	Y	2.53 E-1	24.791	24.802	25.797	-0.012	Y 🟡
	" glycosyl transferase, family 2 [Methylobacillus flagellatus KT]637938278 YP_545481 """														
MFLA1373		4.915	4.040	5.543	1.044	Y	🟡	🟡	Y	1.57 E-1	23.870	23.486	24.691	0.658	Y 🟡
	putative beta (1-6) glucan synthase [Methylobacillus flagellatus KT]637938279 YP_545482														
MFLA1374		0.000	0.000				■	■			0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938280 YP_545483														
MFLA1375		0.000	0.000				■	■			0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938281 YP_545484														
MFLA1376		0.000	0.000				■	■			0.000	0.000			■
	GtrA-like protein [Methylobacillus flagellatus KT]637938282 YP_545485														



ORF	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA1377		0.521	2.689	2.979	-1.056	Y 🟡 🟡 Y	7.77 E-2	18.463	22.395	22.486	-2.873	Y 🟡
	" glycosyl transferase, family 2 [Methylobacillus flagellatus KT]637938283 YP_545486 """											
MFLA1378		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938284 YP_545487											
MFLA1379		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	4Fe-4S cluster binding [Methylobacillus flagellatus KT]637938285 YP_545488											
MFLA1380		2.328	2.595	3.468	0.751	Y 🟡 🟡 Y	1.41 E-1	22.360	22.653	23.514	1.014	Y 🟡
	protein of unknown function UPF0079 [Methylobacillus flagellatus KT]637938286 YP_545489											
MFLA1381		4.357	5.197	5.837	-0.806	Y 🟡 🟡 Y	8.26 E-2	22.888	23.931	24.502	-1.351	Y 🟡
	N-acetylmuramoyl-L-alanine amidase [Methylobacillus flagellatus KT]637938287 YP_545490											
MFLA1382	1.4 E-4	6.306	6.881	7.622	-0.584	G 🟢 🟡 Y	1.38 E-2	24.968	26.261	26.755	-1.327	G 🟢
	beta-lactamase-like protein [Methylobacillus flagellatus KT]637938288 YP_545491											
MFLA1383	0	8.190	9.479	9.974	-1.269	G 🟢 🟡 Y	2.7 E-2	28.257	29.143	29.767	-0.942	G 🟢
	hypothetical protein [Methylobacillus flagellatus KT]637938289 YP_545492											
MFLA1384		3.283	3.928	4.641	-0.651	Y 🟡 🟡 Y	5.87 E-2	21.363	22.539	23.068	-1.298	Y 🟡
	DNA mismatch repair protein MutL [Methylobacillus flagellatus KT]637938290 YP_545493											
MFLA1385		2.307	1.322	2.897	-0.155	Y 🟡 🟡 Y	1.13 E-1	22.404	19.104	22.544	2.096	Y 🟡
	tRNA delta(2)-isopentenylpyrophosphate transferase [Methylobacillus flagellatus KT]637938291 YP_545494											
MFLA1386	2.69 E-2	5.464	5.911	6.705	-0.455	Y 🟡 🟡 Y	1.01 E-2	24.138	25.069	25.677	-0.943	Y 🟡
	" aminotransferase, class I and II [Methylobacillus flagellatus KT]637938292 YP_545495 """											
MFLA1387		3.610	3.739	4.676	-0.193	Y 🟡 🟡 Y	1.4 E-1	22.660	22.425	23.547	0.191	Y 🟡
	twitching motility protein [Methylobacillus flagellatus KT]637938293 YP_545496											
MFLA1388		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) [Methylobacillus flagellatus KT]637938294 YP_545497											
MFLA1389		4.601	4.328	5.471	0.264	Y 🟡 🟡 Y	1.88 E-1	22.483	22.830	23.667	-0.596	Y 🟡
	TPR repeat [Methylobacillus flagellatus KT]637938295 YP_545498											
MFLA1390		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	protein of unknown function DUF752 [Methylobacillus flagellatus KT]637938296 YP_545499											
MFLA1391		2.418	3.787	4.259	-1.181	Y 🟡 🟡 Y	9.64 E-2	21.085	22.461	22.931	-1.092	Y 🟡
	" molybdenum ABC transporter, periplasmic molybdate-binding protein [Methylobacillus flagellatus KT]637938297 YP_545500 """											
MFLA1392		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	" Molybdate ABC transporter, permease protein [Methylobacillus flagellatus KT]637938298 YP_545501 """											
MFLA1393		1.398	2.410	2.991	0.140	Y 🟡 🟡 Y	1.81 E-1	19.914	21.453	21.879	-0.344	Y 🟡
	ABC transporter related [Methylobacillus flagellatus KT]637938299 YP_545502											
MFLA1394		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	Methyltransferase type 12 [Methylobacillus flagellatus KT]637938300 YP_545503											
MFLA1395		4.656	4.964	5.818	-0.283	Y 🟡 🟡 Y	1.02 E-1	24.730	25.088	25.920	-0.313	Y 🟡
	putative phage repressor [Methylobacillus flagellatus KT]637938301 YP_545504											
MFLA1396		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938302 YP_545505											
MFLA1397		0.521		0.521		Y 🟡 🟡 Y		20.272		20.272		Y 🟡
	putative phospholipase [Methylobacillus flagellatus KT]637938303 YP_545506											
MFLA1398	6.66 E-2	5.109	5.543	6.342	-1.015	Y 🟡 🟡 Y	8.9 E-2	23.368	24.244	24.872	-1.568	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938306 YP_545507											



ORF	AM/OH *M Flagellatus* Spectral Count					Regulation				AM/OH *M Flagellatus* Protein Intensity					Consensus	
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio					*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		
MFLA1399	3.92 E-2	5.306	5.298	6.302	-0.103	Y	🟡	🟡	Y	2.48 E-1	24.070	24.139	25.105	-0.119	Y	🟡
	sulfatase [Methylobacillus flagellatus KT]637938307 YP_545508															
MFLA1400	1.59 E-2	3.983	5.700	6.083	-0.712	Y	🟡	🟡	Y	7.49 E-2	21.350	24.683	24.819	-2.289	Y	🟡
	GTP cyclohydrolase I [Methylobacillus flagellatus KT]637938308 YP_545509															
MFLA1401	4 E-2	5.637	5.276	6.468	0.377	Y	🟡	🟡	Y	2.37 E-1	23.259	23.336	24.298	-0.012	Y	🟡
	Chromosome segregation protein SMC [Methylobacillus flagellatus KT]637938309 YP_545510															
MFLA1402	6.09 E-2	5.944	5.929	6.937	-0.031	Y	🟡	🟡	Y	1.82 E-1	25.424	25.729	26.584	-0.585	Y	🟡
	" putative ZipA related protein, possibly involved in cell division [Methylobacillus flagellatus KT]637938310 YP_545511 """															
MFLA1403	4.06 E-2	5.532	4.995	6.289	0.530	Y	🟡	🟡	Y	7.02 E-2	24.521	23.721	25.176	0.712	Y	🟡
	" DNA ligase, NAD-dependent [Methylobacillus flagellatus KT]637938311 YP_545512 """															
MFLA1404		2.710	1.585	3.255	0.035	Y	🟡	🟡	Y	7.72 E-2	20.259	20.107	21.185	-0.895	Y	🟡
	" 3'(2'),5'-bisphosphate nucleotidase [Methylobacillus flagellatus KT]637938312 YP_545513 """															
MFLA1405		4.397	3.584	5.047	0.786	Y	🟡	🟡	Y	1.42 E-1	21.518	22.128	22.855	-1.026	Y	🟡
	TPR repeat [Methylobacillus flagellatus KT]637938313 YP_545514															
MFLA1406		3.199	3.275	4.237	-0.225	Y	🟡	🟡	Y	2.52 E-2	24.232	25.316	25.873	-1.095	Y	🟡
	Conserved TM helix [Methylobacillus flagellatus KT]637938314 YP_545515															
MFLA1407		2.813		2.813		Y	🟡	🟡	Y		20.577		20.577		Y	🟡
	cold-shock DNA-binding domain protein [Methylobacillus flagellatus KT]637938315 YP_545516															
MFLA1408	1.8 E-2	9.340	9.231	10.287	0.110	Y	🟡	🟡	Y	5.57 E-2	29.290	29.684	30.501	-0.414	Y	🟡
	trigger factor [Methylobacillus flagellatus KT]637938316 YP_545517															
MFLA1409	3.4 E-16	7.713	6.830	8.338	0.826	R	🔴	🟡	Y	1.35 E-1	26.727	26.550	27.641	0.158	R	🔴
	" ATP-dependent Clp protease, proteolytic subunit ClpP [Methylobacillus flagellatus KT]637938317 YP_545518 """															
MFLA1410		6.253	6.868	7.593	-0.497	Y	🟡	🟡	Y	2.43 E-2	25.606	26.990	27.458	-1.347	Y	🟡
	" ATP-dependent Clp protease, ATP-binding subunit ClpX [Methylobacillus flagellatus KT]637938318 YP_545519 """															
MFLA1411	1.01 E-7	9.235	8.902	10.078	0.323	Y	🟡	🟡	Y	1.29 E-2	28.683	28.451	29.572	0.232	Y	🟡
	ATP-dependent protease La [Methylobacillus flagellatus KT]637938319 YP_545520															
MFLA1412		6.366	5.826	7.121	0.320	Y	🟡	🟡	Y	2.7 E-1	27.420	27.358	28.389	-1.085	Y	🟡
	histone-like DNA-binding protein [Methylobacillus flagellatus KT]637938320 YP_545521															
MFLA1413	0	9.162	8.141	9.740	1.087	R	🔴	🟡	Y	1.43 E-1	27.899	27.780	28.841	0.119	R	🔴
	PpiC-type peptidyl-prolyl cis-trans isomerase [Methylobacillus flagellatus KT]637938323 YP_545522															
MFLA1414		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938324 YP_545523															
MFLA1415		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938325 YP_545524															
MFLA1416		0.000	0.000				■	■			0.000	0.000				■
	Malto-oligosyltrehalose synthase [Methylobacillus flagellatus KT]637938326 YP_545525															
MFLA1417		0.000	0.000				■	■			0.000	0.000				■
	Malto-oligosyltrehalose trehalohydrolase [Methylobacillus flagellatus KT]637938327 YP_545526															
MFLA1418		0.000	0.000				■	■			0.000	0.000				■
	Trehalose synthase-like protein [Methylobacillus flagellatus KT]637938328 YP_545527															
MFLA1419		0.000	0.000				■	■			0.000	0.000				■
	" alpha amylase, catalytic region [Methylobacillus flagellatus KT]637938329 YP_545528 """															
MFLA1420		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938330 YP_545529															

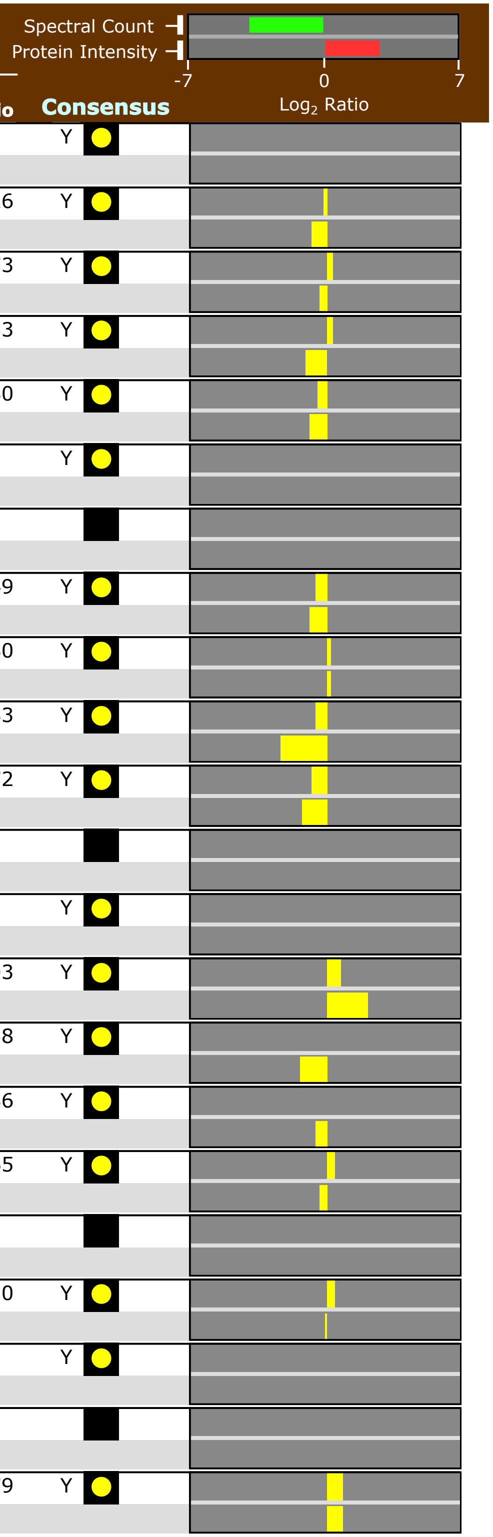


	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity						Spectral Count 🟩 Protein Intensity 🟥 -7 0 7
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	$\log_2$ Ratio
MFLA1421		0.000	0.000			■ ■		0.000	0.000			■	
	phospholipase D/Transphosphatidylase [Methylobacillus flagellatus KT]637938331 YP_545530												
MFLA1422		0.000	0.000			■ ■		0.000	0.000			■	
	Endonuclease/exonuclease/phosphatase [Methylobacillus flagellatus KT]637938332 YP_545531												
MFLA1423		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938333 YP_545532												
MFLA1424		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938334 YP_545533												
MFLA1425		0.000	0.000			■ ■		0.000	0.000			■	
	methyltransferase small [Methylobacillus flagellatus KT]637938335 YP_545534												
MFLA1426		0.000	0.000			■ ■		0.000	0.000			■	
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637938336 YP_545535												
MFLA1427		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938337 YP_545536												
MFLA1428		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938338 YP_545537												
MFLA1429		0.000	0.000			■ ■		0.000	0.000			■	
	copper resistance protein CopC [Methylobacillus flagellatus KT]637938339 YP_545538												
MFLA1430		0.000	0.000			■ ■		0.000	0.000			■	
	copper resistance D [Methylobacillus flagellatus KT]637938340 YP_545539												
MFLA1431		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938341 YP_545540												
MFLA1432		0.000	0.000			■ ■		0.000	0.000			■	
	" cytochrome c, class I [Methylobacillus flagellatus KT]637938342 YP_545541 """												
MFLA1433		0.000	0.000			■ ■		0.000	0.000			■	
	" cytochrome C oxidase, mono-heme subunit/FixO [Methylobacillus flagellatus KT]637938343 YP_545542 """												
MFLA1434		0.000	0.000			■ ■		0.000	0.000			■	
	" cytochrome c oxidase, subunit I [Methylobacillus flagellatus KT]637938344 YP_545543 """												
MFLA1435		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938345 YP_545544												
MFLA1436		0.000	0.000			■ ■		0.000	0.000			■	
	Catalase [Methylobacillus flagellatus KT]637938346 YP_545545												
MFLA1437		0.000	0.000			■ ■		0.000	0.000			■	
	integral membrane protein [Methylobacillus flagellatus KT]637938347 YP_545546												
MFLA1438		0.000	0.000			■ ■		0.000	0.000			■	
	NAD-dependent epimerase/dehydratase [Methylobacillus flagellatus KT]637938348 YP_545547												
MFLA1439		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938349 YP_545548												
MFLA1440		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637938350 YP_545549												
MFLA1441		0.000	0.000			■ ■		0.000	0.000			■	
	Alcohol dehydrogenase GroES-like protein [Methylobacillus flagellatus KT]637938351 YP_545550												
MFLA1442		0.000	0.000			■ ■		0.000	0.000			■	
	fatty acid beta hydroxylase (cytochrome P450) [Methylobacillus flagellatus KT]637938352 YP_545551												

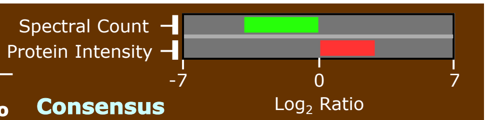
Spectral Count 🟩
Protein Intensity 🟥
-7 0 7
Log$_2$ Ratio

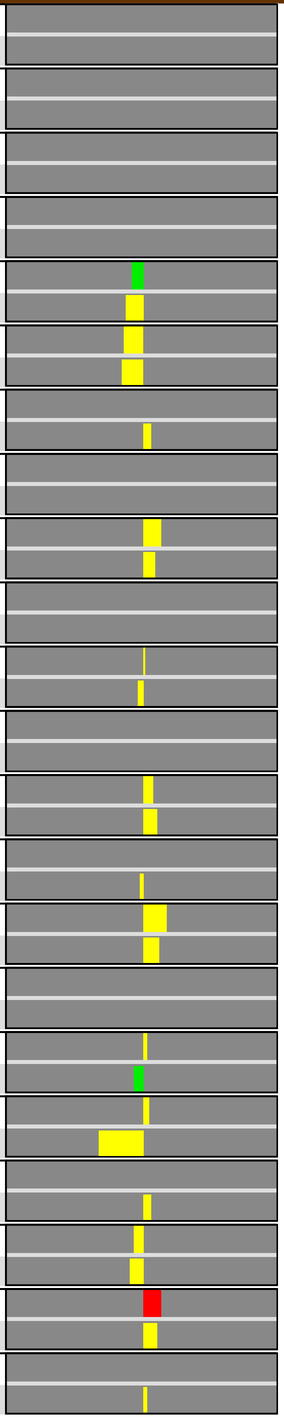
ORF	AM/OH *M Flagellatus* Spectral Count					Regulation				AM/OH *M Flagellatus* Protein Intensity					Consensus		Log$_2$ Ratio
	q-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio					*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio			
MFLA1443		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938353 YP_545552																
MFLA1444			1.807	1.807		Y	🟡	🟡	Y			17.018	17.018		Y	🟡	
	protein of unknown function DUF336 [Methylobacillus flagellatus KT]637938354 YP_545553																
MFLA1445		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938355 YP_545554																
MFLA1446		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938356 YP_545555																
MFLA1447		0.000	0.000				■	■			0.000	0.000				■	
	" cytochrome c oxidase, subunit III [Methylobacillus flagellatus KT]637938357 YP_545556 """																
MFLA1448		0.000	0.000				■	■			0.000	0.000				■	
	Cytochrome-c oxidase [Methylobacillus flagellatus KT]637938358 YP_545557																
MFLA1449		0.000	0.000				■	■			0.000	0.000				■	
	" cytochrome c oxidase, subunit II [Methylobacillus flagellatus KT]637938359 YP_545558 """																
MFLA1450		0.000	0.000				■	■			0.000	0.000				■	
	" cytochrome c, class I [Methylobacillus flagellatus KT]637938360 YP_545559 """																
MFLA1451		0.000	0.000				■	■			0.000	0.000				■	
	Pyrrolo-quinoline quinone [Methylobacillus flagellatus KT]637938361 YP_545560																
MFLA1452		0.000	0.000				■	■			0.000	0.000				■	
	MscS Mechanosensitive ion channel [Methylobacillus flagellatus KT]637938362 YP_545561																
MFLA1453		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938363 YP_545562																
MFLA1454	1.06 E-1	5.093	5.018	6.056	0.053	Y	🟡	🟡	Y	1.82 E-1	24.326	23.935	25.144	0.085	Y	🟡	🟨
	hypothetical protein [Methylobacillus flagellatus KT]637938364 YP_545563																🟨
MFLA1455	1.72 E-4	4.386	5.510	6.055	-1.127	G	🟢	🟡	Y	1.33 E-1	24.763	25.123	25.954	-0.423	G	🟢	🟩
	hypothetical protein [Methylobacillus flagellatus KT]637938365 YP_545564																🟨
MFLA1456		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938366 YP_545565																
MFLA1457		0.000	0.000				■	■			0.000	0.000				■	
	type II and III secretion system protein [Methylobacillus flagellatus KT]637938367 YP_545566																
MFLA1458		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938368 YP_545567																
MFLA1459		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938369 YP_545568																
MFLA1460		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938370 YP_545569																
MFLA1461		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938371 YP_545570																
MFLA1462		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938372 YP_545571																
MFLA1463		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938373 YP_545572																
MFLA1464		1.521	1.000	2.284	0.521	Y	🟡	🟡	Y		20.592	20.191	21.405	0.401	Y	🟡	🟨
	hypothetical protein [Methylobacillus flagellatus KT]637938374 YP_545573																🟨

	AM/OH *M Flagellatus* Spectral Count							AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation		*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA1465		0.813		0.813		Y ●	● Y		20.420		20.420		Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637938375 YP_545574												
MFLA1466		4.467	4.543	5.505	-0.167	Y ●	● Y	6.47 E-2	24.465	25.137	25.840	-0.826	Y ●
	Peptide deformylase [Methylobacillus flagellatus KT]637938377 YP_545575												
MFLA1467		4.964	4.641	5.811	0.316	Y ●	● Y	1.44 E-1	24.855	25.140	26.004	-0.373	Y ●
	5'-methylthioadenosine phosphorylase [Methylobacillus flagellatus KT]637938378 YP_545576												
MFLA1468		4.357	3.991	5.186	0.251	Y ●	● Y	8 E-2	22.264	23.002	23.679	-1.053	Y ●
	Squalene/phytoene synthase [Methylobacillus flagellatus KT]637938379 YP_545577												
MFLA1469		2.795	3.240	4.035	-0.486	Y ●	● Y	1.02 E-1	21.390	22.619	23.132	-0.880	Y ●
	Squalene/phytoene synthase [Methylobacillus flagellatus KT]637938380 YP_545578												
MFLA1470		0.521		0.521		Y ●	● Y		18.602		18.602		Y ●
	amine oxidase [Methylobacillus flagellatus KT]637938381 YP_545579												
MFLA1471		0.000	0.000			■	■		0.000	0.000			■
	membrane protein of unknown function [Methylobacillus flagellatus KT]637938382 YP_545580												
MFLA1472	1.82 E-2	4.926	5.541	6.266	-0.618	Y ●	● Y	4.68 E-2	23.349	24.204	24.839	-0.949	Y ●
	" Glycogen/starch synthases, ADP-glucose type [Methylobacillus flagellatus KT]637938383 YP_545581 """												
MFLA1473	1.07 E-1	5.976	5.727	6.857	0.246	Y ●	● Y	1.65 E-1	25.274	25.090	26.185	0.180	Y ●
	Exonuclease [Methylobacillus flagellatus KT]637938384 YP_545582												
MFLA1474		4.277	4.825	5.577	-0.571	Y ●	● Y	4.5 E-2	22.678	24.519	24.875	-2.383	Y ●
	Ste24 endopeptidase [Methylobacillus flagellatus KT]637938385 YP_545583												
MFLA1475		3.582	3.725	4.655	-0.752	Y ●	● Y	2.01 E-2	22.139	23.287	23.825	-1.272	Y ●
	GTPase EngC [Methylobacillus flagellatus KT]637938386 YP_545584												
MFLA1476		0.000	0.000			■	■		0.000	0.000			■
	histone deacetylase superfamily [Methylobacillus flagellatus KT]637938387 YP_545585												
MFLA1477			3.039	3.039		Y ●	● Y			21.812	21.812		Y ●
	6-pyruvoyl tetrahydrobiopterin synthase [Methylobacillus flagellatus KT]637938388 YP_545586												
MFLA1478		3.691	3.000	4.386	0.691	Y ●	● Y		21.809	19.706	22.111	2.103	Y ●
	" DNA polymerase III, epsilon subunit [Methylobacillus flagellatus KT]637938389 YP_545587 """												
MFLA1479		1.967	1.966	2.966	-0.006	Y ●	● Y	1.05 E-1	20.331	21.218	21.842	-1.358	Y ●
	ribonuclease H [Methylobacillus flagellatus KT]637938390 YP_545588												
MFLA1480		3.899	4.027	4.965	-0.050	Y ●	● Y	7.62 E-2	22.019	22.511	23.286	-0.586	Y ●
	Methyltransferase type 11 [Methylobacillus flagellatus KT]637938391 YP_545589												
MFLA1481		3.930	3.551	4.753	0.362	Y ●	● Y	6.49 E-2	22.371	22.753	23.575	-0.365	Y ●
	Hydroxyacylglutathione hydrolase [Methylobacillus flagellatus KT]637938392 YP_545590												
MFLA1482		0.000	0.000			■	■		0.000	0.000			■
	" Lytic transglycosylase, catalytic [Methylobacillus flagellatus KT]637938393 YP_545591 """												
MFLA1483		5.014	4.581	5.814	0.434	Y ●	● Y	2.21 E-1	23.797	23.871	24.834	-0.110	Y ●
	" extracellular solute-binding protein, family 5 [Methylobacillus flagellatus KT]637938394 YP_545592 """												
MFLA1484		0.521		0.521		Y ●	● Y		19.024		19.024		Y ●
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637938395 YP_545593												
MFLA1485		0.000	0.000			■	■		0.000	0.000			■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637938396 YP_545594												
MFLA1486		6.771	5.802	7.366	0.816	Y ●	● Y	3.09 E-2	27.226	26.464	27.894	0.779	Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637938397 YP_545595												

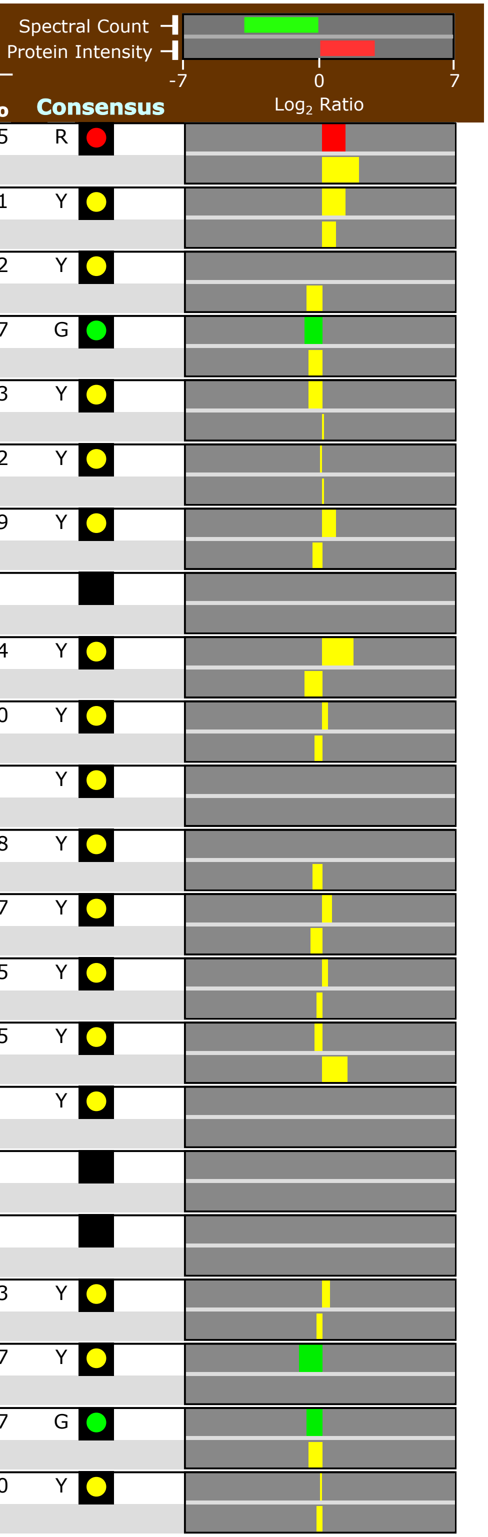


ORF	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA1487		0.000	0.000			■ ■		0.000	0.000			■
	putative hydrolase protein [Methylobacillus flagellatus KT]637938398 YP_545596											
MFLA1488		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938399 YP_545597											
MFLA1489		0.000	0.000			■ ■		0.000	0.000			■
	Arsenical pump membrane protein [Methylobacillus flagellatus KT]637938400 YP_545598											
MFLA1490		0.000	0.000			■ ■		0.000	0.000			■
	putative signal transduction protein with CBS domains [Methylobacillus flagellatus KT]637938401 YP_545599											
MFLA1491	3.85 E-3	5.479	6.049	6.792	-0.620	G 🟢 🟡 Y	2.74 E-2	23.707	24.552	25.190	-0.882	G 🟢
	arsenite-activated ATPase (arsA) [Methylobacillus flagellatus KT]637938402 YP_545600											
MFLA1492		1.106	3.102	3.425	-0.971	Y 🟡 🟡 Y	1.02 E-1	21.623	23.806	24.093	-1.122	Y 🟡
	Arsenical resistance operon trans-acting repressor ArsD [Methylobacillus flagellatus KT]637938403 YP_545601											
MFLA1493		2.328	3.546	4.062	-0.050	Y 🟡 🟡 Y	1.48 E-1	21.016	21.643	22.363	0.445	Y 🟡
	" transcriptional regulator, ArsR family [Methylobacillus flagellatus KT]637938404 YP_545602 """											
MFLA1494		0.000	0.000			■ ■		0.000	0.000			■
	Resolvase-like protein [Methylobacillus flagellatus KT]637938405 YP_545603											
MFLA1495		1.843	0.931	2.458	0.911	Y 🟡 🟡 Y		19.103	18.536	19.848	0.567	Y 🟡
	transposase Tn3 [Methylobacillus flagellatus KT]637938406 YP_545604											
MFLA1496		0.000	0.000			■ ■		0.000	0.000			■
	putative hydrolase protein [Methylobacillus flagellatus KT]637938407 YP_545605											
MFLA1497		4.601	4.456	5.530	0.107	Y 🟡 🟡 Y	1.13 E-1	23.733	23.994	24.869	-0.308	Y 🟡
	TatD-related deoxyribonuclease [Methylobacillus flagellatus KT]637938408 YP_545606											
MFLA1498		0.000	0.000			■ ■		0.000	0.000			■
	type IV pilus assembly PilZ [Methylobacillus flagellatus KT]637938409 YP_545607											
MFLA1499		3.106	2.585	3.869	0.521	Y 🟡 🟡 Y		21.901	21.170	22.581	0.731	Y 🟡
	" DNA polymerase III, delta prime subunit [Methylobacillus flagellatus KT]637938410 YP_545608 """											
MFLA1500		3.700	3.638	4.670	0.044	Y 🟡 🟡 Y	2.7 E-1	21.355	21.312	22.334	-0.181	Y 🟡
	Thymidylate kinase [Methylobacillus flagellatus KT]637938411 YP_545609											
MFLA1501		4.967	3.778	5.492	1.201	Y 🟡 🟡 Y	7.36 E-2	23.642	22.844	24.297	0.770	Y 🟡
	aminodeoxychorismate lyase [Methylobacillus flagellatus KT]637938412 YP_545610											
MFLA1502		0.000	0.000			■ ■		0.000	0.000			■
	" aminotransferase, class IV [Methylobacillus flagellatus KT]637938413 YP_545611 """											
MFLA1503		8.071	7.901	8.989	0.175	Y 🟡 🟢 G	5.49 E-3	27.282	27.822	28.577	-0.541	Y 🟡
	beta-ketoacyl synthase [Methylobacillus flagellatus KT]637938414 YP_545612											
MFLA1504		6.650	6.070	7.389	0.345	Y 🟡 🟡 Y	1.99 E-2	26.728	28.806	29.113	-2.260	Y 🟡
	acyl carrier protein [Methylobacillus flagellatus KT]637938415 YP_545613											
MFLA1505	1.48 E-1	6.439	6.405	7.422	0.030	Y 🟡 🟡 Y	9.8 E-2	26.666	26.232	27.465	0.397	Y 🟡
	3-oxoacyl-(acyl-carrier-protein) reductase [Methylobacillus flagellatus KT]637938416 YP_545614											
MFLA1506	1.05 E-2	6.180	6.629	7.422	-0.460	Y 🟡 🟡 Y	1.23 E-2	24.979	25.657	26.357	-0.686	Y 🟡
	malonyl CoA-acyl carrier protein transacylase [Methylobacillus flagellatus KT]637938417 YP_545615											
MFLA1507	3 E-6	6.115	5.151	6.712	0.864	R 🔴 🟡 Y	3.18 E-2	24.427	23.740	25.124	0.706	R 🔴
	3-oxoacyl-(acyl-carrier-protein) synthase III [Methylobacillus flagellatus KT]637938418 YP_545616											
MFLA1508		2.996	2.966	3.981	0.023	Y 🟡 🟡 Y	1.5 E-1	22.231	21.919	23.084	0.230	Y 🟡
	fatty acid/phospholipid synthesis protein PlsX [Methylobacillus flagellatus KT]637938419 YP_545617											

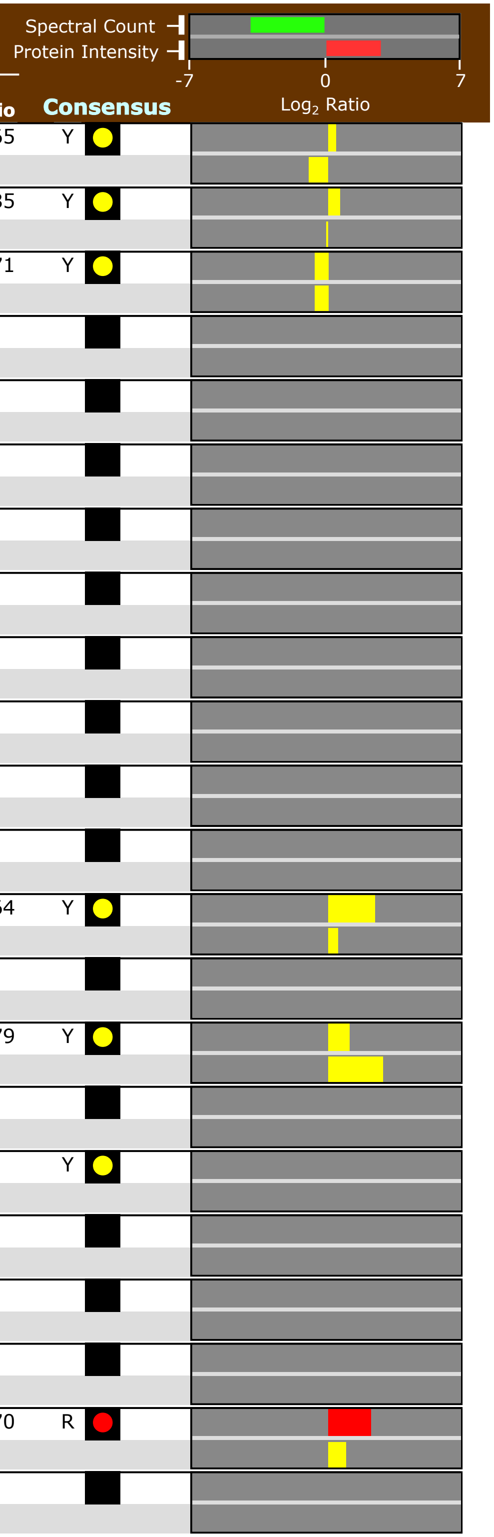


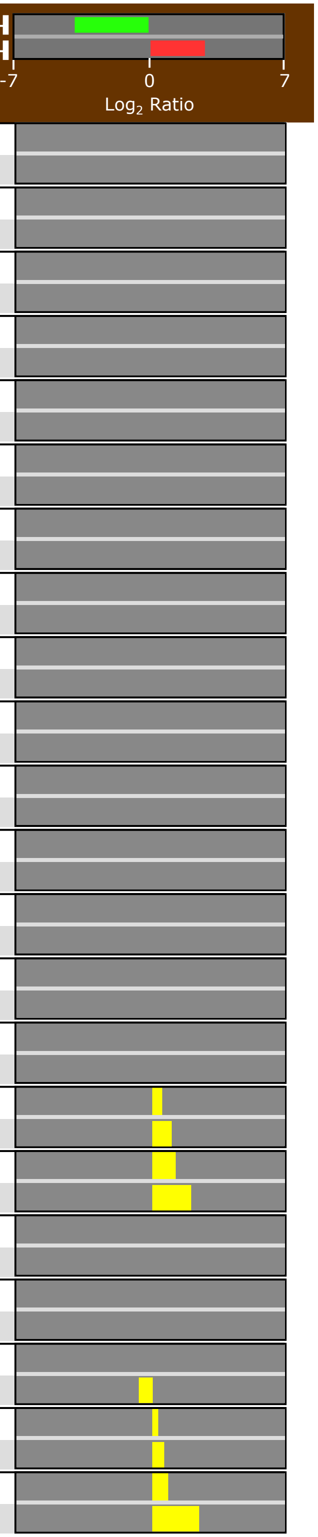


	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	***q*-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**	***q*-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**
MFLA1509	0	7.207	6.064	7.746	1.208	R 🔴 🟡 Y	5.57 E-2	27.305	25.527	27.674	1.935	R 🔴
	ribosomal protein L32 [Methylobacillus flagellatus KT]637938420 YP_545618											
MFLA1510		6.273	4.258	6.592	1.247	Y 🟡 🟡 Y	1.59 E-1	23.418	22.732	24.116	0.681	Y 🟡
	protein of unknown function DUF177 [Methylobacillus flagellatus KT]637938421 YP_545619											
MFLA1511	1.25 E-1	7.230	7.187	8.209	0.037	Y 🟡 🟡 Y	2.12 E-2	26.995	27.755	28.424	-0.802	Y 🟡
	" acetyl-CoA carboxylase, biotin carboxylase [Methylobacillus flagellatus KT]637938422 YP_545620 """											
MFLA1512	0	9.043	9.951	10.567	-0.915	G 🟢 🟡 Y	1.26 E-2	28.807	29.470	30.176	-0.677	G 🟢
	oxaloacetate decarboxylase alpha subunit [Methylobacillus flagellatus KT]637938423 YP_545621											
MFLA1513		2.106	2.806	3.498	-0.700	Y 🟡 🟡 Y		22.641	22.498	23.571	0.143	Y 🟡
	maf protein [Methylobacillus flagellatus KT]637938424 YP_545622											
MFLA1514	1.15 E-2	6.448	6.580	7.515	-0.140	Y 🟡 🟡 Y	1.48 E-1	26.018	25.909	26.964	0.122	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938425 YP_545623											
MFLA1515		3.656	2.000	4.054	0.656	Y 🟡 🟡 Y	1.48 E-1	21.084	20.481	21.813	-0.479	Y 🟡
	Uroporphyrin-III C/tetrapyrrole (Corrin/Porphyrin) methyltransferase [Methylobacillus flagellatus KT]637938426 YP_545624											
MFLA1516		0.000	0.000			■ ■		0.000	0.000			■
	Ribonuclease H [Methylobacillus flagellatus KT]637938427 YP_545625											
MFLA1517		2.843	2.529	3.694	1.584	Y 🟡 🟡 Y	6.31 E-2	20.649	22.571	22.909	-0.914	Y 🟡
	lipid-A-disaccharide synthase [Methylobacillus flagellatus KT]637938428 YP_545626											
MFLA1518	3.03 E-2	6.631	6.276	7.464	0.345	Y 🟡 🟡 Y	3.26 E-2	24.393	24.828	25.627	-0.430	Y 🟡
	acyl-(acyl-carrier-protein)--UDP-N- acetylglucosamine O-acyltransferase [Methylobacillus flagellatus KT]637938429 YP_545627											
MFLA1519		4.623		4.623		Y 🟡 🟡 Y		24.503		24.503		Y 🟡
	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ [Methylobacillus flagellatus KT]637938430 YP_545628											
MFLA1520	5.21 E-2	5.101	5.001	6.052	0.017	Y 🟡 🟡 Y	4.84 E-2	24.359	24.813	25.604	-0.458	Y 🟡
	UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase [Methylobacillus flagellatus KT]637938431 YP_545629											
MFLA1521		8.219	7.758	9.007	0.494	Y 🟡 🟡 Y	3.09 E-2	27.454	28.071	28.795	-0.617	Y 🟡
	outer membrane chaperone Skp (OmpH) [Methylobacillus flagellatus KT]637938432 YP_545630											
MFLA1522	8.78 E-3	7.470	7.185	8.334	0.269	Y 🟡 🟡 Y	1.82 E-2	26.732	27.068	27.909	-0.335	Y 🟡
	surface antigen (D15) [Methylobacillus flagellatus KT]637938433 YP_545631											
MFLA1523		1.106	2.505	2.969	-0.390	Y 🟡 🟡 Y	8.3 E-2	20.833	20.656	21.747	1.345	Y 🟡
	" Peptidase M50, putative membrane-associated zinc metallopeptidase [Methylobacillus flagellatus KT]637938434 YP_545632 """											
MFLA1524			1.000	1.000		Y 🟡 🟡 Y			19.948	19.948		Y 🟡
	1-deoxy-D-xylulose-5-phosphate reductoisomerase [Methylobacillus flagellatus KT]637938435 YP_545633											
MFLA1525		0.000	0.000			■ ■		0.000	0.000			■
	phosphatidate cytidylyltransferase [Methylobacillus flagellatus KT]637938436 YP_545634											
MFLA1526		0.000	0.000			■ ■		0.000	0.000			■
	undecaprenyl diphosphate synthase [Methylobacillus flagellatus KT]637938437 YP_545635											
MFLA1527	2.37 E-2	6.043	5.633	6.852	0.400	Y 🟡 🟡 Y	8.4 E-2	26.318	26.623	27.478	-0.333	Y 🟡
	ribosome recycling factor [Methylobacillus flagellatus KT]637938438 YP_545636											
MFLA1528	0	6.353	7.553	8.074	-1.152	G 🟢 🟡 Y	2.19 E-1	26.210	26.039	27.127	0.007	Y 🟡
	Uridylate kinase [Methylobacillus flagellatus KT]637938439 YP_545637											
MFLA1529	0	10.156	10.904	11.578	-0.824	G 🟢 🟡 Y	1.77 E-2	28.847	29.549	30.240	-0.717	G 🟢
	translation elongation factor Ts [Methylobacillus flagellatus KT]637938440 YP_545638											
MFLA1530	1.07 E-1	8.002	8.121	9.063	-0.118	Y 🟡 🟡 Y	1.05 E-1	29.567	29.835	30.707	-0.290	Y 🟡
	ribosomal protein S2 [Methylobacillus flagellatus KT]637938441 YP_545639											

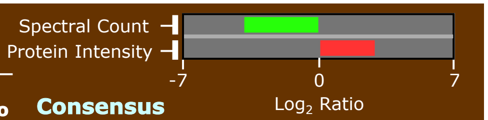


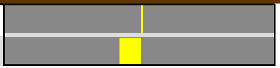
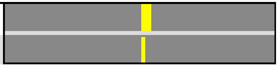
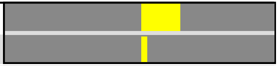
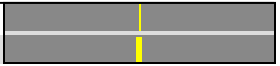
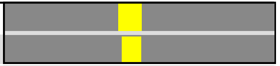
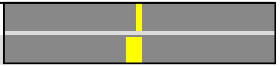
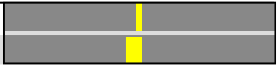
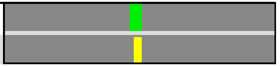
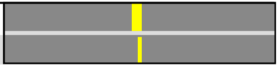
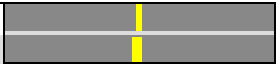
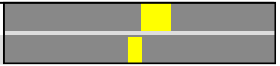
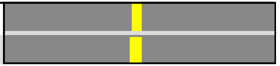
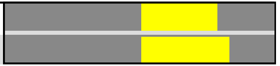
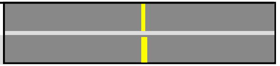
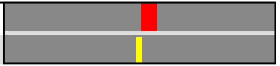
	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**	**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**
MFLA1531	6.46 E-2	5.315	4.915	6.129	0.404	Y 🟡 🟡 Y	1.12 E-2	23.583	24.556	25.150	-0.965	Y 🟡
	" methionine aminopeptidase, type I [Methylobacillus flagellatus KT]637938442 YP_545640 """											
MFLA1532		5.120	4.360	5.789	0.605	Y 🟡 🟡 Y	1.93 E-1	22.702	22.284	23.508	-0.085	Y 🟡
	" UTP-GlnB (protein PII) uridylyltransferase, GlnD [Methylobacillus flagellatus KT]637938443 YP_545641 """											
MFLA1533		7.979	8.451	9.235	-0.658	Y 🟡 🟡 Y	5.77 E-2	27.163	27.855	28.550	-0.671	Y 🟡
	" protein of unknown function DUF861, cupin_3 [Methylobacillus flagellatus KT]637938444 YP_545642 """											
MFLA1534		0.000	0.000			■ ■		0.000	0.000			■
	Alkanesulfonate monooxygenase [Methylobacillus flagellatus KT]637938445 YP_545643											
MFLA1535		0.000	0.000			■ ■		0.000	0.000			■
	Alkanesulfonate monooxygenase [Methylobacillus flagellatus KT]637938446 YP_545644											
MFLA1536		0.000	0.000			■ ■		0.000	0.000			■
	Haloacid dehalogenase-like hydrolase [Methylobacillus flagellatus KT]637938447 YP_545645											
MFLA1537		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938448 YP_545646											
MFLA1538		0.000	0.000			■ ■		0.000	0.000			■
	nitroreductase [Methylobacillus flagellatus KT]637938449 YP_545647											
MFLA1539		0.000	0.000			■ ■		0.000	0.000			■
	" extracellular solute-binding protein, family 5 [Methylobacillus flagellatus KT]637938450 YP_545648 """											
MFLA1540		0.000	0.000			■ ■		0.000	0.000			■
	ABC transporter related [Methylobacillus flagellatus KT]637938451 YP_545649											
MFLA1541		0.000	0.000			■ ■		0.000	0.000			■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637938452 YP_545650											
MFLA1542		0.000	0.000			■ ■		0.000	0.000			■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637938453 YP_545651											
MFLA1543		4.547	2.254	4.815	2.440	Y 🟡 🟡 Y	1.41 E-2	21.557	21.098	22.346	0.464	Y 🟡
	" HAD-superfamily hydrolase subfamily IA, variant 3 [Methylobacillus flagellatus KT]637938454 YP_545652 """											
MFLA1544		0.000	0.000			■ ■		0.000	0.000			■
	luciferase-like protein [Methylobacillus flagellatus KT]637938455 YP_545653											
MFLA1545		1.106	0.000	1.656	1.106	Y 🟡 🟡 Y		20.238	17.459	20.434	2.779	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938456 YP_545654											
MFLA1546		0.000	0.000			■ ■		0.000	0.000			■
	" thermophilic desulfurizing enzyme, TdsB protein [Methylobacillus flagellatus KT]637938457 YP_545655 """											
MFLA1547		0.521		0.521		Y 🟡 🟡 Y		17.575		17.575		Y 🟡
	TonB-dependent receptor [Methylobacillus flagellatus KT]637938458 YP_545656											
MFLA1548		0.000	0.000			■ ■		0.000	0.000			■
	ABC transporter related [Methylobacillus flagellatus KT]637938459 YP_545657											
MFLA1549		0.000	0.000			■ ■		0.000	0.000			■
	ABC transporter related [Methylobacillus flagellatus KT]637938460 YP_545658											
MFLA1550		0.000	0.000			■ ■		0.000	0.000			■
	" thermophilic desulfurizing enzyme, TdsB protein [Methylobacillus flagellatus KT]637938461 YP_545659 """											
MFLA1551	0	8.423	6.268	8.715	2.163	R 🔴 🟡 Y	1.1 E-2	27.073	26.207	27.704	0.870	R 🔴
	Peroxidase [Methylobacillus flagellatus KT]637938462 YP_545660											
MFLA1552		0.000	0.000			■ ■		0.000	0.000			■
	protein of unknown function DUF81 [Methylobacillus flagellatus KT]637938464 YP_545661											



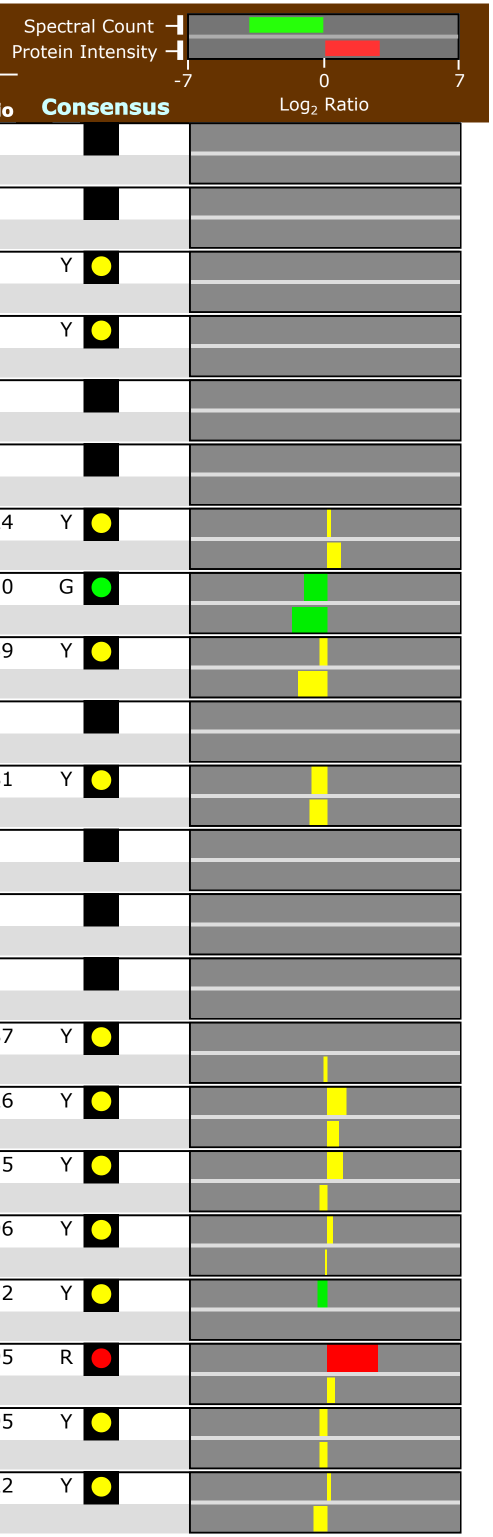


ORF	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA1553		0.521		0.521		Y ● ● Y		18.261		18.261		Y ●
	" DNA polymerase III, epsilon subunit [Methylobacillus flagellatus KT]637938465 YP_545662 """											
MFLA1554		0.000	0.000			■ ■		0.000	0.000			■
	ABC transporter related [Methylobacillus flagellatus KT]637938466 YP_545663											
MFLA1555		1.106		1.106		Y ● ● Y		21.855		21.855		Y ●
	ABC transporter related [Methylobacillus flagellatus KT]637938467 YP_545664											
MFLA1556		0.000	0.000			■ ■		0.000	0.000			■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637938468 YP_545665											
MFLA1557		0.000	0.000			■ ■		0.000	0.000			■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637938469 YP_545666											
MFLA1558		0.000	0.000			■ ■		0.000	0.000			■
	Biopolymer transport protein ExbD/TolR [Methylobacillus flagellatus KT]637938470 YP_545667											
MFLA1559		0.000	0.000			■ ■		0.000	0.000			■
	MotA/TolQ/ExbB proton channel [Methylobacillus flagellatus KT]637938471 YP_545668											
MFLA1560		0.000	0.000			■ ■		0.000	0.000			■
	TonB-like protein [Methylobacillus flagellatus KT]637938472 YP_545669											
MFLA1561		0.000	0.000			■ ■		0.000	0.000			■
	ABC transporter related [Methylobacillus flagellatus KT]637938473 YP_545670											
MFLA1562		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938474 YP_545671											
MFLA1563			0.000	0.000		Y ● ● Y			17.301	17.301		Y ●
	" sulfonate ABC transporter, periplasmic sulfonate-binding protein SsuA [Methylobacillus flagellatus KT]637938475 YP_545672 """											
MFLA1564		0.000	0.000			■ ■		0.000	0.000			■
	" sulfonate ABC transporter, periplasmic sulfonate-binding protein SsuA [Methylobacillus flagellatus KT]637938476 YP_545673 """											
MFLA1565		0.000	0.000			■ ■		0.000	0.000			■
	" monooxygenase, putative [Methylobacillus flagellatus KT]637938477 YP_545674 """											
MFLA1566		0.000	0.000			■ ■		0.000	0.000			■
	class II aldolase/adducin-like protein [Methylobacillus flagellatus KT]637938478 YP_545675											
MFLA1567		1.106		1.106		Y ● ● Y		18.169		18.169		Y ●
	" sigma-54 factor, interaction region [Methylobacillus flagellatus KT]637938479 YP_545676 """											
MFLA1568		4.312	3.857	5.103	0.453	Y ● ● Y	4.08 E-2	22.820	21.814	23.403	0.960	Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637938480 YP_545677											
MFLA1569		1.843	1.710	2.778	1.169	Y ● ● Y	2.81 E-2	21.839	20.887	22.440	1.973	Y ●
	NADPH-dependent FMN reductase [Methylobacillus flagellatus KT]637938481 YP_545678											
MFLA1570			1.000	1.000		Y ● ● Y			22.848	22.848		Y ●
	methyl-accepting chemotaxis sensory transducer [Methylobacillus flagellatus KT]637938482 YP_545679											
MFLA1571		0.000	0.000			■ ■		0.000	0.000			■
	adenylate/guanylate cyclase [Methylobacillus flagellatus KT]637938483 YP_545680											
MFLA1572	7.45 E-2	6.261	6.286	7.273	0.010	Y ● ● Y	5.44 E-2	24.229	25.028	25.683	-0.742	Y ●
	" DNA polymerase III, subunits gamma and tau [Methylobacillus flagellatus KT]637938484 YP_545681 """											
MFLA1573	4.46 E-2	7.154	6.881	8.024	0.269	Y ● ● Y	4.59 E-2	26.715	26.042	27.417	0.642	Y ●
	conserved hypothetical protein 103 [Methylobacillus flagellatus KT]637938485 YP_545682											
MFLA1574		3.718	2.871	4.356	0.820	Y ● ● Y	2.8 E-2	23.872	21.471	24.122	2.365	Y ●
	recombination protein RecR [Methylobacillus flagellatus KT]637938486 YP_545683											

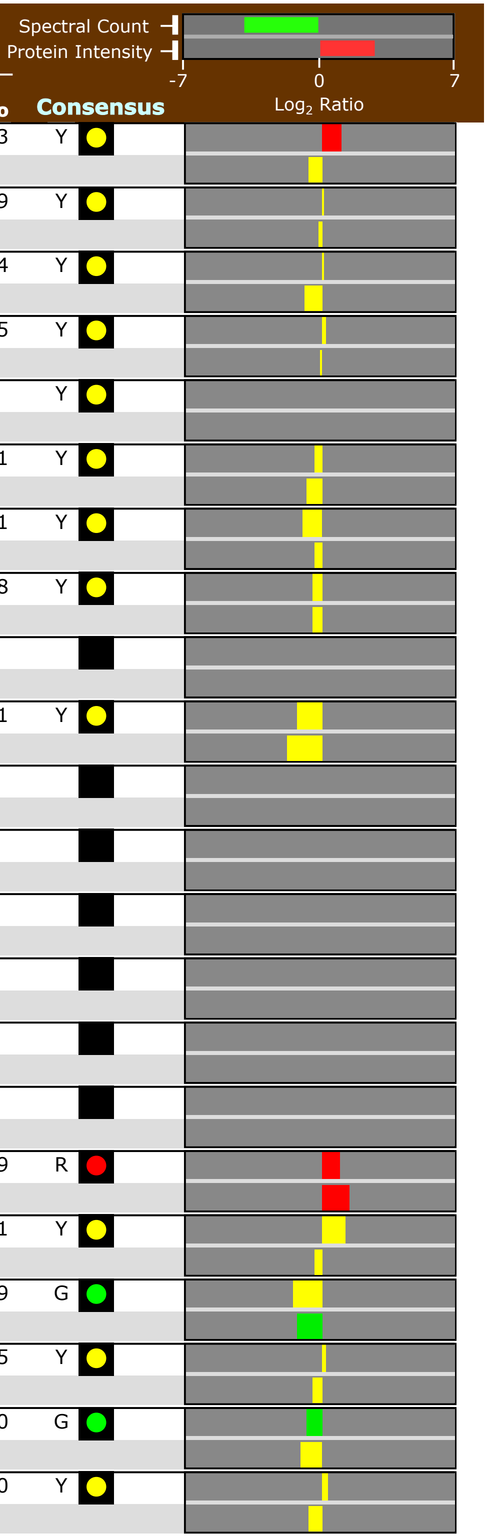


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity							
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	**Consensus**		Log$_2$ Ratio
MFLA1575		3.802	3.117	4.500	0.147	Y	🟡	🟡	Y	2.29 E-1	21.880	22.124	23.007	-1.127	Y	🟡	
	phosphoglycolate phosphatase [Methylobacillus flagellatus KT]637938487 YP_545684																
MFLA1576		4.683	4.219	5.470	0.469	Y	🟡	🟡	Y	1.51 E-1	24.302	24.114	25.211	0.236	Y	🟡	
	ubiquinone biosynthesis O-methyltransferase [Methylobacillus flagellatus KT]637938488 YP_545685																
MFLA1577		4.397	1.322	4.559	2.028	Y	🟡	🟡	Y	1.83 E-1	22.099	20.502	22.511	0.343	Y	🟡	
	amidohydrolase [Methylobacillus flagellatus KT]637938489 YP_545686																
MFLA1578		11.873	11.956	12.915	-0.093	Y	🟡	🟡	Y	8.26 E-2	30.921	31.201	32.068	-0.301	Y	🟡	
	OmpA/MotB [Methylobacillus flagellatus KT]637938490 YP_545687																
MFLA1579		0.521	2.710	2.996	-1.153	Y	🟡	🟡	Y	1.17 E-1	19.309	21.380	21.688	-0.977	Y	🟡	
	protein of unknown function DUF556 [Methylobacillus flagellatus KT]637938491 YP_545688																
MFLA1580		2.600		2.600		Y	🟡	🟡	Y		20.720		20.720		Y	🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637938492 YP_545689																
MFLA1581		4.312	2.871	4.765	1.440	Y	🟡	🟡	Y	6.85 E-2	22.077	21.618	22.866	0.455	Y	🟡	
	" dihydropteroate synthase, DHPS [Methylobacillus flagellatus KT]637938493 YP_545690 """																
MFLA1582		4.324	4.627	5.484	-0.317	Y	🟡	🟡	Y	4.29 E-2	23.318	24.137	24.785	-0.780	Y	🟡	
	flavoprotein [Methylobacillus flagellatus KT]637938494 YP_545691																
MFLA1583		7.867	8.096	8.986	-0.342	Y	🟡	🟡	Y	1.11 E-2	27.055	27.878	28.525	-0.835	Y	🟡	
	Adenylosuccinate synthase [Methylobacillus flagellatus KT]637938495 YP_545692																
MFLA1584	1.79 E-3	6.112	6.656	7.410	-0.563	G	🟢	🟡	Y	4.4 E-2	24.657	25.057	25.870	-0.417	G	🟢	
	" tRNA synthetase, class II (G, H, P and S) [Methylobacillus flagellatus KT]637938496 YP_545693 """																
MFLA1585		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938497 YP_545694																
MFLA1586	1.06 E-3	6.956	7.409	8.200	-0.457	Y	🟡	🟡	Y	9.54 E-2	27.345	27.588	28.472	-0.239	Y	🟡	
	HflC protein [Methylobacillus flagellatus KT]637938498 YP_545695																
MFLA1587	1.1 E-2	7.294	7.606	8.458	-0.317	Y	🟡	🟡	Y	2.12 E-2	27.460	27.905	28.699	-0.456	Y	🟡	
	HflK protein [Methylobacillus flagellatus KT]637938499 YP_545696																
MFLA1588		3.120	0.585	3.350	1.535	Y	🟡	🟡	Y	2.28 E-1	20.919	20.181	21.596	-0.717	Y	🟡	
	Small GTP-binding protein domain [Methylobacillus flagellatus KT]637938500 YP_545697																
MFLA1589		7.194	6.790	8.006	0.480	Y	🟡	🟡	Y	2.58 E-1	26.897	26.956	27.927	-0.039	Y	🟡	
	Host factor Hfq [Methylobacillus flagellatus KT]637938501 YP_545698																
MFLA1590		6.693	7.108	7.915	-0.483	Y	🟡	🟡	Y	1.12 E-1	25.736	26.197	26.985	-0.626	Y	🟡	
	glutamyl-tRNA synthetase [Methylobacillus flagellatus KT]637938502 YP_545699																
MFLA1591		5.610	1.825	5.711	3.936	Y	🟡	🟡	Y	1.49 E-2	24.634	20.149	24.697	4.473	Y	🟡	
	" RND efflux system, outer membrane lipoprotein, NodT [Methylobacillus flagellatus KT]637938503 YP_545700 """																
MFLA1592		6.328	6.212	7.272	0.205	Y	🟡	🟡	Y	4.59 E-2	25.469	25.186	26.335	0.293	Y	🟡	
	Hydrophobe/amphiphile efflux-1 HAE1 [Methylobacillus flagellatus KT]637938504 YP_545701																
MFLA1593	1.55 E-5	6.386	5.541	7.025	0.846	R	🔴	🟡	Y	3.82 E-2	25.806	26.083	26.951	-0.272	Y	🟡	
	secretion protein HlyD [Methylobacillus flagellatus KT]637938505 YP_545702																
MFLA1594		0.521		0.521		Y	🟡	🟡	Y		18.754		18.754		Y	🟡	
	" transcriptional regulator, TetR family [Methylobacillus flagellatus KT]637938506 YP_545703 """																
MFLA1595		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938507 YP_545704																
MFLA1596		4.562		4.562		Y	🟡	🟡	Y		22.894		22.894		Y	🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637938508 YP_545705																

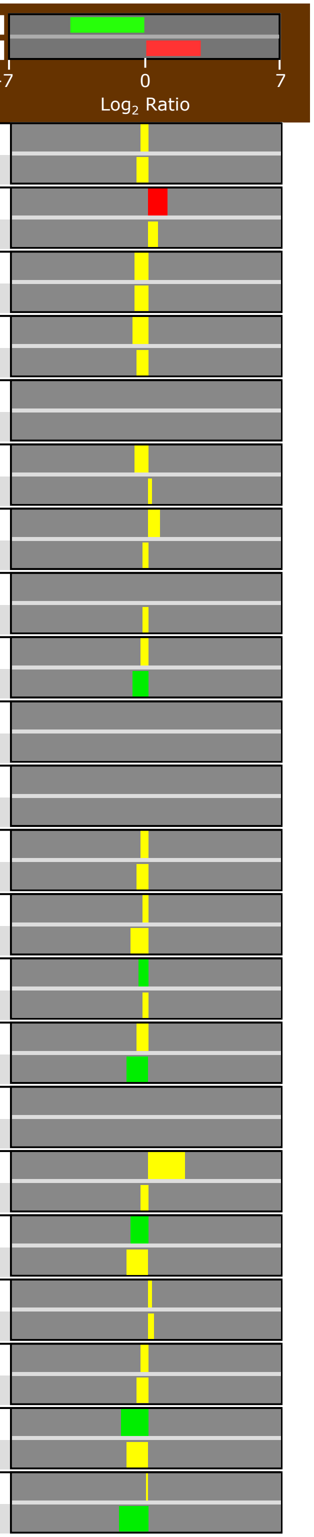
ORF	AM/OH *M Flagellatus* Spectral Count							AM/OH *M Flagellatus* Protein Intensity					
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation		*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA1597		0.000	0.000			■	■		0.000	0.000			■
	zinc/iron permease [Methylobacillus flagellatus KT]637938509 YP_545706												
MFLA1598		0.000	0.000			■	■		0.000	0.000			■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637938510 YP_545707												
MFLA1599			0.000	0.000		Y ●	● Y			20.894	20.894		Y ●
	" TonB-dependent receptor, plug [Methylobacillus flagellatus KT]637938511 YP_545708 """												
MFLA1600			5.280	5.280		Y ●	● Y			24.148	24.148		Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637938512 YP_545709												
MFLA1601		0.000	0.000			■	■		0.000	0.000			■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637938513 YP_545710												
MFLA1602		0.000	0.000			■	■		0.000	0.000			■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637938514 YP_545711												
MFLA1603		3.761	3.483	4.628	0.236	Y ●	● Y	1.75 E-2	23.179	22.449	23.860	0.724	Y ●
	" TonB-dependent receptor, plug [Methylobacillus flagellatus KT]637938515 YP_545712 """												
MFLA1604	0	8.351	9.569	10.085	-1.216	G ●	● G	4.1 E-3	27.511	29.302	29.668	-1.810	G ●
	Haemin-degrading [Methylobacillus flagellatus KT]637938516 YP_545713												
MFLA1605		5.947	6.335	7.154	-0.358	Y ●	● Y	7.63 E-2	24.846	26.628	26.996	-1.459	Y ●
	periplasmic binding protein [Methylobacillus flagellatus KT]637938517 YP_545714												
MFLA1606		0.000	0.000			■	■		0.000	0.000			■
	transport system permease protein [Methylobacillus flagellatus KT]637938518 YP_545715												
MFLA1607		2.418	3.162	3.837	-0.834	Y ●	● Y	7.36 E-2	20.463	21.312	21.949	-0.881	Y ●
	ABC transporter related [Methylobacillus flagellatus KT]637938519 YP_545716												
MFLA1608		0.000	0.000			■	■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938520 YP_545717												
MFLA1609		0.000	0.000			■	■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938521 YP_545718												
MFLA1610		0.000	0.000			■	■		0.000	0.000			■
	" Cupin 2, conserved barrel [Methylobacillus flagellatus KT]637938522 YP_545719 """												
MFLA1611		3.804	3.750	4.777	0.027	Y ●	● Y	1.7 E-1	22.629	22.779	23.706	-0.187	Y ●
	protein of unknown function DUF152 [Methylobacillus flagellatus KT]637938523 YP_545720												
MFLA1612		2.328	2.649	3.497	0.994	Y ●	● Y	1.55 E-1	22.353	22.882	23.641	0.626	Y ●
	" Pseudouridine synthase, RluD [Methylobacillus flagellatus KT]637938524 YP_545721 """												
MFLA1613		5.050	4.202	5.687	0.813	Y ●	● Y	5.33 E-2	23.488	23.919	24.720	-0.415	Y ●
	putative competence lipoprotein precursor [Methylobacillus flagellatus KT]637938525 YP_545722												
MFLA1614		6.825	6.483	7.664	0.305	Y ●	● Y	2.77 E-1	25.956	25.965	26.961	-0.096	Y ●
	Small GTP-binding protein domain [Methylobacillus flagellatus KT]637938526 YP_545723												
MFLA1615	1.43 E-3	6.215	6.738	7.500	-0.517	G ●	● Y	2.42 E-1	26.203	26.248	27.225	-0.032	Y ●
	Pyrrolo-quinoline quinone [Methylobacillus flagellatus KT]637938527 YP_545724												
MFLA1616	0	7.311	4.771	7.540	2.570	R ●	● Y	1.26 E-1	24.573	24.008	25.318	0.395	R ●
	hypothetical protein [Methylobacillus flagellatus KT]637938528 YP_545725												
MFLA1617		4.591	5.104	5.870	-0.449	Y ●	● Y	8.22 E-2	23.831	24.240	25.050	-0.395	Y ●
	ABC transporter related [Methylobacillus flagellatus KT]637938529 YP_545726												
MFLA1618		3.398	4.219	4.866	0.203	Y ●	● Y	1.06 E-1	21.923	23.683	24.056	-0.722	Y ●
	ABC transporter related [Methylobacillus flagellatus KT]637938530 YP_545727												



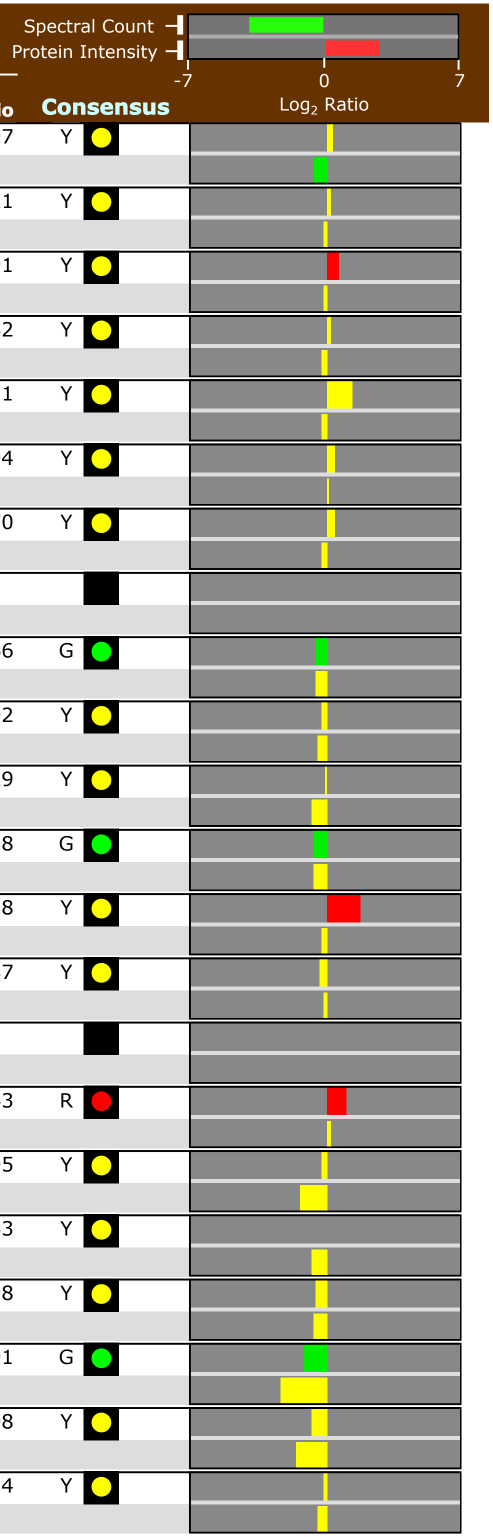
ORF	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA1619	0	7.914	6.881	8.488	1.029	R	🔴	🟡	Y	1.25 E-2	26.322	26.991	27.695	-0.683	Y	🟡
	histidyl-tRNA synthetase [Methylobacillus flagellatus KT]637938531 YP_545728															
MFLA1620	8.43 E-2	6.221	6.074	7.150	0.139	Y	🟡	🟡	Y	1.83 E-1	25.338	25.503	26.423	-0.229	Y	🟡
	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase [Methylobacillus flagellatus KT]637938532 YP_545729															
MFLA1621		4.638	4.344	5.499	0.107	Y	🟡	🟡	Y	1.29 E-1	24.790	25.326	26.083	-0.914	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938533 YP_545730															
MFLA1622	1.39 E-1	5.661	5.456	6.562	0.206	Y	🟡	🟡	Y	2.39 E-1	24.254	24.331	25.293	-0.105	Y	🟡
	Tetratricopeptide TPR_2 [Methylobacillus flagellatus KT]637938534 YP_545731															
MFLA1623			2.435	2.435		Y	🟡	🟡	Y			21.762	21.762		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938535 YP_545732															
MFLA1624	1.07 E-11	8.832	9.259	10.061	-0.435	Y	🟡	🟡	Y	4.79 E-2	28.518	29.222	29.912	-0.811	Y	🟡
	Nucleoside-diphosphate kinase [Methylobacillus flagellatus KT]637938536 YP_545733															
MFLA1625		4.025	4.919	5.540	-0.960	Y	🟡	🟡	Y	1.26 E-1	23.920	24.268	25.105	-0.421	Y	🟡
	" RNA methyltransferase TrmH, group 3 [Methylobacillus flagellatus KT]637938537 YP_545734 """															
MFLA1626		7.082	7.470	8.289	-0.465	Y	🟡	🟡	Y	4.65 E-2	25.882	26.343	27.131	-0.498	Y	🟡
	Ribonuclease R [Methylobacillus flagellatus KT]637938538 YP_545735															
MFLA1627		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938540 YP_545736															
MFLA1628		0.521	1.807	2.303	-1.287	Y	🟡	🟡	Y		20.854	22.674	23.034	-1.821	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938542 YP_545737															
MFLA1629		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938543 YP_545738															
MFLA1630		0.000	0.000				■	■			0.000	0.000				■
	outer membrane efflux protein [Methylobacillus flagellatus KT]637938544 YP_545739															
MFLA1631		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938545 YP_545740															
MFLA1632		0.000	0.000				■	■			0.000	0.000				■
	acriflavin resistance protein [Methylobacillus flagellatus KT]637938546 YP_545741															
MFLA1633		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938547 YP_545742															
MFLA1634		0.000	0.000				■	■			0.000	0.000				■
	small multidrug resistance protein [Methylobacillus flagellatus KT]637938548 YP_545743															
MFLA1635	1.11 E-4	5.951	5.075	6.578	0.900	R	🔴	🔴	R	9.92 E-3	25.981	24.619	26.455	1.359	R	🔴
	membrane protein-like protein [Methylobacillus flagellatus KT]637938549 YP_545744															
MFLA1636		5.064	3.820	5.572	1.173	Y	🟡	🟡	Y	3.96 E-2	23.700	24.074	24.899	-0.381	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938550 YP_545745															
MFLA1637		2.746	4.012	4.513	-1.550	Y	🟡	🟢	G	8.35 E-3	22.127	23.387	23.891	-1.269	G	🟢
	hypothetical protein [Methylobacillus flagellatus KT]637938551 YP_545746															
MFLA1638	1.28 E-1	5.530	5.303	6.421	0.224	Y	🟡	🟡	Y	2.42 E-1	24.265	24.081	25.176	-0.505	Y	🟡
	type II secretion system protein [Methylobacillus flagellatus KT]637938552 YP_545747															
MFLA1639	2.71 E-3	4.799	5.628	6.273	-0.820	G	🟢	🟡	Y	1.66 E-2	24.202	25.300	25.853	-1.110	G	🟢
	type II secretion system protein [Methylobacillus flagellatus KT]637938553 YP_545748															
MFLA1640	1.58 E-2	6.807	6.515	7.668	0.268	Y	🟡	🟡	Y	3.74 E-2	25.378	26.022	26.735	-0.670	Y	🟡
	type II secretion system protein E [Methylobacillus flagellatus KT]637938554 YP_545749															



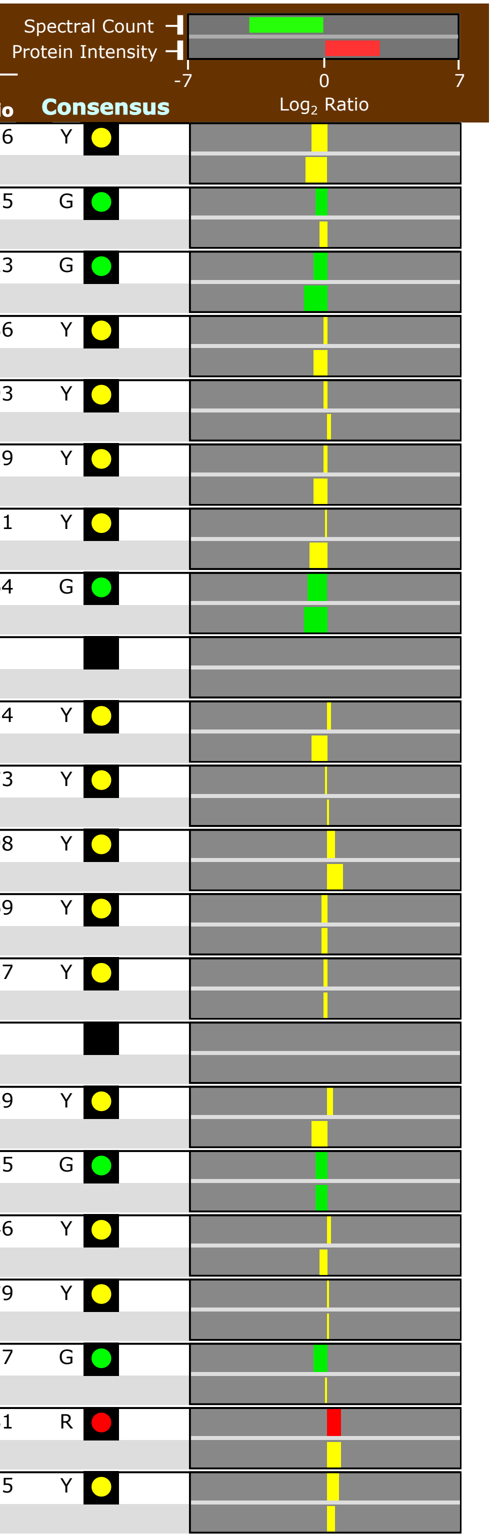
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA1641	2.05 E-5	7.879	8.292	9.100	-0.408	Y	🟡	🟡	Y	6.47 E-2	27.776	28.321	29.074	-0.576	Y	🟡
	pilus assembly protein CpaE [Methylobacillus flagellatus KT]637938555 YP_545750															
MFLA1642	0	9.673	8.660	10.253	0.987	R	🔴	🟡	Y	2.1 E-2	28.939	28.399	29.694	0.534	R	🔴
	type II and III secretion system protein [Methylobacillus flagellatus KT]637938556 YP_545751															
MFLA1643		6.038	6.505	7.290	-0.667	Y	🟡	🟡	Y	2.87 E-2	25.991	26.672	27.371	-0.715	Y	🟡
	Flp pilus assembly CpaB [Methylobacillus flagellatus KT]637938557 YP_545752															
MFLA1644		1.398	2.170	2.835	-0.772	Y	🟡	🟡	Y		21.768	22.407	23.122	-0.639	Y	🟡
	TadE-like protein [Methylobacillus flagellatus KT]637938558 YP_545753															
MFLA1645		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" peptidase A24A, prepilin type IV [Methylobacillus flagellatus KT]637938559 YP_545754 """															
MFLA1646		4.347	5.036	5.732	-0.749	Y	🟡	🟡	Y	2.02 E-1	23.342	23.190	24.268	0.227	Y	🟡
	transcriptional coactivator/pterin dehydratase [Methylobacillus flagellatus KT]637938560 YP_545755															
MFLA1647		6.575	5.737	7.216	0.580	Y	🟡	🟡	Y	1.14 E-1	24.713	25.021	25.875	-0.267	Y	🟡
	aspartate/glutamate/uridylate kinase [Methylobacillus flagellatus KT]637938561 YP_545756															
MFLA1648		4.933	4.924	5.928	0.016	Y	🟡	🟡	Y	2.27 E-1	23.457	23.640	24.552	-0.262	Y	🟡
	" para-aminobenzoate synthase, component I [Methylobacillus flagellatus KT]637938562 YP_545757 """															
MFLA1649	4.49 E-2	5.110	5.447	6.288	-0.399	Y	🟡	🟢	G	4.58 E-3	23.353	24.151	24.806	-0.800	G	🟢
	" S-layer protein, putative [Methylobacillus flagellatus KT]637938563 YP_545758 """															
MFLA1650			1.346	1.346		Y	🟡	🟡	Y			18.789	18.789		Y	🟡
	protein of unknown function DUF201 [Methylobacillus flagellatus KT]637938564 YP_545759															
MFLA1651			2.095	2.095		Y	🟡	🟡	Y			21.131	21.131		Y	🟡
	histidine biosynthesis [Methylobacillus flagellatus KT]637938565 YP_545760															
MFLA1652	0	9.866	10.260	11.077	-0.380	Y	🟡	🟡	Y	8.58 E-2	30.470	31.102	31.820	-0.559	Y	🟡
	formaldehyde-activating enzyme [Methylobacillus flagellatus KT]637938566 YP_545761															
MFLA1653		7.931	8.271	9.111	-0.302	Y	🟡	🟡	Y	2.28 E-2	28.559	29.413	30.049	-0.882	Y	🟡
	sugar isomerase (SIS) [Methylobacillus flagellatus KT]637938567 YP_545762															
MFLA1654	0	11.036	11.572	12.329	-0.548	G	🟢	🟡	Y	9.62 E-2	32.621	32.881	33.757	-0.251	G	🟢
	Orotidine 5'-phosphate decarboxylase [Methylobacillus flagellatus KT]637938568 YP_545763															
MFLA1655		10.396	10.951	11.700	-0.642	Y	🟡	🟢	G	4.58 E-3	31.060	32.157	32.710	-1.105	G	🟢
	transaldolase [Methylobacillus flagellatus KT]637938569 YP_545764															
MFLA1656			2.095	2.095		Y	🟡	🟡	Y			21.262	21.262		Y	🟡
	triphosphoribosyl-dephospho-CoA protein [Methylobacillus flagellatus KT]637938570 YP_545765															
MFLA1657		2.691	1.915	3.354	1.856	Y	🟡	🟡	Y	1.77 E-1	19.253	21.026	21.396	-0.433	Y	🟡
	S6 modification enzyme RimK [Methylobacillus flagellatus KT]637938571 YP_545766															
MFLA1658	0	8.501	9.398	10.018	-0.888	G	🟢	🟡	Y	5.48 E-2	28.507	29.418	30.033	-1.126	G	🟢
	Methenyltetrahydromethanopterin cyclohydrolase [Methylobacillus flagellatus KT]637938572 YP_545767															
MFLA1659		4.323	3.778	5.076	0.171	Y	🟡	🟡	Y	1.41 E-1	23.096	22.549	23.848	0.320	Y	🟡
	protein of unknown function DUF201 [Methylobacillus flagellatus KT]637938573 YP_545768															
MFLA1660	5.32 E-13	9.512	9.872	10.703	-0.352	Y	🟡	🟡	Y	2.94 E-2	29.078	29.719	30.434	-0.627	Y	🟡
	" methylene tetrahydromethanopterin dehydrogenase/methylenetetrahydrofolate dehydrogenase, putative [Methylobacillus flagellatus KT]637938574 YP_545769 """															
MFLA1661	0	6.150	7.503	7.980	-1.353	G	🟢	🟡	Y	2.29 E-2	24.147	25.131	25.721	-1.077	G	🟢
	GHMP kinase group 1 [Methylobacillus flagellatus KT]637938575 YP_545770															
MFLA1662		7.380	7.550	8.467	-0.140	Y	🟡	🟢	G	8.64 E-3	25.900	27.356	27.805	-1.493	G	🟢
	formylmethanofuran dehydrogenase [Methylobacillus flagellatus KT]637938576 YP_545771															



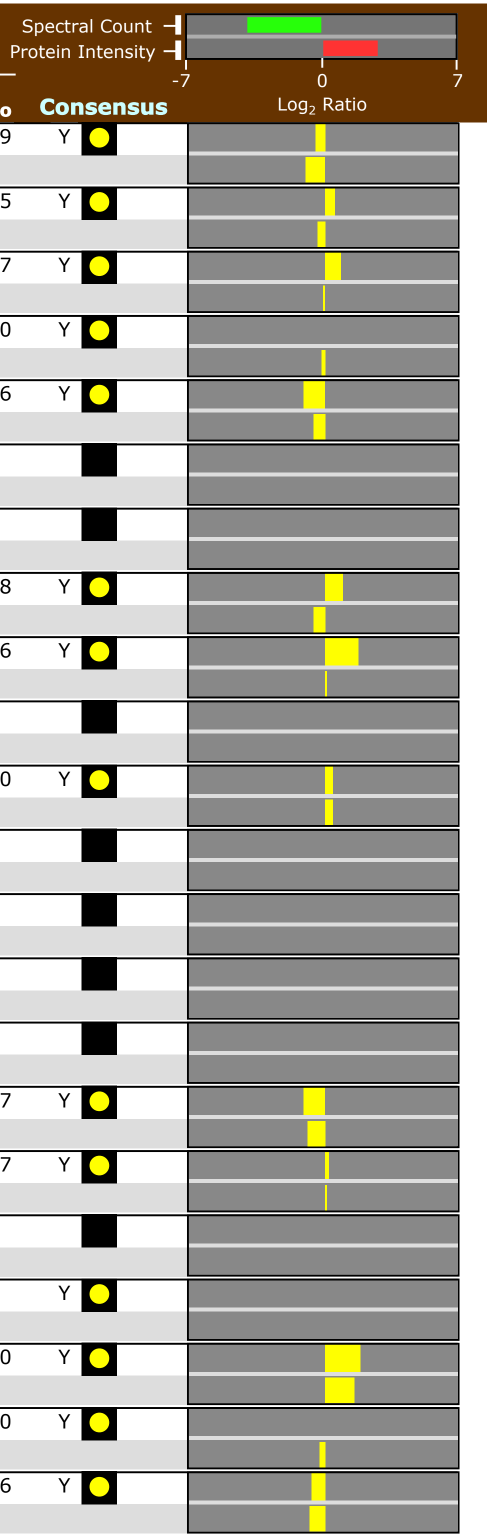
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA1663	2.48 E-4	8.715	8.461	9.594	0.265	Y	🟡	🟢	G	6.36 E-3	28.144	28.841	29.534	-0.697	Y	🟡
	Amidohydrolase 3 [Methylobacillus flagellatus KT]637938577 YP_545772															
MFLA1664	5.14 E-2	7.499	7.349	8.426	0.163	Y	🟡	🟡	Y	9.14 E-2	27.446	27.662	28.558	-0.221	Y	🟡
	Formylmethanofuran--tetrahydromethanopterin N-formyltransferase [Methylobacillus flagellatus KT]637938578 YP_545773															
MFLA1665	0	9.169	8.546	9.891	0.624	R	🔴	🟡	Y	8.8 E-2	27.475	27.659	28.570	-0.191	Y	🟡
	Formylmethanofuran dehydrogenase [Methylobacillus flagellatus KT]637938579 YP_545774															
MFLA1666		6.587	6.166	7.392	0.217	Y	🟡	🟡	Y	1.16 E-1	26.686	26.959	27.829	-0.282	Y	🟡
	OmpA/MotB [Methylobacillus flagellatus KT]637938580 YP_545775															
MFLA1667		1.521	1.184	2.362	1.347	Y	🟡	🟡	Y	1.87 E-1	19.992	21.583	21.997	-0.311	Y	🟡
	protein of unknown function UPF0029 [Methylobacillus flagellatus KT]637938581 YP_545776															
MFLA1668	1.95 E-2	6.075	5.704	6.901	0.365	Y	🟡	🟡	Y	2 E-1	25.195	25.104	26.150	0.094	Y	🟡
	" protein of unknown function DUF853, NPT hydrolase putative [Methylobacillus flagellatus KT]637938582 YP_545777 """															
MFLA1669		4.956	4.545	5.765	0.422	Y	🟡	🟡	Y	2.32 E-1	23.848	24.018	24.935	-0.270	Y	🟡
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637938583 YP_545778 """															
MFLA1670		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF81 [Methylobacillus flagellatus KT]637938584 YP_545779															
MFLA1671	9.25 E-5	6.543	7.145	7.875	-0.606	G	🟢	🟡	Y	8.22 E-2	26.313	26.836	27.598	-0.566	G	🟢
	nitrite and sulphite reductase 4Fe-4S region [Methylobacillus flagellatus KT]637938585 YP_545780															
MFLA1672	9.72 E-2	5.916	6.189	7.059	-0.275	Y	🟡	🟡	Y	9.23 E-2	25.304	25.727	26.531	-0.502	Y	🟡
	Uncharacterised conserved protein UCP030820 [Methylobacillus flagellatus KT]637938586 YP_545781															
MFLA1673	10 E-2	6.663	6.787	7.726	-0.137	Y	🟡	🟡	Y	2.7 E-2	25.754	26.607	27.243	-0.829	Y	🟡
	" Sulfate adenylyltransferase, small subunit [Methylobacillus flagellatus KT]637938587 YP_545782 """															
MFLA1674	5.29 E-10	7.151	7.858	8.547	-0.706	G	🟢	🟡	Y	3.18 E-2	26.634	27.251	27.975	-0.658	G	🟢
	" Sulfate adenylyltransferase, large subunit [Methylobacillus flagellatus KT]637938588 YP_545783 """															
MFLA1675	3.38 E-14	6.052	4.143	6.393	1.745	R	🔴	🟡	Y	2.62 E-1	25.256	25.315	26.286	-0.318	Y	🟡
	" 4Fe-4S ferredoxin, iron-sulfur binding [Methylobacillus flagellatus KT]637938589 YP_545784 """															
MFLA1676		5.836	6.304	7.089	-0.379	Y	🟡	🟡	Y	2.02 E-1	25.266	25.429	26.350	-0.187	Y	🟡
	short-chain alcohol dehydrogenase [Methylobacillus flagellatus KT]637938590 YP_545785															
MFLA1677		0.000	0.000				■	■			0.000	0.000				■
	Drug resistance transporter Bcr/CflA subfamily [Methylobacillus flagellatus KT]637938591 YP_545786															
MFLA1678	9.29 E-5	5.508	4.497	6.089	0.958	R	🔴	🟡	Y	1.83 E-1	24.882	24.564	25.732	0.243	R	🔴
	Cyclopropane-fatty-acyl-phospholipid synthase [Methylobacillus flagellatus KT]637938592 YP_545787															
MFLA1679	3.34 E-2	5.789	6.112	6.960	-0.316	Y	🟡	🟡	Y	1.12 E-2	24.786	26.114	26.598	-1.405	Y	🟡
	phosphoadenosine phosphosulfate reductase [Methylobacillus flagellatus KT]637938593 YP_545788															
MFLA1680		4.424	4.450	5.437	0.008	Y	🟡	🟡	Y	3.22 E-2	22.617	23.380	24.049	-0.783	Y	🟡
	Coenzyme PQQ biosynthesis protein E [Methylobacillus flagellatus KT]637938594 YP_545789															
MFLA1681		1.843	3.441	3.852	-0.577	Y	🟡	🟡	Y	8.26 E-2	21.655	23.367	23.751	-0.698	Y	🟡
	coenzyme PQQ synthesis D [Methylobacillus flagellatus KT]637938595 YP_545790															
MFLA1682	3.73 E-15	6.033	7.086	7.653	-1.249	G	🟢	🟡	Y	1.29 E-2	23.162	25.114	25.446	-2.391	G	🟢
	Coenzyme PQQ biosynthesis protein C [Methylobacillus flagellatus KT]637938596 YP_545791															
MFLA1683		4.240	4.957	5.643	-0.836	Y	🟡	🟡	Y	4.26 E-2	23.480	24.787	25.276	-1.608	Y	🟡
	Coenzyme PQQ biosynthesis protein B [Methylobacillus flagellatus KT]637938597 YP_545792															
MFLA1684	1.03 E-2	6.183	6.315	7.250	-0.203	Y	🟡	🟡	Y	9.62 E-2	25.204	25.633	26.434	-0.514	Y	🟡
	histidinol-phosphate aminotransferase [Methylobacillus flagellatus KT]637938598 YP_545793															

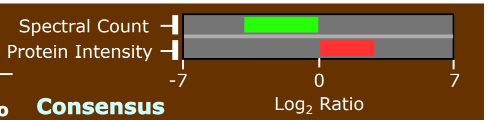


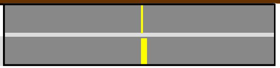
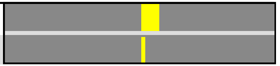
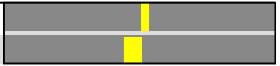
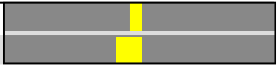
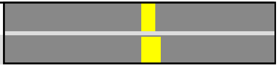
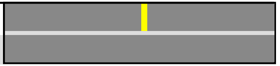
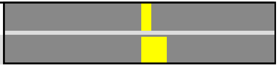
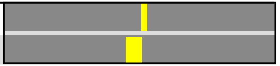
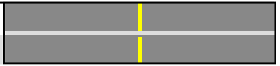
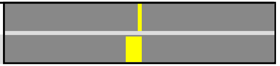
	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA1685		3.482	4.407	5.018	-0.761	Y 🟡 🟡 Y	1.24 E-2	22.831	23.877	24.447	-1.056	Y 🟡
	diguanylate cyclase (GGDEF domain) [Methylobacillus flagellatus KT]637938599 YP_545794											
MFLA1686	3.7 E-3	5.697	6.222	6.983	-0.572	G 🟢 🟡 Y	3.1 E-2	24.437	24.799	25.629	-0.355	G 🟢
	chorismate mutase [Methylobacillus flagellatus KT]637938600 YP_545795											
MFLA1687	4.57 E-3	4.918	5.632	6.319	-0.723	G 🟢 🟢 G	7.38 E-3	24.219	25.420	25.941	-1.223	G 🟢
	phosphoserine aminotransferase [Methylobacillus flagellatus KT]637938601 YP_545796											
MFLA1688	3.82 E-2	7.481	7.704	8.597	-0.226	Y 🟡 🟡 Y	1.11 E-2	26.779	27.469	28.165	-0.686	Y 🟡
	" DNA gyrase, A subunit [Methylobacillus flagellatus KT]637938602 YP_545797 """											
MFLA1689		8.046	8.069	9.057	-0.156	Y 🟡 🟡 Y	1.33 E-1	29.247	29.016	30.136	0.193	Y 🟡
	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen [Methylobacillus flagellatus KT]637938603 YP_545798											
MFLA1690	1.19 E-2	7.202	7.424	8.317	-0.246	Y 🟡 🟡 Y	1.03 E-2	27.471	28.123	28.833	-0.659	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938604 YP_545799											
MFLA1691	4.63 E-2	6.387	6.520	7.455	-0.109	Y 🟡 🟡 Y	2.74 E-2	25.420	26.278	26.912	-0.911	Y 🟡
	O-succinylhomoserine sulfhydrylase [Methylobacillus flagellatus KT]637938605 YP_545800											
MFLA1692	3.88 E-13	6.550	7.515	8.112	-0.992	G 🟢 🟢 G	8.91 E-3	25.953	27.120	27.651	-1.164	G 🟢
	amidophosphoribosyltransferase [Methylobacillus flagellatus KT]637938606 YP_545801											
MFLA1693		0.000	0.000			■ ■		0.000	0.000			■
	Colicin V production protein [Methylobacillus flagellatus KT]637938607 YP_545802											
MFLA1694		2.328	2.170	3.251	0.158	Y 🟡 🟡 Y		19.835	20.589	21.260	-0.754	Y 🟡
	Sporulation related [Methylobacillus flagellatus KT]637938608 YP_545803											
MFLA1695		3.763	3.705	4.734	-0.060	Y 🟡 🟡 Y	2.3 E-1	22.756	22.571	23.667	0.073	Y 🟡
	FolC bifunctional protein [Methylobacillus flagellatus KT]637938609 YP_545804											
MFLA1696	1.97 E-2	5.593	5.347	6.475	0.355	Y 🟡 🟡 Y	9.44 E-2	25.245	24.604	25.960	0.798	Y 🟡
	" acetyl-CoA carboxylase, carboxyl transferase, beta subunit [Methylobacillus flagellatus KT]637938610 YP_545805 """											
MFLA1697		6.385	6.626	7.510	-0.258	Y 🟡 🟡 Y	6.85 E-2	25.887	26.162	27.031	-0.269	Y 🟡
	" tryptophan synthase, alpha subunit [Methylobacillus flagellatus KT]637938611 YP_545806 """											
MFLA1698		6.475	6.776	7.633	-0.192	Y 🟡 🟡 Y	1.29 E-1	26.196	26.424	27.315	-0.237	Y 🟡
	" tryptophan synthase, beta subunit [Methylobacillus flagellatus KT]637938612 YP_545807 """											
MFLA1699		0.000	0.000			■ ■		0.000	0.000			■
	Phosphoribosylanthranilate isomerase [Methylobacillus flagellatus KT]637938613 YP_545808											
MFLA1700		3.259	2.966	4.120	0.286	Y 🟡 🟡 Y	7.05 E-2	21.153	21.986	22.629	-0.759	Y 🟡
	tRNA pseudouridine synthase A [Methylobacillus flagellatus KT]637938614 YP_545809											
MFLA1701	8.26 E-12	7.658	8.238	8.977	-0.630	G 🟢 🟢 G	4.1 E-3	27.148	27.702	28.452	-0.555	G 🟢
	hypothetical protein [Methylobacillus flagellatus KT]637938615 YP_545810											
MFLA1702	1.27 E-2	7.021	6.843	7.935	0.158	Y 🟡 🟡 Y	1.08 E-2	25.957	26.399	27.195	-0.446	Y 🟡
	aspartate-semialdehyde dehydrogenase [Methylobacillus flagellatus KT]637938616 YP_545811											
MFLA1703	1.84 E-2	7.645	7.503	8.576	0.120	Y 🟡 🟡 Y	2.22 E-1	26.747	26.670	27.709	0.079	Y 🟡
	3-isopropylmalate dehydrogenase [Methylobacillus flagellatus KT]637938617 YP_545812											
MFLA1704	2.75 E-8	6.813	7.558	8.233	-0.745	G 🟢 🟡 Y	2 E-1	26.441	26.555	27.499	-0.117	G 🟢
	" 3-isopropylmalate dehydratase, small subunit [Methylobacillus flagellatus KT]637938618 YP_545813 """											
MFLA1705	2.82 E-6	7.112	6.444	7.817	0.658	R 🔴 🟡 Y	2.01 E-2	26.978	26.297	27.677	0.681	R 🔴
	" 3-isopropylmalate dehydratase, large subunit [Methylobacillus flagellatus KT]637938619 YP_545814 """											
MFLA1706		7.234	6.521	7.921	0.630	Y 🟡 🟡 Y	3.92 E-2	25.563	25.143	26.368	0.415	Y 🟡
	protein of unknown function DUF520 [Methylobacillus flagellatus KT]637938620 YP_545815											



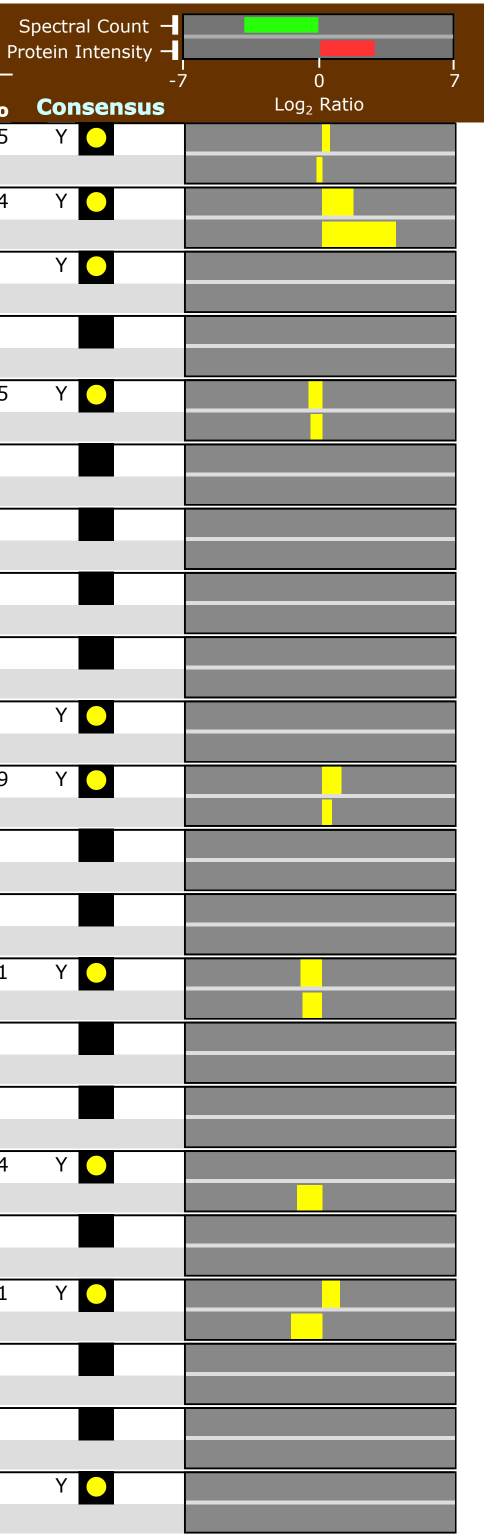
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA1707	3.14 E-2	4.135	5.672	6.099	-0.514	Y	●	●	Y	4.79 E-2	22.388	24.440	24.752	-1.049	Y	●
	protein of unknown function DUF1255 [Methylobacillus flagellatus KT]637938621 YP_545816															
MFLA1708	8.11 E-7	8.162	7.656	8.931	0.499	Y	●	●	Y	2.04 E-1	26.720	26.920	27.823	-0.385	Y	●
	Argininosuccinate synthase [Methylobacillus flagellatus KT]637938622 YP_545817															
MFLA1709		7.100	6.046	7.667	0.778	Y	●	●	Y	2.24 E-1	25.831	25.611	26.725	-0.137	Y	●
	ornithine carbamoyltransferase [Methylobacillus flagellatus KT]637938623 YP_545818															
MFLA1710	1.8 E-2	6.733	6.721	7.727	-0.043	Y	●	●	Y	1.33 E-1	25.731	25.865	26.800	-0.150	Y	●
	acetylornithine and succinylornithine aminotransferases [Methylobacillus flagellatus KT]637938624 YP_545819															
MFLA1711		1.674	2.739	3.303	-1.071	Y	●	●	Y	4.59 E-2	21.184	21.771	22.507	-0.646	Y	●
	Rieske (2Fe-2S) region [Methylobacillus flagellatus KT]637938625 YP_545820															
MFLA1712		0.000	0.000				■	■			0.000	0.000				■
	" protein of unknown function DUF6, transmembrane [Methylobacillus flagellatus KT]637938626 YP_545821 """															
MFLA1713		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938627 YP_545822															
MFLA1714		4.497	3.659	5.138	0.855	Y	●	●	Y	1.44 E-1	22.810	23.221	24.030	-0.578	Y	●
	" two component transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637938628 YP_545823 """															
MFLA1715		3.844	2.184	4.241	1.664	Y	●	●	Y	1.84 E-1	22.438	21.954	23.216	0.066	Y	●
	multi-sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637938629 YP_545824															
MFLA1716		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938630 YP_545825															
MFLA1717		2.892	2.649	3.776	0.418	Y	●	●	Y	2.5 E-1	23.140	23.045	24.093	0.380	Y	●
	Pyrrolo-quinoline quinone [Methylobacillus flagellatus KT]637938631 YP_545826															
MFLA1718		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637938632 YP_545827															
MFLA1719		0.000	0.000				■	■			0.000	0.000				■
	Sel1 [Methylobacillus flagellatus KT]637938633 YP_545828															
MFLA1720		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938634 YP_545829															
MFLA1721		0.000	0.000				■	■			0.000	0.000				■
	Na+/Pi-cotransporter [Methylobacillus flagellatus KT]637938635 YP_545830															
MFLA1722		2.461	3.551	4.107	-1.091	Y	●	●	Y	2.49 E-2	21.258	22.157	22.776	-0.917	Y	●
	methyltransferase small [Methylobacillus flagellatus KT]637938636 YP_545831															
MFLA1723	3.66 E-2	6.511	6.379	7.446	0.151	Y	●	●	Y	1.43 E-1	25.550	25.455	26.504	0.087	Y	●
	L-sorbosone dehydrogenase [Methylobacillus flagellatus KT]637938637 YP_545832															
MFLA1724		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938638 YP_545833															
MFLA1725		2.106		2.106		Y	●	●	Y		21.572		21.572		Y	●
	metal dependent phosphohydrolase [Methylobacillus flagellatus KT]637938639 YP_545834															
MFLA1726		4.705	2.941	5.078	1.786	Y	●	●	Y	4.87 E-2	22.050	20.428	22.456	1.510	Y	●
	Glutamate-ammonia-ligase adenylyltransferase [Methylobacillus flagellatus KT]637938640 YP_545835															
MFLA1727	4.8 E-2	6.904	6.939	7.922	-0.048	Y	●	●	Y	1.17 E-1	26.257	26.540	27.405	-0.320	Y	●
	Acetate--CoA ligase [Methylobacillus flagellatus KT]637938641 YP_545836															
MFLA1728		3.710	4.288	5.028	-0.667	Y	●	●	Y	1.39 E-1	24.585	25.053	25.837	-0.816	Y	●
	protein of unknown function DUF442 [Methylobacillus flagellatus KT]637938642 YP_545837															



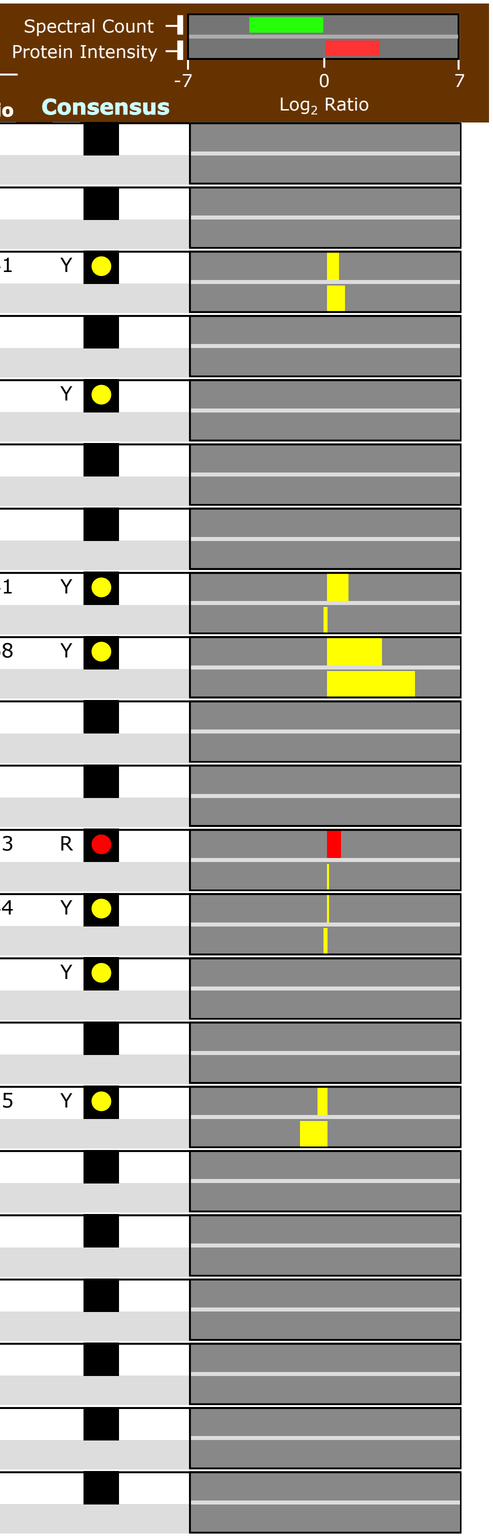


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity							
ORF	**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**				**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**		
MFLA1729		0.813	1.769	2.369	0.055	Y	●	●	Y	9.73 E-2	19.536	20.222	20.919	0.323	Y	●	
	" HAD-superfamily hydrolase subfamily IA, variant 3 [Methylobacillus flagellatus KT]637938643 YP_545838 """																
MFLA1730		0.000	0.000				■	■			0.000	0.000				■	
	transcriptional regulator [Methylobacillus flagellatus KT]637938644 YP_545839																
MFLA1731		0.000	0.000				■	■			0.000	0.000				■	
	Antibiotic biosynthesis monooxygenase [Methylobacillus flagellatus KT]637938645 YP_545840																
MFLA1732		0.000	0.000				■	■			0.000	0.000				■	
	" Alcohol dehydrogenase, zinc-binding [Methylobacillus flagellatus KT]637938646 YP_545841 """																
MFLA1733		3.283	3.321	4.302	0.036	Y	●	●	Y	1.6 E-2	20.491	22.057	22.477	-1.760	Y	●	
	beta-lactamase-like protein [Methylobacillus flagellatus KT]637938647 YP_545842																
MFLA1734		4.938	4.036	5.556	0.877	Y	●	●	Y	1.63 E-1	23.299	23.042	24.176	0.195	Y	●	
	" transcriptional regulator, Crp/Fnr family [Methylobacillus flagellatus KT]637938648 YP_545843 """																
MFLA1735		2.543	1.966	3.283	0.362	Y	●	●	Y	4.19 E-2	21.163	21.928	22.596	-0.868	Y	●	
	hypothetical protein [Methylobacillus flagellatus KT]637938649 YP_545844																
MFLA1736		0.000	0.000				■	■			0.000	0.000				■	
	response regulator receiver domain protein (CheY-like) [Methylobacillus flagellatus KT]637938650 YP_545845																
MFLA1737	2.15 E-2	5.172	5.757	6.494	-0.587	Y	●	●	Y	2.56 E-2	23.520	24.632	25.181	-1.281	Y	●	
	peptide chain release factor 3 [Methylobacillus flagellatus KT]637938651 YP_545846																
MFLA1738			0.585	0.585		Y	●	●	Y			20.129	20.129		Y	●	
	hypothetical protein [Methylobacillus flagellatus KT]637938652 YP_545847																
MFLA1739		3.736	2.649	4.292	1.397	Y	●	●	Y	1.59 E-1	21.004	21.507	22.278	-0.697	Y	●	
	" glycosyl transferase, group 1 [Methylobacillus flagellatus KT]637938653 YP_545848 """																
MFLA1740		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938654 YP_545849																
MFLA1741		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938655 YP_545850																
MFLA1742			1.000	1.000		Y	●	●	Y			18.349	18.349		Y	●	
	hypothetical protein [Methylobacillus flagellatus KT]637938656 YP_545851																
MFLA1743		2.843	2.170	3.545	0.673	Y	●	●	Y		21.259	20.269	21.847	0.990	Y	●	
	ABC transporter related [Methylobacillus flagellatus KT]637938657 YP_545852																
MFLA1744	7.68 E-2	5.222	4.900	6.070	0.314	Y	●	●	Y	2.54 E-1	22.367	22.320	23.343	-0.013	Y	●	
	hypothetical protein [Methylobacillus flagellatus KT]637938658 YP_545853																
MFLA1745		3.159	2.334	3.805	0.494	Y	●	●	Y	7.52 E-2	22.843	21.326	23.275	1.320	Y	●	
	Nitrilase/cyanide hydratase and apolipoprotein N-acyltransferase [Methylobacillus flagellatus KT]637938659 YP_545854																
MFLA1746		5.921	5.459	6.708	0.276	Y	●	●	Y	5.48 E-2	25.353	26.052	26.744	-0.796	Y	●	
	" peptidase U62, modulator of DNA gyrase [Methylobacillus flagellatus KT]637938660 YP_545855 """																
MFLA1747	9.04 E-2	6.921	7.103	8.015	-0.177	Y	●	●	Y	2.4 E-1	26.693	26.800	27.747	-0.248	Y	●	
	hypothetical protein [Methylobacillus flagellatus KT]637938661 YP_545856																
MFLA1748	5.18 E-2	5.832	5.947	6.890	-0.159	Y	●	●	Y	1.39 E-1	24.045	24.511	25.297	-0.813	Y	●	
	transcription-repair coupling factor [Methylobacillus flagellatus KT]637938662 YP_545857																
MFLA1749		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938663 YP_545858																
MFLA1750		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637938664 YP_545859																

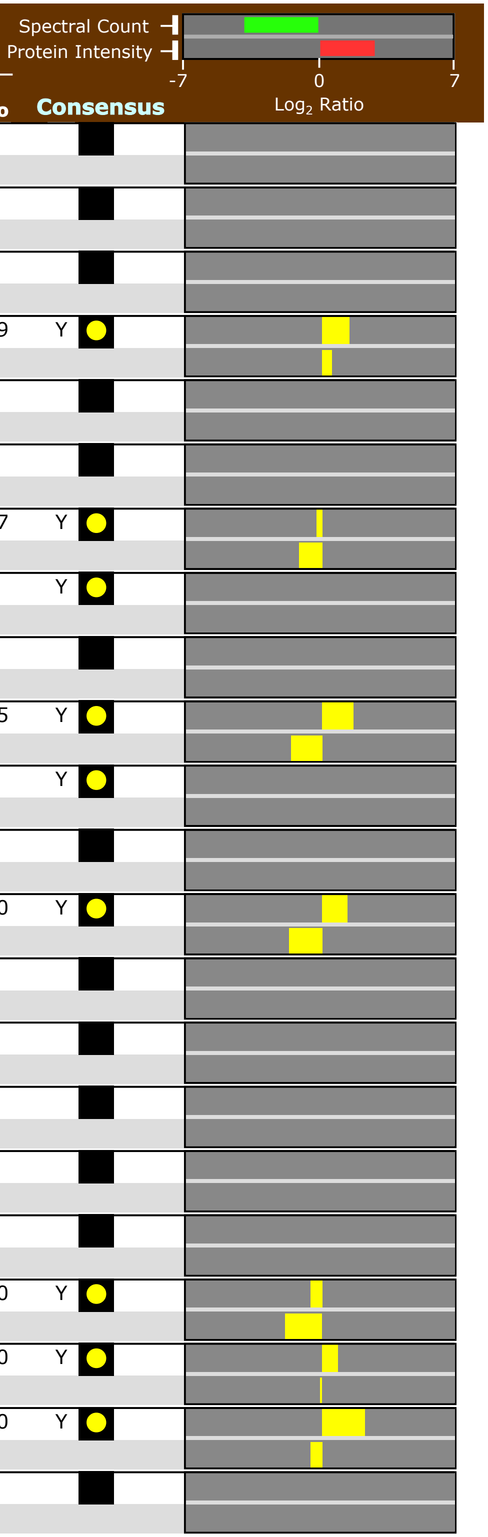
ORF	AM/OH *M Flagellatus* Spectral Count *q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	AM/OH *M Flagellatus* Protein Intensity *q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA1751		4.444	3.871	5.186	0.352	Y ● ● Y	2.66 E-1	22.500	22.446	23.473	-0.255	Y ●
	UvrD/REP helicase [Methylobacillus flagellatus KT]637938665 YP_545860											
MFLA1752		3.608	3.177	4.408	1.585	Y ● ● Y	2.45 E-2	23.648	21.017	23.864	3.834	Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637938666 YP_545861											
MFLA1753		2.418		2.418		Y ● ● Y		20.314		20.314		Y ●
	GreA/GreB family elongation factor [Methylobacillus flagellatus KT]637938667 YP_545862											
MFLA1754		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938668 YP_545863											
MFLA1755		7.205	7.901	8.594	-0.724	Y ● ● Y	6.99 E-2	27.301	28.012	28.700	-0.645	Y ●
	translation elongation factor P [Methylobacillus flagellatus KT]637938669 YP_545864											
MFLA1756		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938670 YP_545865											
MFLA1757		0.000	0.000			■ ■		0.000	0.000			■
	ammonium transporter [Methylobacillus flagellatus KT]637938671 YP_545866											
MFLA1758		0.000	0.000			■ ■		0.000	0.000			■
	uracil-DNA glycosylase [Methylobacillus flagellatus KT]637938672 YP_545867											
MFLA1759		0.000	0.000			■ ■		0.000	0.000			■
	Radical SAM [Methylobacillus flagellatus KT]637938673 YP_545868											
MFLA1760		0.521		0.521		Y ● ● Y		19.006		19.006		Y ●
	CheW protein [Methylobacillus flagellatus KT]637938674 YP_545869											
MFLA1761		1.843	1.915	2.879	1.008	Y ● ● Y	6.08 E-2	20.486	20.983	21.755	0.509	Y ●
	" two component transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637938675 YP_545870 """											
MFLA1762		0.000	0.000			■ ■		0.000	0.000			■
	periplasmic sensor hybrid histidine kinase [Methylobacillus flagellatus KT]637938676 YP_545871											
MFLA1763		0.000	0.000			■ ■		0.000	0.000			■
	HupE/UreJ protein [Methylobacillus flagellatus KT]637938677 YP_545872											
MFLA1764		2.967	4.044	4.604	-1.067	Y ● ● Y	3.98 E-2	21.709	22.542	23.185	-0.951	Y ●
	urease accessory protein UreG [Methylobacillus flagellatus KT]637938678 YP_545873											
MFLA1765		0.000	0.000			■ ■		0.000	0.000			■
	Urease accessory protein UreF [Methylobacillus flagellatus KT]637938679 YP_545874											
MFLA1766		0.000	0.000			■ ■		0.000	0.000			■
	UreE urease accessory-like protein [Methylobacillus flagellatus KT]637938680 YP_545875											
MFLA1767		3.341	3.435	4.389	-0.041	Y ● ● Y	2.52 E-2	21.264	22.477	22.995	-1.264	Y ●
	" urease, alpha subunit [Methylobacillus flagellatus KT]637938681 YP_545876 """											
MFLA1768		0.000	0.000			■ ■		0.000	0.000			■
	" urease, beta subunit [Methylobacillus flagellatus KT]637938682 YP_545877 """											
MFLA1769		1.843	0.931	2.458	0.911	Y ● ● Y		18.323	19.965	20.366	-1.641	Y ●
	" urease, gamma subunit [Methylobacillus flagellatus KT]637938683 YP_545878 """											
MFLA1770		0.000	0.000			■ ■		0.000	0.000			■
	Urease accessory protein UreD [Methylobacillus flagellatus KT]637938684 YP_545879											
MFLA1771		0.000	0.000			■ ■		0.000	0.000			■
	ABC transporter related [Methylobacillus flagellatus KT]637938685 YP_545880											
MFLA1772		1.106		1.106		Y ● ● Y		19.410		19.410		Y ●
	ABC transporter related [Methylobacillus flagellatus KT]637938686 YP_545881											



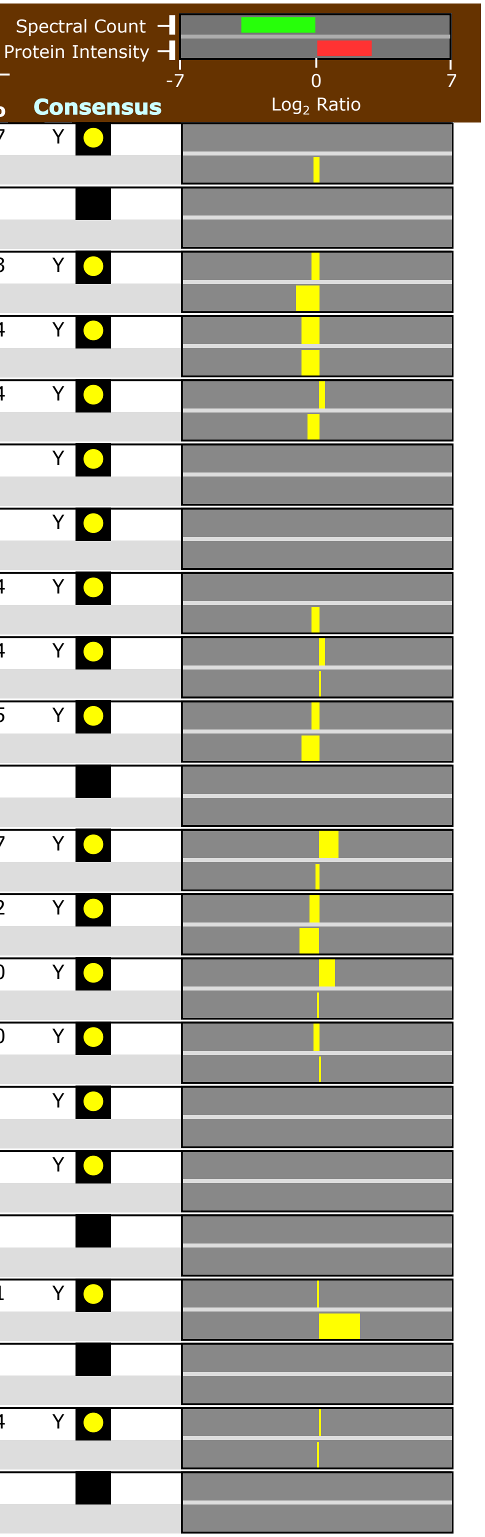
	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA1773		0.000	0.000			■ ■		0.000	0.000			■
	inner-membrane translocator [Methylobacillus flagellatus KT]637938687 YP_545882											
MFLA1774		0.000	0.000			■ ■		0.000	0.000			■
	inner-membrane translocator [Methylobacillus flagellatus KT]637938688 YP_545883											
MFLA1775		5.432	4.861	6.175	0.576	Y 🟡 🟡 Y	1.02 E-1	25.078	24.095	25.669	0.941	Y 🟡
	Twin-arginine translocation pathway signal [Methylobacillus flagellatus KT]637938689 YP_545884											
MFLA1776		0.000	0.000			■ ■		0.000	0.000			■
	" Glutamine amidotransferase, class-II [Methylobacillus flagellatus KT]637938690 YP_545885 """											
MFLA1777			2.844	2.844		Y 🟡 🟡 Y			21.445	21.445		Y 🟡
	Formamidase [Methylobacillus flagellatus KT]637938691 YP_545886											
MFLA1778		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938692 YP_545887											
MFLA1779		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938693 YP_545888											
MFLA1780		4.918	3.875	5.489	1.134	Y 🟡 🟡 Y	1.34 E-1	21.561	22.727	23.259	-0.241	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938694 YP_545889											
MFLA1781		3.106	0.346	3.304	2.759	Y 🟡 🟡 Y		25.783	21.316	25.847	4.468	Y 🟡
	putative prophage repressor [Methylobacillus flagellatus KT]637938695 YP_545890											
MFLA1782		0.000	0.000			■ ■		0.000	0.000			■
	[Methylobacillus flagellatus KT]639329602											
MFLA1783		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938696 YP_545891											
MFLA1784	1.26 E-5	7.100	6.432	7.804	0.682	R 🔴 🟡 Y	2.21 E-1	24.480	24.399	25.440	0.113	R 🔴
	nitrilotriacetate monooxygenase component A [Methylobacillus flagellatus KT]637938697 YP_545892											
MFLA1785	1.48 E-1	7.393	7.339	8.366	0.052	Y 🟡 🟡 Y	9.05 E-2	26.983	27.238	28.116	-0.244	Y 🟡
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637938698 YP_545893											
MFLA1786		2.328		2.328		Y 🟡 🟡 Y		20.066		20.066		Y 🟡
	Na+/solute symporter [Methylobacillus flagellatus KT]637938699 YP_545894											
MFLA1787		0.000	0.000			■ ■		0.000	0.000			■
	Conserved TM helix [Methylobacillus flagellatus KT]637938700 YP_545895											
MFLA1788		4.460	4.379	5.420	-0.541	Y 🟡 🟡 Y	1.17 E-1	22.568	23.256	23.953	-1.415	Y 🟡
	protein of unknown function UPF0061 [Methylobacillus flagellatus KT]637938701 YP_545896											
MFLA1789		0.000	0.000			■ ■		0.000	0.000			■
	luciferase-like protein [Methylobacillus flagellatus KT]637938702 YP_545897											
MFLA1790		0.000	0.000			■ ■		0.000	0.000			■
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637938703 YP_545898 """											
MFLA1791		0.000	0.000			■ ■		0.000	0.000			■
	Alpha/beta hydrolase fold-3 [Methylobacillus flagellatus KT]637938704 YP_545899											
MFLA1792		0.000	0.000			■ ■		0.000	0.000			■
	secretion protein HlyD [Methylobacillus flagellatus KT]637938705 YP_545900											
MFLA1793		0.000	0.000			■ ■		0.000	0.000			■
	Hydrophobe/amphiphile efflux-1 HAE1 [Methylobacillus flagellatus KT]637938706 YP_545901											
MFLA1794		0.000	0.000			■ ■		0.000	0.000			■
	" RND efflux system, outer membrane lipoprotein, NodT [Methylobacillus flagellatus KT]637938707 YP_545902 """											

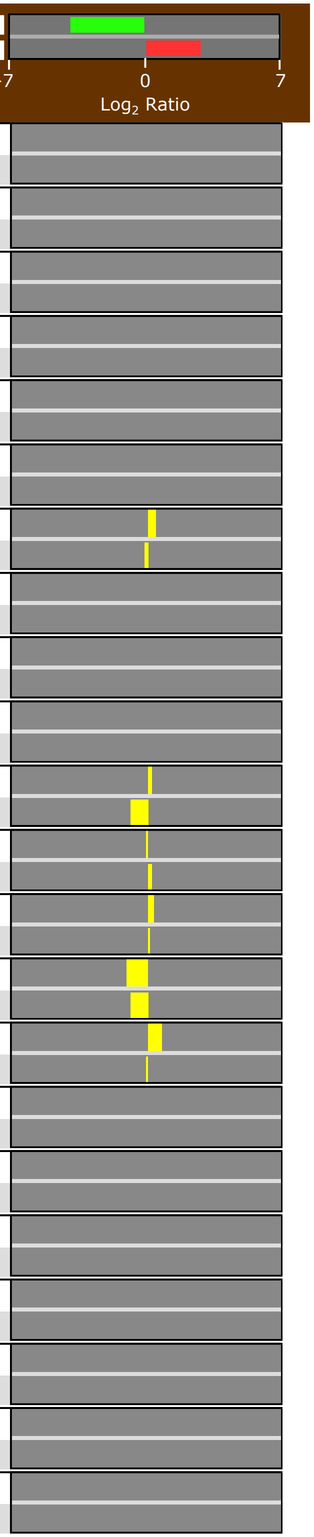


ORF	AM/OH *M Flagellatus* Spectral Count					Regulation	AM/OH *M Flagellatus* Protein Intensity					Consensus
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio		*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	
MFLA1795		0.000	0.000			■ ■		0.000	0.000			■
	Lysine exporter protein (LYSE/YGGA) [Methylobacillus flagellatus KT]637938708 YP_545903											
MFLA1796		0.000	0.000			■ ■		0.000	0.000			■
	transport-associated [Methylobacillus flagellatus KT]637938709 YP_545904											
MFLA1797		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938710 YP_545905											
MFLA1798		4.477	3.464	5.058	1.418	Y ● ● Y	7.11 E-2	22.874	22.284	23.609	0.539	Y ●
	Twin-arginine translocation pathway signal [Methylobacillus flagellatus KT]637938711 YP_545906											
MFLA1799		0.000	0.000			■ ■		0.000	0.000			■
	major facilitator superfamily MFS_1 [Methylobacillus flagellatus KT]637938712 YP_545907											
MFLA1800		0.000	0.000			■ ■		0.000	0.000			■
	putative transcriptional regulator [Methylobacillus flagellatus KT]637938713 YP_545908											
MFLA1801	1.74 E-2	5.357	5.555	6.460	-0.324	Y ● ● Y	1.53 E-2	24.157	25.284	25.828	-1.197	Y ●
	NAD-dependent epimerase/dehydratase [Methylobacillus flagellatus KT]637938714 YP_545909											
MFLA1802			0.000	0.000		Y ● ● Y			18.588	18.588		Y ●
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637938715 YP_545910											
MFLA1803		0.000	0.000			■ ■		0.000	0.000			■
	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase [Methylobacillus flagellatus KT]637938719 YP_545911											
MFLA1804		2.106	1.540	2.850	1.640	Y ● ● Y	1.06 E-1	18.671	21.401	21.604	-1.615	Y ●
	" excinuclease ABC, C subunit [Methylobacillus flagellatus KT]637938720 YP_545912 """											
MFLA1805		2.398		2.398		Y ● ● Y		22.376		22.376		Y ●
	4-oxalocrotonate tautomerase [Methylobacillus flagellatus KT]637938721 YP_545913											
MFLA1806		0.000	0.000			■ ■		0.000	0.000			■
	cation diffusion facilitator family transporter [Methylobacillus flagellatus KT]637938722 YP_545914											
MFLA1807		2.521	2.398	3.461	1.347	Y ● ● Y	5.54 E-2	19.988	22.690	22.896	-1.690	Y ●
	protein of unknown function DUF519 [Methylobacillus flagellatus KT]637938723 YP_545915											
MFLA1808		0.000	0.000			■ ■		0.000	0.000			■
	Uncharacterized protein UPF0114 [Methylobacillus flagellatus KT]637938724 YP_545916											
MFLA1809		0.000	0.000			■ ■		0.000	0.000			■
	protein of unknown function DUF81 [Methylobacillus flagellatus KT]637938725 YP_545917											
MFLA1810		0.000	0.000			■ ■		0.000	0.000			■
	" protein of unknown function DUF395, YeeE/YedE [Methylobacillus flagellatus KT]637938726 YP_545918 """											
MFLA1811		0.000	0.000			■ ■		0.000	0.000			■
	" protein of unknown function DUF395, YeeE/YedE [Methylobacillus flagellatus KT]637938727 YP_545919 """											
MFLA1812		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938728 YP_545920											
MFLA1813	3.81 E-2	4.803	5.366	6.112	-0.583	Y ● ● Y	1.07 E-2	21.752	23.657	23.999	-1.890	Y ●
	protein of unknown function DUF442 [Methylobacillus flagellatus KT]637938729 YP_545921											
MFLA1814		3.273	2.459	3.923	0.813	Y ● ● Y		20.854	20.935	21.895	-0.080	Y ●
	beta-lactamase-like protein [Methylobacillus flagellatus KT]637938730 YP_545922											
MFLA1815		2.691	1.540	3.227	2.225	Y ● ● Y	1.59 E-1	18.052	19.882	20.239	-0.600	Y ●
	" sigma54 specific transcriptional regulator, Fis family [Methylobacillus flagellatus KT]637938731 YP_545923 """											
MFLA1816		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938732 YP_545924											

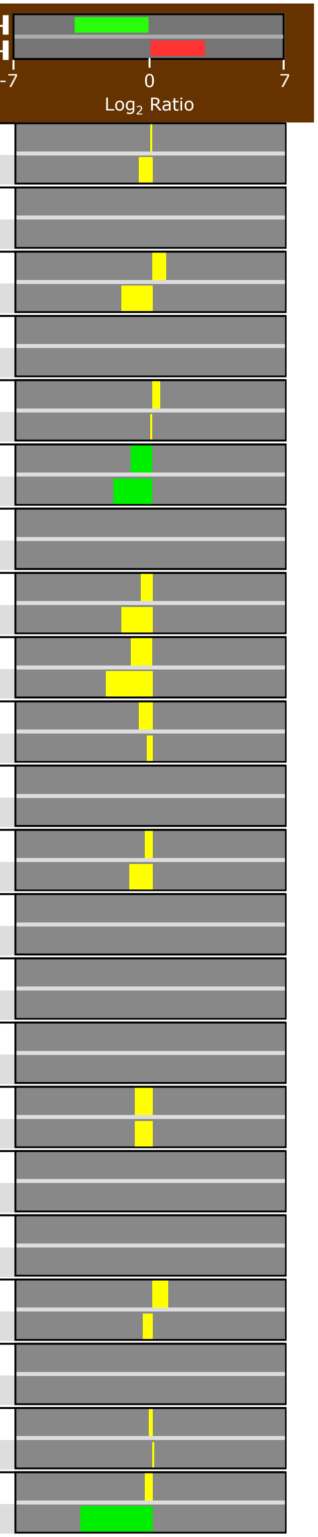


ORF	AM/OH *M Flagellatus* Spectral Count					Regulation	AM/OH *M Flagellatus* Protein Intensity					Consensus
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio		*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	
MFLA1817	7.21 E-2	8.205	8.181	9.193	0.015	Y ● ● Y	1.66 E-2	27.784	28.062	28.930	-0.277	Y ●
	Aconitate hydratase [Methylobacillus flagellatus KT]637938733 YP_545925											
MFLA1818		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938734 YP_545926											
MFLA1819	3.08 E-4	7.618	7.976	8.808	-0.369	Y ● ● Y	1.23 E-2	27.020	28.185	28.717	-1.233	Y ●
	adenylosuccinate lyase [Methylobacillus flagellatus KT]637938735 YP_545927											
MFLA1820		3.210	4.056	4.694	-0.884	Y ● ● Y	4.62 E-2	21.868	22.666	23.322	-0.944	Y ●
	surface antigen (D15) [Methylobacillus flagellatus KT]637938736 YP_545928											
MFLA1821		4.532	4.373	5.455	0.277	Y ● ● Y	1.83 E-1	22.642	23.086	23.881	-0.634	Y ●
	protein of unknown function DUF490 [Methylobacillus flagellatus KT]637938737 YP_545929											
MFLA1822			3.945	3.945		Y ● ● Y			23.660	23.660		Y ●
	protein of unknown function DUF88 [Methylobacillus flagellatus KT]637938738 YP_545930											
MFLA1823			0.000	0.000		Y ● ● Y			18.843	18.843		Y ●
	flavodoxin/nitric oxide synthase [Methylobacillus flagellatus KT]637938739 YP_545931											
MFLA1824	9.34 E-2	6.065	6.038	7.051	-0.004	Y ● ● Y	5.47 E-2	24.819	25.234	26.041	-0.424	Y ●
	stationary-phase survival protein SurE [Methylobacillus flagellatus KT]637938740 YP_545932											
MFLA1825		4.974	4.641	5.817	0.337	Y ● ● Y	1.92 E-1	23.235	23.077	24.158	0.124	Y ●
	protein-L-isoaspartate O-methyltransferase [Methylobacillus flagellatus KT]637938741 YP_545933											
MFLA1826		4.624	5.013	5.832	-0.385	Y ● ● Y	2.27 E-2	23.628	24.481	25.116	-0.915	Y ●
	peptidase M23B [Methylobacillus flagellatus KT]637938742 YP_545934											
MFLA1827		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938743 YP_545935											
MFLA1828		3.580	1.322	3.854	0.988	Y ● ● Y	2.72 E-1	22.822	21.790	23.396	-0.227	Y ●
	thioredoxin-related [Methylobacillus flagellatus KT]637938744 YP_545936											
MFLA1829	2.03 E-2	5.725	6.229	6.999	-0.504	Y ● ● Y	4.08 E-2	26.711	27.615	28.233	-0.992	Y ●
	nitroreductase [Methylobacillus flagellatus KT]637938745 YP_545937											
MFLA1830		8.090	7.343	8.764	0.761	Y ● ● Y	2.66 E-1	25.857	25.886	26.872	-0.080	Y ●
	NADH:flavin oxidoreductase/NADH oxidase [Methylobacillus flagellatus KT]637938746 YP_545938											
MFLA1831	2.99 E-2	6.762	7.088	7.934	-0.327	Y ● ● Y	2.67 E-1	26.740	26.689	27.715	0.070	Y ●
	YceI [Methylobacillus flagellatus KT]637938747 YP_545939											
MFLA1832			4.125	4.125		Y ● ● Y			22.840	22.840		Y ●
	NADPH-dependent FMN reductase [Methylobacillus flagellatus KT]637938748 YP_545940											
MFLA1833		1.106		1.106		Y ● ● Y		19.141		19.141		Y ●
	Pirin-like protein [Methylobacillus flagellatus KT]637938749 YP_545941											
MFLA1834		0.000	0.000			■ ■		0.000	0.000			■
	protein of unknown function DUF540 [Methylobacillus flagellatus KT]637938750 YP_545942											
MFLA1835		0.521	0.585	1.553	-0.064	Y ● ● Y		22.106	20.006	22.409	2.101	Y ●
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637938751 YP_545943 """											
MFLA1836		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938752 YP_545944											
MFLA1837		4.757	4.641	5.700	0.086	Y ● ● Y	2.59 E-1	23.087	23.016	24.052	-0.074	Y ●
	" ATPase associated with various cellular activities, AAA_3 [Methylobacillus flagellatus KT]637938753 YP_545945 """											
MFLA1838		0.000	0.000			■ ■		0.000	0.000			■
	protein of unknown function DUF58 [Methylobacillus flagellatus KT]637938754 YP_545946											



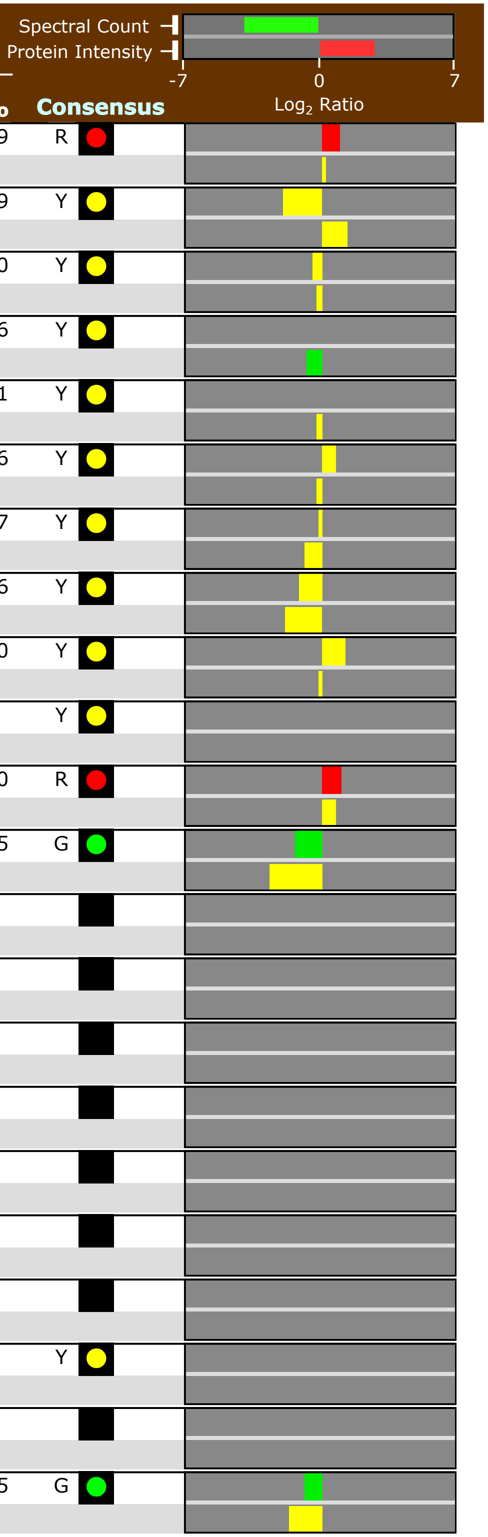


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA1839		2.106		2.106		Y	●	●	Y		19.211		19.211		Y	●
	transglutaminase-like protein [Methylobacillus flagellatus KT]637938755 YP_545947															
MFLA1840		1.674		1.674		Y	●	●	Y		19.665		19.665		Y	●
	" CMP/dCMP deaminase, zinc-binding [Methylobacillus flagellatus KT]637938756 YP_545948 """															
MFLA1841		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938757 YP_545949															
MFLA1842		0.000	0.000				■	■			0.000	0.000				■
	Rhomboid-like protein [Methylobacillus flagellatus KT]637938758 YP_545950															
MFLA1843		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function UPF0005 [Methylobacillus flagellatus KT]637938759 YP_545951															
MFLA1844		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637938760 YP_545952															
MFLA1845	4.72 E-2	5.169	4.766	5.982	0.395	Y	●	●	Y	1.87 E-1	23.637	23.771	24.706	-0.168	Y	●
	Beta-N-acetylhexosaminidase [Methylobacillus flagellatus KT]637938761 YP_545953															
MFLA1846		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF165 [Methylobacillus flagellatus KT]637938762 YP_545954															
MFLA1847		0.000	0.000				■	■			0.000	0.000				■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637938763 YP_545955															
MFLA1848		0.000	0.000				■	■			0.000	0.000				■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637938764 YP_545956															
MFLA1849		2.761	1.346	3.220	0.224	Y	●	●	Y	1.3 E-1	19.939	19.654	20.803	-0.939	Y	●
	ErfK/YbiS/YcfS/YnhG [Methylobacillus flagellatus KT]637938765 YP_545957															
MFLA1850		4.391	4.471	5.431	-0.094	Y	●	●	Y	1.6 E-1	22.709	22.247	23.497	0.224	Y	●
	" extracellular solute-binding protein, family 5 [Methylobacillus flagellatus KT]637938766 YP_545958 """															
MFLA1851	1.42 E-2	5.167	4.788	5.990	0.303	Y	●	●	Y	1.73 E-1	24.007	23.579	24.809	0.143	Y	●
	" RNA methyltransferase, TrmA family [Methylobacillus flagellatus KT]637938767 YP_545959 """															
MFLA1852		3.726	4.261	5.018	-1.091	Y	●	●	Y	7.9 E-2	23.018	23.700	24.399	-0.924	Y	●
	hypothetical protein [Methylobacillus flagellatus KT]637938768 YP_545960															
MFLA1853		3.552	2.844	4.241	0.710	Y	●	●	Y	2.02 E-1	22.595	22.751	23.675	-0.074	Y	●
	hypothetical protein [Methylobacillus flagellatus KT]637938769 YP_545961															
MFLA1854		0.813		0.813		Y	●	●	Y		23.707		23.707		Y	●
	hypothetical protein [Methylobacillus flagellatus KT]637938770 YP_545962															
MFLA1855		0.000	0.000				■	■			0.000	0.000				■
	" putative transcriptional regulator, CopG family [Methylobacillus flagellatus KT]637938771 YP_545963 """															
MFLA1856		0.000	0.000				■	■			0.000	0.000				■
	Glutamate--ammonia ligase [Methylobacillus flagellatus KT]637938772 YP_545964															
MFLA1857		0.000	0.000				■	■			0.000	0.000				■
	ABC transporter related [Methylobacillus flagellatus KT]637938773 YP_545965															
MFLA1858		0.000	0.000				■	■			0.000	0.000				■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637938774 YP_545966															
MFLA1859		0.000	0.000				■	■			0.000	0.000				■
	ABC transport system substrate-binding protein [Methylobacillus flagellatus KT]637938775 YP_545967															
MFLA1860		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938776 YP_545968															

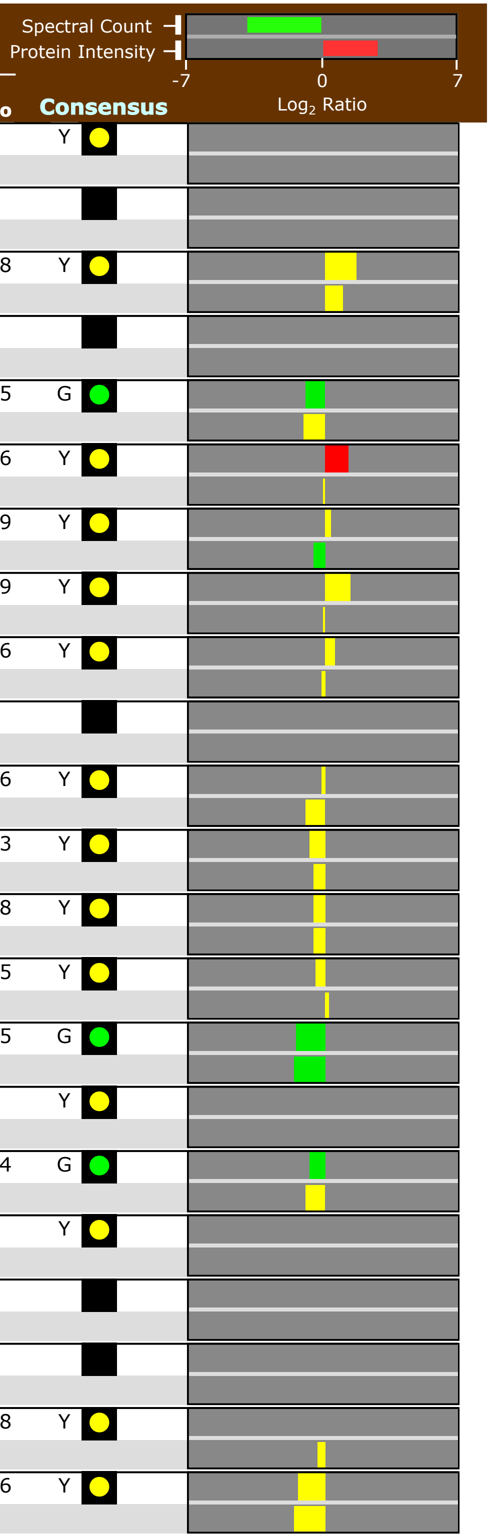


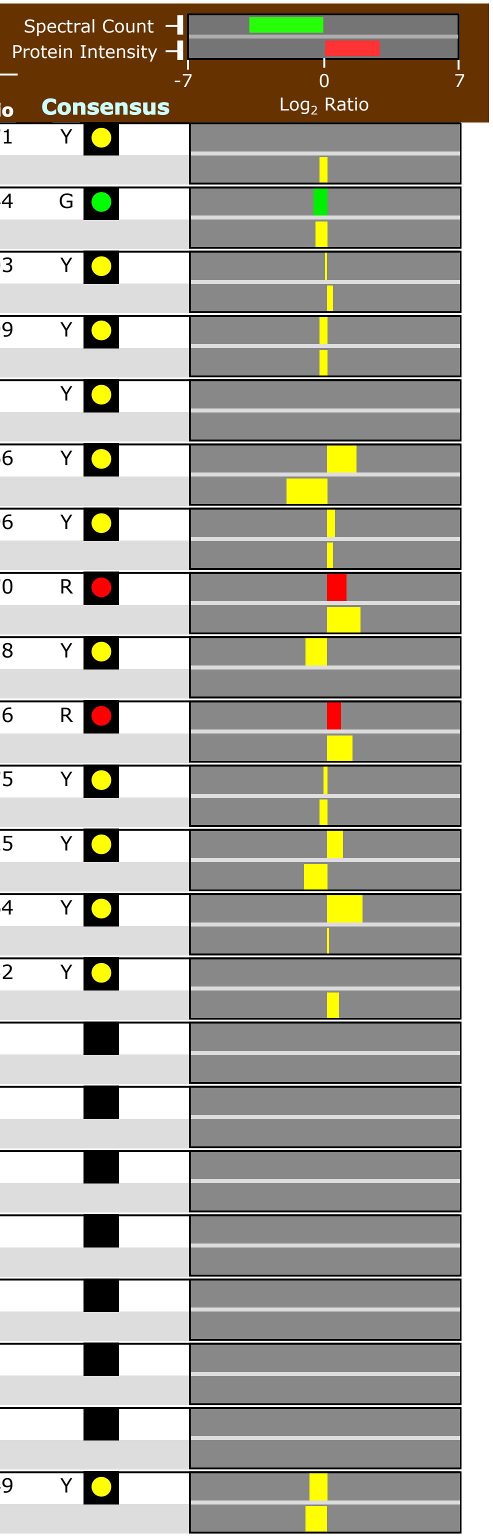
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA1861	1.08 E-1	5.004	5.117	6.061	-0.117	Y	🟡	🟡	Y	2.05 E-2	24.335	25.039	25.729	-0.729	Y	🟡
	cysteine synthase B [Methylobacillus flagellatus KT]637938777 YP_545969															
MFLA1862			2.739	2.739		Y	🟡	🟡	Y			20.712	20.712		Y	🟡
	Disulphide bond formation protein DsbB [Methylobacillus flagellatus KT]637938778 YP_545970															
MFLA1863		2.980	3.261	4.127	0.722	Y	🟡	🟡	Y	8.42 E-2	19.049	21.706	21.918	-1.608	Y	🟡
	" exodeoxyribonuclease VII, large subunit [Methylobacillus flagellatus KT]637938779 YP_545971 """															
MFLA1864			1.322	1.322		Y	🟡	🟡	Y			19.954	19.954		Y	🟡
	TfoX-like protein [Methylobacillus flagellatus KT]637938780 YP_545972															
MFLA1865		4.960	4.431	5.720	0.442	Y	🟡	🟡	Y	2.13 E-1	24.613	24.791	25.705	-0.099	Y	🟡
	" peptidase M48, Ste24p [Methylobacillus flagellatus KT]637938781 YP_545973 """															
MFLA1866	0	9.075	10.162	10.718	-1.090	G	🟢	🟢	G	7.38 E-3	26.760	28.757	29.079	-2.003	G	🟢
	" 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase [Methylobacillus flagellatus KT]637938782 YP_545974 """															
MFLA1867			2.095	2.095		Y	🟡	🟡	Y			21.120	21.120		Y	🟡
	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) [Methylobacillus flagellatus KT]637938783 YP_545975															
MFLA1868		3.937	4.526	5.261	-0.641	Y	🟡	🟡	Y	3.98 E-2	22.955	24.146	24.670	-1.621	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938784 YP_545976															
MFLA1869	1.15 E-1	4.604	5.233	5.953	-1.121	Y	🟡	🟡	Y	2.34 E-2	22.136	23.957	24.317	-2.363	Y	🟡
	succinyl-diaminopimelate desuccinylase [Methylobacillus flagellatus KT]637938785 YP_545977															
MFLA1870		3.691	5.366	5.759	-0.671	Y	🟡	🟡	Y	1.44 E-1	22.826	24.116	24.610	-0.267	Y	🟡
	" modification methylase, HemK family [Methylobacillus flagellatus KT]637938786 YP_545978 """															
MFLA1871		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF202 [Methylobacillus flagellatus KT]637938787 YP_545979															
MFLA1872		4.470	4.370	5.421	-0.352	Y	🟡	🟡	Y	1.69 E-1	22.151	22.607	23.397	-1.159	Y	🟡
	" Pseudouridine synthase, Rsu [Methylobacillus flagellatus KT]637938788 YP_545980 """															
MFLA1873			0.346	0.346		Y	🟡	🟡	Y			19.695	19.695		Y	🟡
	putative transcriptional regulator [Methylobacillus flagellatus KT]637938789 YP_545981															
MFLA1874		0.000	0.000				■	■			0.000	0.000				■
	chromosome segregation and condensation protein ScpA [Methylobacillus flagellatus KT]637938790 YP_545982															
MFLA1875		0.000	0.000				■	■			0.000	0.000				■
	peptidase M50 [Methylobacillus flagellatus KT]637938791 YP_545983															
MFLA1876		4.128	4.869	5.545	-0.943	Y	🟡	🟡	Y	6.37 E-2	24.523	25.235	25.923	-0.893	Y	🟡
	Sua5/YciO/YrdC/YwlC [Methylobacillus flagellatus KT]637938792 YP_545984															
MFLA1877		2.543		2.543		Y	🟡	🟡	Y		20.434		20.434		Y	🟡
	PHP-like protein [Methylobacillus flagellatus KT]637938793 YP_545985															
MFLA1878		0.000	0.000				■	■			0.000	0.000				■
	intracellular septation protein A [Methylobacillus flagellatus KT]637938794 YP_545986															
MFLA1879		3.608	2.806	4.262	0.802	Y	🟡	🟡	Y		20.648	21.114	21.900	-0.466	Y	🟡
	YCII-related [Methylobacillus flagellatus KT]637938795 YP_545987															
MFLA1880			0.000	0.000		Y	🟡	🟡	Y			20.543	20.543		Y	🟡
	BolA-like protein [Methylobacillus flagellatus KT]637938796 YP_545988															
MFLA1881		8.541	8.732	9.640	-0.161	Y	🟡	🟡	Y	1.55 E-1	28.952	28.805	29.880	0.132	Y	🟡
	PpiC-type peptidyl-prolyl cis-trans isomerase [Methylobacillus flagellatus KT]637938797 YP_545989															
MFLA1882		4.080	4.473	5.290	-0.434	Y	🟡	🟢	G	4.1 E-3	19.859	23.278	23.407	-3.661	G	🟢
	peptidase M61 [Methylobacillus flagellatus KT]637938798 YP_545990															

ORF	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
	q-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA1883	6.28 E-5	6.104	5.247	6.738	0.900	R 🔴 🟡 Y	1.86 E-1	23.359	23.019	24.199	0.159	R 🔴
	iron permease FTR1 [Methylobacillus flagellatus KT]637938799 YP_545991											
MFLA1884		1.398	4.410	4.579	-1.975	Y 🟡 🟡 Y	1.23 E-2	23.634	23.306	24.479	1.329	Y 🟡
	Glyoxalase/bleomycin resistance protein/dioxygenase [Methylobacillus flagellatus KT]637938800 YP_545992											
MFLA1885		6.957	7.443	8.221	-0.516	Y 🟡 🟡 Y	1.33 E-1	27.902	28.198	29.058	-0.290	Y 🟡
	" nitrogen regulatory protein P-II (GlnB, GlnK) [Methylobacillus flagellatus KT]637938801 YP_545993 """											
MFLA1886		4.271	4.230	5.251	0.027	Y 🟡 🟢 G	8.9 E-3	22.699	23.528	24.172	-0.826	Y 🟡
	NAD+ synthetase [Methylobacillus flagellatus KT]637938802 YP_545994											
MFLA1887	1.3 E-2	6.263	6.225	7.244	-0.040	Y 🟡 🟡 Y	1.03 E-1	25.040	25.329	26.192	-0.311	Y 🟡
	Ankyrin [Methylobacillus flagellatus KT]637938803 YP_545995											
MFLA1888		7.239	6.321	7.852	0.742	Y 🟡 🟡 Y	1.23 E-1	25.004	25.252	26.133	-0.286	Y 🟡
	" succinyl-CoA synthetase, alpha subunit [Methylobacillus flagellatus KT]637938804 YP_545996 """											
MFLA1889	8.81 E-2	6.502	6.742	7.627	-0.243	Y 🟡 🟡 Y	1.13 E-2	25.674	26.549	27.176	-0.877	Y 🟡
	" succinyl-CoA synthetase, beta subunit [Methylobacillus flagellatus KT]637938805 YP_545997 """											
MFLA1890		2.710	3.915	4.435	-1.214	Y 🟡 🟡 Y	3.18 E-2	22.537	24.037	24.474	-1.946	Y 🟡
	phosphoserine phosphatase SerB [Methylobacillus flagellatus KT]637938806 YP_545998											
MFLA1891		7.902	6.882	8.480	1.187	Y 🟡 🟡 Y	1.62 E-1	24.703	24.931	25.821	-0.170	Y 🟡
	" peptidyl-prolyl cis-trans isomerase, cyclophilin type [Methylobacillus flagellatus KT]637938807 YP_545999 """											
MFLA1892			1.807	1.807		Y 🟡 🟡 Y			19.846	19.846		Y 🟡
	" transcriptional regulator, GntR family [Methylobacillus flagellatus KT]637938808 YP_546000 """											
MFLA1893	0	8.310	7.283	8.886	1.028	R 🔴 🟡 Y	2.74 E-2	27.529	26.831	28.222	0.680	R 🔴
	beta-ketoacyl synthase [Methylobacillus flagellatus KT]637938809 YP_546001											
MFLA1894	8.21 E-8	4.731	5.978	6.485	-1.375	G 🟢 🟡 Y	1.12 E-2	23.376	25.496	25.794	-2.675	G 🟢
	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabA [Methylobacillus flagellatus KT]637938810 YP_546002											
MFLA1895		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	" ATPase associated with various cellular activities, AAA_3 [Methylobacillus flagellatus KT]637938811 YP_546003 """											
MFLA1896		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938812 YP_546004											
MFLA1897		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938813 YP_546005											
MFLA1898		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	" von Willebrand factor, type A [Methylobacillus flagellatus KT]637938814 YP_546006 """											
MFLA1899		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938815 YP_546007											
MFLA1900		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	" von Willebrand factor, type A [Methylobacillus flagellatus KT]637938816 YP_546008 """											
MFLA1901		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938817 YP_546009											
MFLA1902		1.521		1.521		Y 🟡 🟡 Y		19.695		19.695		Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938818 YP_546010											
MFLA1903		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938819 YP_546011											
MFLA1904	2.78 E-3	4.552	5.431	6.058	-0.877	G 🟢 🟡 Y	2.76 E-2	23.532	25.259	25.640	-1.665	G 🟢
	glycine cleavage T protein (aminomethyl transferase) [Methylobacillus flagellatus KT]637938820 YP_546012											



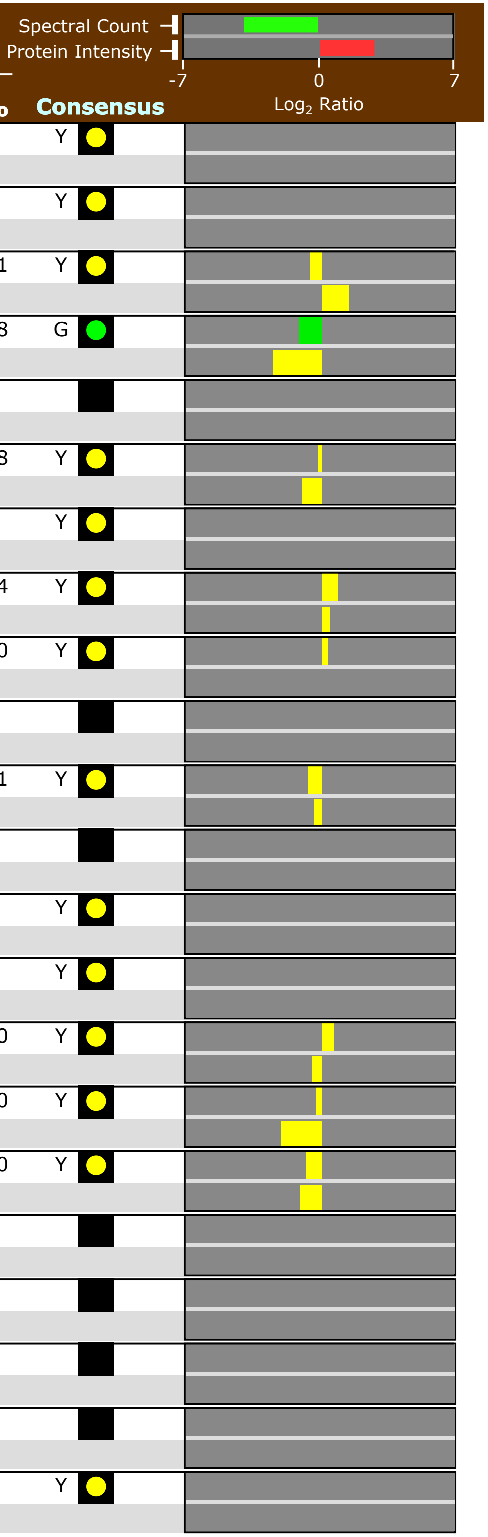
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA1905		2.328		2.328		Y	🟡	🟡	Y		18.339		18.339		Y	🟡
	TonB-dependent receptor [Methylobacillus flagellatus KT]637938821 YP_546013															
MFLA1906		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938822 YP_546014															
MFLA1907		2.761	0.000	2.959	1.571	Y	🟡	🟡	Y	1.33 E-1	20.834	18.720	21.134	0.948	Y	🟡
	diguanylate cyclase (GGDEF domain) [Methylobacillus flagellatus KT]637938823 YP_546015															
MFLA1908		0.000	0.000				■	■			0.000	0.000				■
	Septum formation initiator [Methylobacillus flagellatus KT]637938824 YP_546016															
MFLA1909	0	8.704	9.712	10.294	-1.035	G	🟢	🟡	Y	1.13 E-2	27.333	28.404	28.966	-1.105	G	🟢
	Phosphopyruvate hydratase [Methylobacillus flagellatus KT]637938825 YP_546017															
MFLA1910	9.45 E-6	5.353	4.087	5.854	1.204	R	🔴	🟡	Y	2.15 E-1	23.951	24.072	25.013	-0.066	Y	🟡
	2-dehydro-3-deoxyphosphooctonate aldolase [Methylobacillus flagellatus KT]637938826 YP_546018															
MFLA1911	1.02 E-2	7.202	6.880	8.050	0.331	Y	🟡	🟢	G	4.58 E-3	26.193	26.781	27.517	-0.589	Y	🟡
	CTP synthase [Methylobacillus flagellatus KT]637938827 YP_546019															
MFLA1912		1.521	1.184	2.362	1.347	Y	🟡	🟡	Y	2.27 E-1	20.373	21.520	22.058	-0.069	Y	🟡
	YjeF-related protein-like protein [Methylobacillus flagellatus KT]637938828 YP_546020															
MFLA1913		2.106	2.788	3.487	0.479	Y	🟡	🟡	Y	1.52 E-1	20.477	21.737	22.240	-0.236	Y	🟡
	Initiation factor 2B alpha/beta/delta [Methylobacillus flagellatus KT]637938829 YP_546021															
MFLA1914		0.000	0.000				■	■			0.000	0.000				■
	TatD-related deoxyribonuclease [Methylobacillus flagellatus KT]637938830 YP_546022															
MFLA1915		3.937	4.079	5.010	-0.214	Y	🟡	🟡	Y	4.29 E-2	21.725	22.607	23.233	-1.016	Y	🟡
	riboflavin biosynthesis protein RibD [Methylobacillus flagellatus KT]637938831 YP_546023															
MFLA1916		3.571	4.398	5.043	-0.811	Y	🟡	🟡	Y	1.23 E-1	22.498	22.984	23.762	-0.563	Y	🟡
	Protein of unknown function DUF193 [Methylobacillus flagellatus KT]637938832 YP_546024															
MFLA1917		8.029	8.627	9.359	-0.598	Y	🟡	🟡	Y	1.11 E-2	27.577	28.185	28.913	-0.608	Y	🟡
	Glycine hydroxymethyltransferase [Methylobacillus flagellatus KT]637938833 YP_546025															
MFLA1918		4.552	5.040	5.816	-0.494	Y	🟡	🟡	Y	1.93 E-1	23.854	23.553	24.712	0.175	Y	🟡
	" hydro-lyases, Fe-S type, tartrate/fumarate subfamily, alpha region [Methylobacillus flagellatus KT]637938834 YP_546026 """															
MFLA1919	0	7.337	8.510	9.040	-1.451	G	🟢	🟢	G	8.35 E-3	25.040	26.604	27.025	-1.595	G	🟢
	NADH:flavin oxidoreductase/NADH oxidase [Methylobacillus flagellatus KT]637938835 YP_546027															
MFLA1920			4.184	4.184		Y	🟡	🟡	Y			22.804	22.804		Y	🟡
	protein of unknown function DUF528 [Methylobacillus flagellatus KT]637938836 YP_546028															
MFLA1921	3.57 E-9	6.828	7.582	8.254	-0.770	G	🟢	🟡	Y	1.23 E-2	26.996	28.001	28.584	-1.014	G	🟢
	Phosphoglucomutase [Methylobacillus flagellatus KT]637938837 YP_546029															
MFLA1922			1.322	1.322		Y	🟡	🟡	Y			20.788	20.788		Y	🟡
	" peptidase A2A, retrovirus, catalytic [Methylobacillus flagellatus KT]637938838 YP_546030 """															
MFLA1923		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938839 YP_546031															
MFLA1924		0.000	0.000				■	■			0.000	0.000				■
	" acetyltransferase, GNAT family [Methylobacillus flagellatus KT]637938840 YP_546032 """															
MFLA1925	1.39 E-1	5.926	5.940	6.933	-0.025	Y	🟡	🟡	Y	2.46 E-2	26.126	26.497	27.323	-0.378	Y	🟡
	phosphoglucomutase/phosphomannomutase alpha/beta/alpha domain I [Methylobacillus flagellatus KT]637938841 YP_546033															
MFLA1926		3.173	4.479	4.969	-1.408	Y	🟡	🟡	Y	1.38 E-2	23.112	24.699	25.113	-1.616	Y	🟡
	cyclic nucleotide-binding domain (cNMP-BD) protein [Methylobacillus flagellatus KT]637938843 YP_546034															

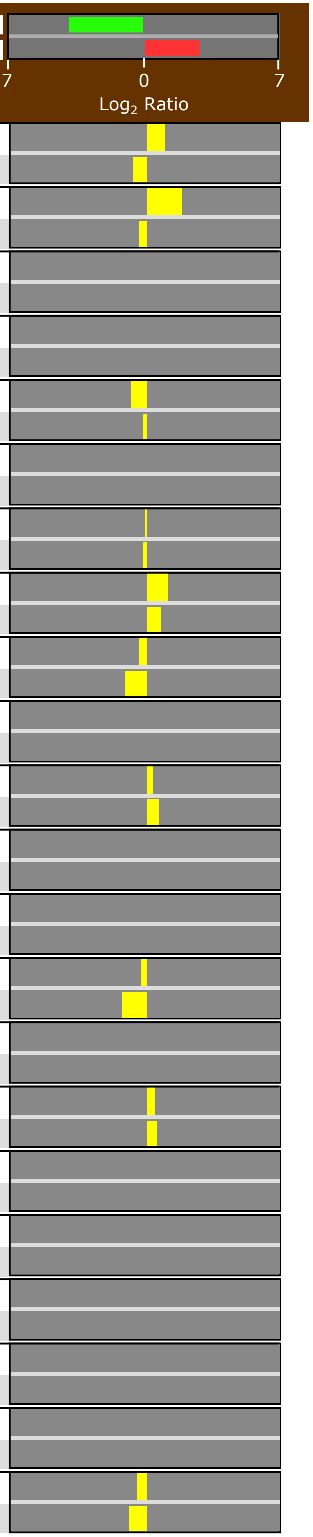




ORF	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
	q-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA1927		3.552	3.568	4.560	-0.019	Y 🟡 🟡 Y	1.1 E-2	22.361	22.733	23.559	-0.371	Y 🟡
	" transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637938844 YP_546035 """											
MFLA1928	4.33 E-3	4.922	5.654	6.334	-0.712	G 🟢 🟡 Y	1.15 E-1	24.707	25.294	26.030	-0.644	G 🟢
	" Chemotaxis phosphatase, CheZ [Methylobacillus flagellatus KT]637938845 YP_546036 """											
MFLA1929	5.88 E-2	6.443	6.568	7.507	-0.148	Y 🟡 🟡 Y	7.12 E-3	26.363	26.060	27.220	0.303	Y 🟡
	response regulator receiver domain protein (CheY-like) [Methylobacillus flagellatus KT]637938846 YP_546037											
MFLA1930		6.015	6.190	7.105	-0.352	Y 🟡 🟡 Y	1.28 E-1	24.706	25.033	25.879	-0.399	Y 🟡
	response regulator receiver (CheY-like) modulated CheB methylesterase [Methylobacillus flagellatus KT]637938847 YP_546038											
MFLA1931			1.322	1.322		Y 🟡 🟡 Y			19.550	19.550		Y 🟡
	" CheD, stimulates methylation of MCP proteins [Methylobacillus flagellatus KT]637938848 YP_546039 """											
MFLA1932		1.521	0.000	1.952	1.521	Y 🟡 🟡 Y		18.477	20.543	20.852	-2.066	Y 🟡
	" MCP methyltransferase, CheR-type [Methylobacillus flagellatus KT]637938849 YP_546040 """											
MFLA1933		7.154	6.764	7.972	0.360	Y 🟡 🟡 Y	1.67 E-1	26.534	26.134	27.347	0.296	Y 🟡
	methyl-accepting chemotaxis sensory transducer with Pas/Pac sensor [Methylobacillus flagellatus KT]637938850 YP_546041											
MFLA1934	1.09 E-11	7.394	6.459	8.001	0.965	R 🔴 🟡 Y	1.08 E-2	27.681	26.023	28.078	1.670	R 🔴
	methyl-accepting chemotaxis sensory transducer [Methylobacillus flagellatus KT]637938851 YP_546042											
MFLA1935		2.328	4.388	4.698	-1.054	Y 🟡 🟡 Y	2.7 E-1	23.374	24.393	24.972	0.018	Y 🟡
	CheW protein [Methylobacillus flagellatus KT]637938852 YP_546043											
MFLA1936	7.26 E-5	6.623	6.039	7.360	0.663	R 🔴 🟡 Y	9.5 E-2	26.589	25.075	27.022	1.336	R 🔴
	CheA signal transduction histidine kinases [Methylobacillus flagellatus KT]637938853 YP_546044											
MFLA1937		4.581	4.884	5.741	-0.214	Y 🟡 🟡 Y	1.5 E-1	24.150	24.571	25.376	-0.375	Y 🟡
	response regulator receiver domain protein (CheY-like) [Methylobacillus flagellatus KT]637938854 YP_546045											
MFLA1938		2.398	2.627	3.517	0.772	Y 🟡 🟡 Y	1.57 E-2	20.526	22.751	23.030	-1.225	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938855 YP_546046											
MFLA1939		4.087	2.295	4.453	1.786	Y 🟡 🟡 Y	2.19 E-1	22.392	22.315	23.354	0.064	Y 🟡
	OmpA/MotB [Methylobacillus flagellatus KT]637938856 YP_546047											
MFLA1940		3.408	3.353	4.381	-0.015	Y 🟡 🟡 Y	1.08 E-1	21.918	21.172	22.593	0.552	Y 🟡
	putative chemotaxis transmembrane protein MotA [Methylobacillus flagellatus KT]637938857 YP_546048											
MFLA1941		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938858 YP_546049											
MFLA1942		0.000	0.000			■ ■		0.000	0.000			■
	flagellar transcriptional activator FlhC [Methylobacillus flagellatus KT]637938859 YP_546050											
MFLA1943		0.000	0.000			■ ■		0.000	0.000			■
	flagellar transcriptional activator [Methylobacillus flagellatus KT]637938860 YP_546051											
MFLA1944		0.000	0.000			■ ■		0.000	0.000			■
	flagellar biosynthetic protein FlhB [Methylobacillus flagellatus KT]637938861 YP_546052											
MFLA1945		0.000	0.000			■ ■		0.000	0.000			■
	flagellar biosynthesis protein FlhA [Methylobacillus flagellatus KT]637938862 YP_546053											
MFLA1946		0.000	0.000			■ ■		0.000	0.000			■
	" GTP-binding signal recognition particle SRP54, G-domain [Methylobacillus flagellatus KT]637938863 YP_546054 """											
MFLA1947		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637938864 YP_546055											
MFLA1948		4.107	5.001	5.622	-0.898	Y 🟡 🟡 Y	7.33 E-2	23.351	24.189	24.830	-1.149	Y 🟡
	sigma 28 (Flagella/Sporulation) [Methylobacillus flagellatus KT]637938865 YP_546056											

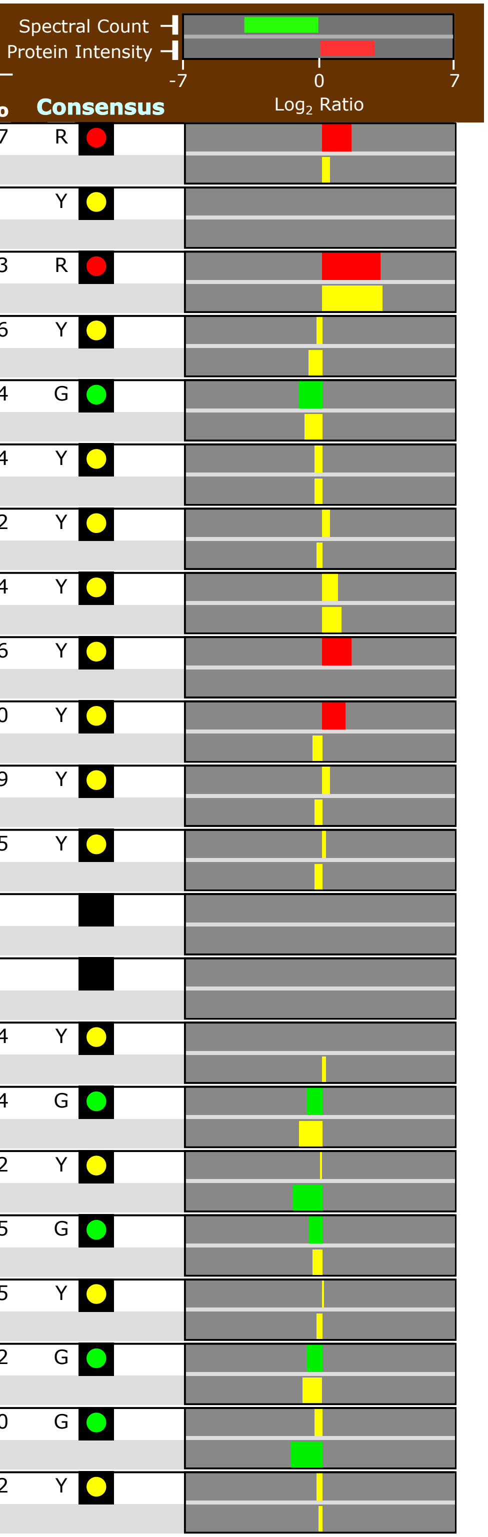
ORF	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA1949		1.813		1.813		Y ● ● Y		18.936		18.936		Y ●
	MotA/TolQ/ExbB proton channel [Methylobacillus flagellatus KT]637938866 YP_546057											
MFLA1950			0.346	0.346		Y ● ● Y			19.211	19.211		Y ●
	OmpA/MotB [Methylobacillus flagellatus KT]637938867 YP_546058											
MFLA1951		3.364	3.000	4.193	-0.637	Y ● ● Y	1.4 E-1	23.189	20.330	23.375	1.441	Y ●
	FlgN [Methylobacillus flagellatus KT]637938868 YP_546059											
MFLA1952	1.56 E-4	4.784	5.746	6.343	-1.194	G ● ● Y	3.84 E-2	24.434	25.872	26.325	-2.498	G ●
	" anti-sigma-28 factor, FlgM [Methylobacillus flagellatus KT]637938869 YP_546060 """											
MFLA1953		0.000	0.000			■ ■		0.000	0.000			■
	Flageller protein FlgA [Methylobacillus flagellatus KT]637938870 YP_546061											
MFLA1954		1.521	2.769	3.275	-0.238	Y ● ● Y	1.06 E-1	20.158	22.197	22.511	-0.978	Y ●
	flagellar basal-body rod protein FlgB [Methylobacillus flagellatus KT]637938871 YP_546062											
MFLA1955			2.949	2.949		Y ● ● Y			22.505	22.505		Y ●
	flagellar basal-body rod protein FlgC [Methylobacillus flagellatus KT]637938872 YP_546063											
MFLA1956		2.521	2.949	3.751	0.762	Y ● ● Y	1.02 E-1	21.901	22.560	23.268	0.354	Y ●
	flagellar hook capping protein [Methylobacillus flagellatus KT]637938873 YP_546064											
MFLA1957	7.09 E-2	5.874	5.561	6.726	0.318	Y ● ● Y	2.32 E-2	24.738	24.693	25.716	0.030	Y ●
	protein of unknown function DUF1078-like protein [Methylobacillus flagellatus KT]637938874 YP_546065											
MFLA1958		0.000	0.000			■ ■		0.000	0.000			■
	Flagellar basal-body rod FlgF [Methylobacillus flagellatus KT]637938875 YP_546066											
MFLA1959		4.451	4.823	5.649	-0.653	Y ● ● Y	1.43 E-1	22.094	22.692	23.424	-0.441	Y ●
	Flagellar basal-body rod FlgG [Methylobacillus flagellatus KT]637938876 YP_546067											
MFLA1960		0.000	0.000			■ ■		0.000	0.000			■
	flagellar L-ring protein [Methylobacillus flagellatus KT]637938877 YP_546068											
MFLA1961			1.668	1.668		Y ● ● Y			21.210	21.210		Y ●
	flagellar P-ring protein [Methylobacillus flagellatus KT]637938878 YP_546069											
MFLA1962			0.931	0.931		Y ● ● Y			19.976	19.976		Y ●
	Mannosyl-glycoprotein endo-beta-N-acetylglucosamidase [Methylobacillus flagellatus KT]637938879 YP_546070											
MFLA1963		3.621	4.147	4.908	0.626	Y ● ● Y	1.75 E-1	21.810	23.607	23.972	-0.460	Y ●
	Flagellar hook-associated protein [Methylobacillus flagellatus KT]637938880 YP_546071											
MFLA1964		3.621	4.893	5.393	-0.257	Y ● ● Y	2.87 E-2	20.367	23.469	23.628	-2.100	Y ●
	flagellin-like protein [Methylobacillus flagellatus KT]637938881 YP_546072											
MFLA1965		3.967	4.790	5.437	-0.778	Y ● ● Y	4.25 E-2	22.753	23.913	24.446	-1.130	Y ●
	diguanylate phosphodiesterase (EAL domain) [Methylobacillus flagellatus KT]637938882 YP_546073											
MFLA1966		0.000	0.000			■ ■		0.000	0.000			■
	flagellar biosynthetic protein FliR [Methylobacillus flagellatus KT]637938883 YP_546074											
MFLA1967		0.000	0.000			■ ■		0.000	0.000			■
	flagellar biosynthetic protein FliQ [Methylobacillus flagellatus KT]637938884 YP_546075											
MFLA1968		0.000	0.000			■ ■		0.000	0.000			■
	flagellar biosynthetic protein FliP [Methylobacillus flagellatus KT]637938885 YP_546076											
MFLA1969		0.000	0.000			■ ■		0.000	0.000			■
	" flagellar biosynthesis protein, FliO [Methylobacillus flagellatus KT]637938886 YP_546077 """											
MFLA1970			1.000	1.000		Y ● ● Y			22.695	22.695		Y ●
	Flagellar motor switch FliN [Methylobacillus flagellatus KT]637938887 YP_546078											



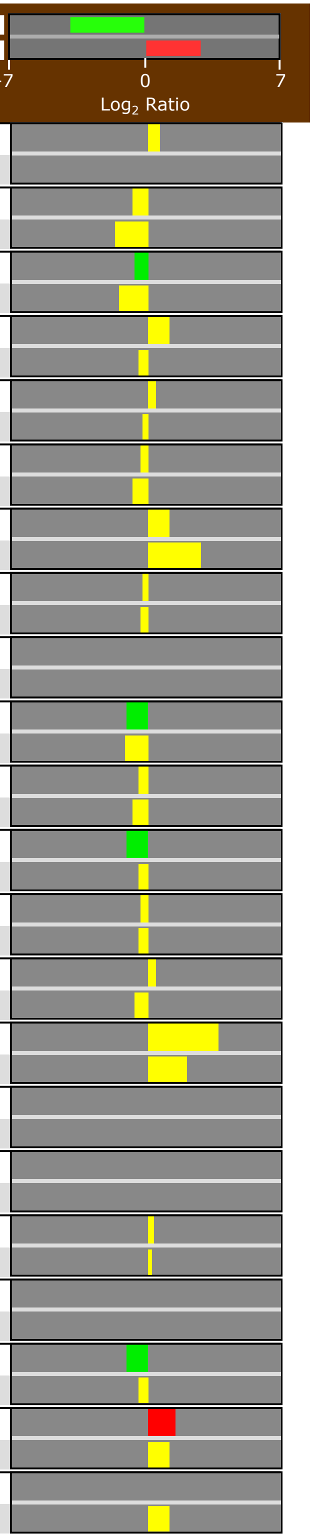


ORF	AM/OH *M Flagellatus* Spectral Count *q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation	AM/OH *M Flagellatus* Protein Intensity *q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA1971		3.147	2.529	3.871	0.862	Y ● ● Y	1.06 E-1	21.955	22.483	23.243	-0.720	Y ●
	flagellar motor switch protein FliM [Methylobacillus flagellatus KT]637938888 YP_546079											
MFLA1972		3.691	2.941	4.364	1.771	Y ● ● Y	1.54 E-1	21.528	22.971	23.423	-0.378	Y ●
	flagellar basal body-associated protein FliL [Methylobacillus flagellatus KT]637938889 YP_546080											
MFLA1973			0.585	0.585		Y ● ● Y			21.008	21.008		Y ●
	flagellar hook-length control protein [Methylobacillus flagellatus KT]637938890 YP_546081											
MFLA1974		0.000	0.000			■ ■		0.000	0.000			■
	Flagellar export FliJ [Methylobacillus flagellatus KT]637938891 YP_546082											
MFLA1975		0.521	1.322	1.976	-0.801	Y ● ● Y		21.897	22.140	23.024	-0.243	Y ●
	ATPase FliI/YscN [Methylobacillus flagellatus KT]637938892 YP_546083											
MFLA1976		0.000	0.000			■ ■		0.000	0.000			■
	flagellar assembly protein FliH [Methylobacillus flagellatus KT]637938893 YP_546084											
MFLA1977		4.424	4.630	5.531	-0.125	Y ● ● Y	1.79 E-1	21.937	22.209	23.079	-0.167	Y ●
	flagellar motor switch protein FliG [Methylobacillus flagellatus KT]637938894 YP_546085											
MFLA1978		3.591	2.505	4.148	1.076	Y ● ● Y	9.02 E-2	22.152	21.451	22.843	0.741	Y ●
	flagellar M-ring protein FliF [Methylobacillus flagellatus KT]637938895 YP_546086											
MFLA1979		3.173	2.516	3.882	-0.446	Y ● ● Y	2.42 E-2	20.687	20.797	21.743	-1.112	Y ●
	flagellar hook-basal body complex protein (FliE) [Methylobacillus flagellatus KT]637938896 YP_546087											
MFLA1980		0.000	0.000			■ ■		0.000	0.000			■
	putative flagellar biosynthetic protein [Methylobacillus flagellatus KT]637938897 YP_546088											
MFLA1981		3.532	3.184	4.368	0.316	Y ● ● Y	1.01 E-1	20.605	20.104	21.376	0.648	Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637938898 YP_546089											
MFLA1982		0.000	0.000			■ ■		0.000	0.000			■
	flagellar protein FliT [Methylobacillus flagellatus KT]637938899 YP_546090											
MFLA1983		0.000	0.000			■ ■		0.000	0.000			■
	flagellar protein FliS [Methylobacillus flagellatus KT]637938900 YP_546091											
MFLA1984		6.316	6.505	7.414	-0.320	Y ● ● Y	4.46 E-2	23.965	25.313	25.791	-1.270	Y ●
	flagellar hook-associated 2-like protein [Methylobacillus flagellatus KT]637938901 YP_546092											
MFLA1985		0.000	0.000			■ ■		0.000	0.000			■
	flagellar protein FlaG protein [Methylobacillus flagellatus KT]637938902 YP_546093											
MFLA1986	0	10.684	10.301	11.505	0.383	Y ● ● Y	1.07 E-1	30.769	30.207	31.515	0.452	Y ●
	flagellin-like protein [Methylobacillus flagellatus KT]637938903 YP_546094											
MFLA1987			2.739	2.739		Y ● ● Y			21.126	21.126		Y ●
	" two component transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637938904 YP_546095 """											
MFLA1988		0.813		0.813		Y ● ● Y		19.600		19.600		Y ●
	putative signal transduction histidine kinase [Methylobacillus flagellatus KT]637938905 YP_546096											
MFLA1989		0.000	0.000			■ ■		0.000	0.000			■
	TonB-dependent receptor [Methylobacillus flagellatus KT]637938906 YP_546097											
MFLA1990		3.066		3.066		Y ● ● Y		20.950		20.950		Y ●
	putative regulatory lipoprotein [Methylobacillus flagellatus KT]637938907 YP_546098											
MFLA1991		0.000	0.000			■ ■		0.000	0.000			■
	protein of unknown function DUF1111 [Methylobacillus flagellatus KT]637938908 YP_546099											
MFLA1992		3.561	3.551	4.556	-0.480	Y ● ● Y	1.67 E-1	20.315	20.816	21.587	-0.858	Y ●
	sulphate transporter [Methylobacillus flagellatus KT]637938909 YP_546100											

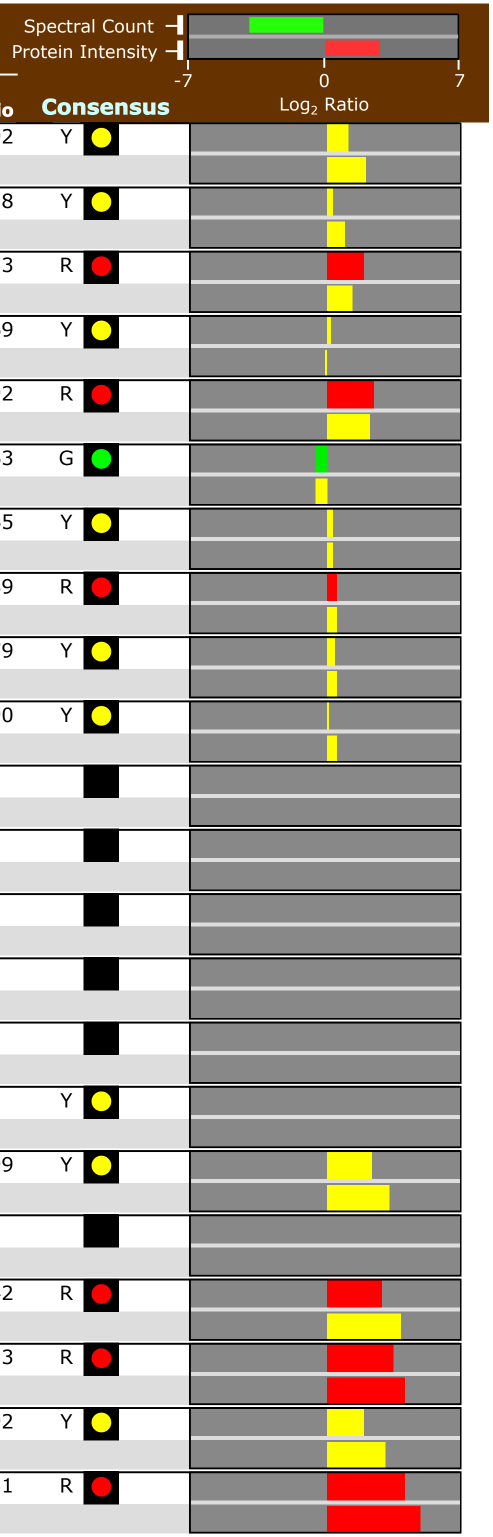
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	q-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				q-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA1993	2.04 E-13	6.029	4.318	6.414	1.504	R	🔴	🟡	Y	1.36 E-1	24.919	24.173	25.594	0.397	R	🔴
	TonB-dependent siderophore receptor [Methylobacillus flagellatus KT]637938910 YP_546101															
MFLA1994		2.398		2.398		Y	🟡	🟡	Y		22.890		22.890		Y	🟡
	protein of unknown function DUF779 [Methylobacillus flagellatus KT]637938911 YP_546102															
MFLA1995	0	10.426	7.433	10.597	2.984	R	🔴	🟡	Y	1.3 E-2	29.615	26.513	29.774	3.073	R	🔴
	Lactaldehyde dehydrogenase [Methylobacillus flagellatus KT]637938912 YP_546103															
MFLA1996		5.837	6.104	6.976	-0.262	Y	🟡	🟡	Y	1.1 E-2	24.323	25.054	25.734	-0.726	Y	🟡
	" transcriptional regulator, MerR family [Methylobacillus flagellatus KT]637938914 YP_546104 """															
MFLA1997	5.82 E-13	5.725	6.937	7.454	-1.155	G	🟢	🟡	Y	1.41 E-2	24.513	25.381	26.011	-0.874	G	🟢
	" integration host factor, alpha subunit [Methylobacillus flagellatus KT]637938915 YP_546105 """															
MFLA1998		6.119	6.569	7.361	-0.408	Y	🟡	🟡	Y	9.29 E-2	25.157	25.505	26.341	-0.364	Y	🟡
	" phenylalanyl-tRNA synthetase, beta subunit [Methylobacillus flagellatus KT]637938916 YP_546106 """															
MFLA1999	3.19 E-2	5.922	5.476	6.716	0.429	Y	🟡	🟡	Y	1.5 E-1	23.706	24.088	24.910	-0.252	Y	🟡
	" phenylalanyl-tRNA synthetase, alpha subunit [Methylobacillus flagellatus KT]637938917 YP_546107 """															
MFLA2000		5.165	4.056	5.714	0.844	Y	🟡	🟡	Y	1.08 E-2	27.550	26.572	28.143	0.994	Y	🟡
	ribosomal protein L20 [Methylobacillus flagellatus KT]637938918 YP_546108															
MFLA2001	1.98 E-6	5.206	4.729	5.987	1.521	R	🔴	🟡	Y	2.78 E-1	22.454	23.451	24.037	0.026	Y	🟡
	ribosomal protein L35 [Methylobacillus flagellatus KT]637938919 YP_546109															
MFLA2002	2.53 E-14	7.015	5.986	7.590	1.231	R	🔴	🟡	Y	4.63 E-2	25.580	26.112	26.871	-0.510	Y	🟡
	translation initiation factor IF-3 [Methylobacillus flagellatus KT]637938920 YP_546110															
MFLA2003	1.87 E-4	7.796	7.405	8.614	0.372	Y	🟡	🟡	Y	1.29 E-1	26.104	26.447	27.286	-0.439	Y	🟡
	threonyl-tRNA synthetase [Methylobacillus flagellatus KT]637938921 YP_546111															
MFLA2004		3.692	3.540	4.618	0.190	Y	🟡	🟡	Y	1.98 E-1	23.035	23.326	24.188	-0.405	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938922 YP_546112															
MFLA2005		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938923 YP_546113															
MFLA2006		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938924 YP_546114															
MFLA2007		4.740	4.707	5.724	-0.047	Y	🟡	🟡	Y	9.62 E-2	24.010	23.839	24.927	0.184	Y	🟡
	UDP-glucose 4-epimerase [Methylobacillus flagellatus KT]637938925 YP_546115															
MFLA2008	0	8.578	9.352	10.017	-0.757	G	🟢	🟡	Y	1.07 E-2	27.065	28.298	28.809	-1.224	G	🟢
	" dTDP-glucose 4,6-dehydratase [Methylobacillus flagellatus KT]637938926 YP_546116 """															
MFLA2009	1.38 E-1	6.725	6.793	7.759	-0.062	Y	🟡	🟢	G	9.51 E-3	25.522	26.994	27.438	-1.462	Y	🟡
	glucose-1-phosphate thymidylyltransferase [Methylobacillus flagellatus KT]637938927 YP_546117															
MFLA2010	7.12 E-6	6.620	7.287	7.992	-0.665	G	🟢	🟡	Y	3.7 E-2	26.522	26.969	27.763	-0.465	G	🟢
	" dTDP-4-dehydrorhamnose 3,5-epimerase [Methylobacillus flagellatus KT]637938928 YP_546118 """															
MFLA2011	1.35 E-1	6.203	6.074	7.140	0.134	Y	🟡	🟡	Y	1.66 E-2	26.444	26.767	27.614	-0.325	Y	🟡
	dTDP-4-dehydrorhamnose reductase [Methylobacillus flagellatus KT]637938929 YP_546119															
MFLA2012	1.79 E-11	7.167	7.888	8.572	-0.753	G	🟢	🟡	Y	1.35 E-2	26.811	27.776	28.373	-1.002	G	🟢
	Mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase [Methylobacillus flagellatus KT]637938930 YP_546120															
MFLA2013	4.43 E-2	5.911	6.310	7.124	-0.398	Y	🟡	🟢	G	1.12 E-7	24.176	25.766	26.180	-1.590	G	🟢
	" glycosyltransferase, RfaG [Methylobacillus flagellatus KT]637938931 YP_546121 """															
MFLA2014	2.45 E-2	6.303	6.599	7.459	-0.325	Y	🟡	🟡	Y	9.11 E-2	26.006	26.161	27.086	-0.162	Y	🟡
	" glycoside hydrolase, family 5 [Methylobacillus flagellatus KT]637938932 YP_546122 """															



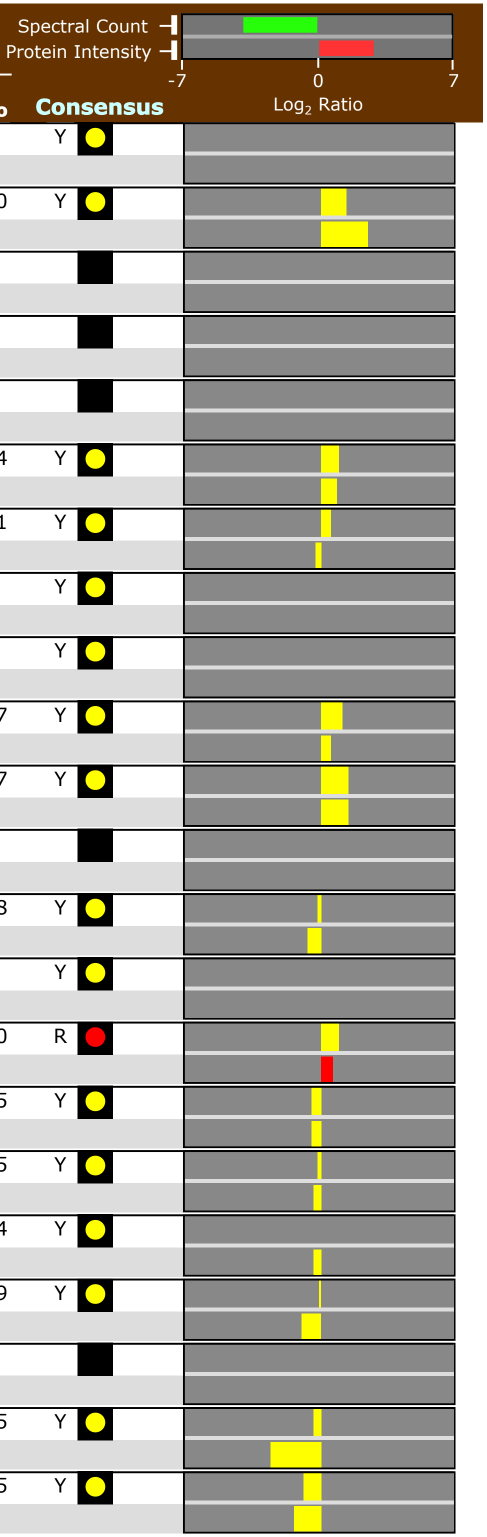
	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA2015		4.799	4.194	5.528	0.625	Y 🟡 🟡 Y	2.16 E-1	23.106	22.861	23.989	-0.041	Y 🟡
	" glycosyl transferase, group 1 [Methylobacillus flagellatus KT]637938933 YP_546123 """											
MFLA2016		0.813	2.595	2.963	-0.764	Y 🟡 🟡 Y	9.53 E-2	19.647	22.454	22.647	-1.728	Y 🟡
	" glycosyl transferase, family 2 [Methylobacillus flagellatus KT]637938934 YP_546124 """											
MFLA2017	6.31 E-3	5.056	5.726	6.429	-0.701	G 🟢 🟡 Y	5.13 E-2	23.821	24.925	25.476	-1.535	G 🟢
	" glycosyl transferase, family 2 [Methylobacillus flagellatus KT]637938935 YP_546125 """											
MFLA2018		2.106	1.000	2.656	1.106	Y 🟡 🟡 Y		22.226	22.757	23.516	-0.530	Y 🟡
	O-antigen polymerase [Methylobacillus flagellatus KT]637938936 YP_546126											
MFLA2019		6.144	5.679	6.931	0.366	Y 🟡 🟡 Y	1.28 E-1	24.796	25.025	25.915	-0.258	Y 🟡
	nitroreductase [Methylobacillus flagellatus KT]637938937 YP_546127											
MFLA2020		7.026	7.308	8.174	-0.419	Y 🟡 🟡 Y	2.81 E-2	25.909	26.673	27.341	-0.796	Y 🟡
	polysaccharide pyruvyl transferase [Methylobacillus flagellatus KT]637938938 YP_546128											
MFLA2021		1.106	0.000	1.656	1.106	Y 🟡 🟡 Y		20.761	18.104	20.974	2.657	Y 🟡
	polysaccharide biosynthesis protein [Methylobacillus flagellatus KT]637938939 YP_546129											
MFLA2022		4.087	4.435	5.272	-0.325	Y 🟡 🟡 Y	1.28 E-1	23.860	24.209	25.045	-0.422	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938940 YP_546130											
MFLA2023		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938941 YP_546131											
MFLA2024	0	7.376	8.437	9.002	-1.079	G 🟢 🟡 Y	4.87 E-2	26.292	27.254	27.852	-1.241	G 🟢
	Protein-tyrosine kinase [Methylobacillus flagellatus KT]637938942 YP_546132											
MFLA2025		7.380	7.747	8.575	-0.452	Y 🟡 🟡 Y	1.38 E-2	27.001	27.780	28.442	-0.786	Y 🟡
	lipopolysaccharide biosynthesis [Methylobacillus flagellatus KT]637938943 YP_546133											
MFLA2026	0	6.785	7.925	8.465	-1.150	G 🟢 🟡 Y	2.44 E-2	27.371	27.825	28.616	-0.468	G 🟢
	polysaccharide export protein [Methylobacillus flagellatus KT]637938944 YP_546134											
MFLA2027	5.73 E-6	7.968	8.389	9.194	-0.427	Y 🟡 🟡 Y	1.01 E-2	28.563	29.019	29.809	-0.455	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938945 YP_546135											
MFLA2028	6.62 E-2	5.719	5.326	6.536	0.390	Y 🟡 🟡 Y	6.6 E-2	23.863	24.469	25.198	-0.728	Y 🟡
	sugar transferase [Methylobacillus flagellatus KT]637938946 YP_546136											
MFLA2029		5.549	0.931	5.607	3.556	Y 🟡 🟡 Y	1.26 E-1	24.671	21.388	24.812	1.960	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938947 YP_546137											
MFLA2030		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	Abortive infection protein [Methylobacillus flagellatus KT]637938948 YP_546138											
MFLA2031		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	" TonB-dependent receptor, plug [Methylobacillus flagellatus KT]637938949 YP_546139 """											
MFLA2032		3.913	4.625	5.312	0.311	Y 🟡 🟡 Y	1.96 E-1	20.781	21.633	22.269	0.180	Y 🟡
	2OG-Fe(II) oxygenase [Methylobacillus flagellatus KT]637938951 YP_546140											
MFLA2033			3.162	3.162		Y 🟡 🟡 Y			20.844	20.844		Y 🟡
	Pyridoxal-dependent decarboxylase [Methylobacillus flagellatus KT]637938952 YP_546141											
MFLA2034	0	7.079	8.176	8.729	-1.144	G 🟢 🟡 Y	7.05 E-2	28.918	29.390	30.173	-0.524	G 🟢
	" MxaD protein, putative [Methylobacillus flagellatus KT]637938953 YP_546142 """											
MFLA2035	2.62 E-6	5.530	4.090	5.983	1.402	R 🔴 🟡 Y	1.49 E-2	24.662	23.518	25.200	1.139	R 🔴
	" MxaL protein, putative [Methylobacillus flagellatus KT]637938954 YP_546143 """											
MFLA2036		4.517	4.557	5.537	-0.013	Y 🟡 🟡 Y	5.71 E-2	24.792	23.698	25.346	1.138	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938955 YP_546144											

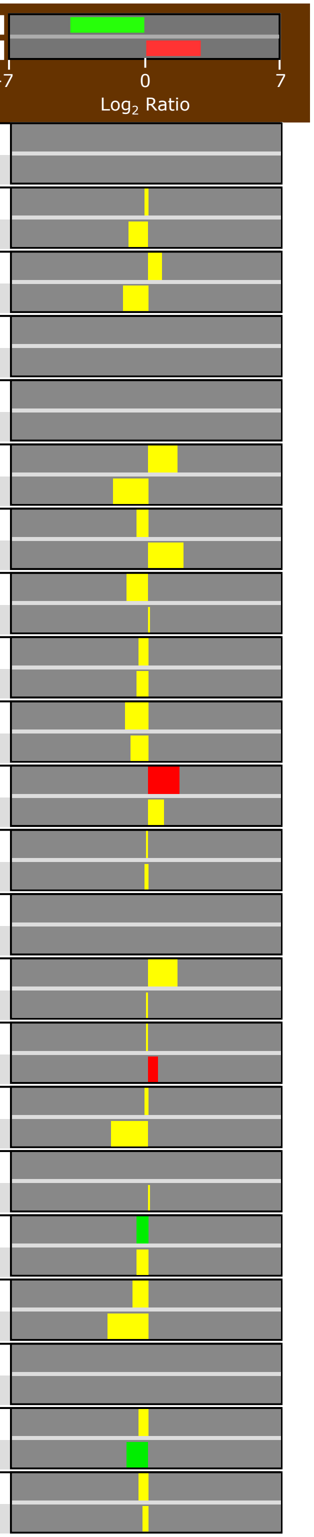


	AM/OH *M Flagellatus* Spectral Count							AM/OH *M Flagellatus* Protein Intensity					
ORF	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation		q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA2037		4.940	3.643	5.433	1.057	Y 🟡	🟡 Y	7.24 E-2	24.347	21.931	24.595	1.992	Y 🟡
	" von Willebrand factor, type A [Methylobacillus flagellatus KT]637938956 YP_546145 """												
MFLA2038	1.39 E-2	5.753	5.406	6.590	0.347	Y 🟡	🟡 Y	6.44 E-2	25.216	24.408	25.868	0.938	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938957 YP_546146												
MFLA2039	7.88 E-8	5.596	3.684	5.936	1.882	R 🔴	🟡 Y	9.53 E-2	23.060	21.451	23.469	1.253	R 🔴
	hypothetical protein [Methylobacillus flagellatus KT]637938958 YP_546147												
MFLA2040		8.101	7.931	9.019	0.181	Y 🟡	🟡 Y	2.07 E-1	27.735	27.822	28.779	-0.069	Y 🟡
	" ATPase associated with various cellular activities, AAA_3 [Methylobacillus flagellatus KT]637938959 YP_546148 """												
MFLA2041	0	6.289	4.926	6.763	2.365	R 🔴	🟡 Y	3.14 E-2	27.309	26.161	27.846	2.192	R 🔴
	" methanol dehydrogenase, beta subunit [Methylobacillus flagellatus KT]637938960 YP_546149 """												
MFLA2042	2.64 E-9	7.338	7.955	8.679	-0.622	G 🟢	🟡 Y	7.52 E-2	28.994	29.473	30.253	-0.563	G 🟢
	" cytochrome c, class I [Methylobacillus flagellatus KT]637938961 YP_546150 """												
MFLA2043	3.05 E-4	8.645	8.362	9.510	0.290	Y 🟡	🟡 Y	1.14 E-1	29.761	29.453	30.615	0.265	Y 🟡
	" extracellular solute-binding protein, family 3 [Methylobacillus flagellatus KT]637938962 YP_546151 """												
MFLA2044	0	12.179	11.631	12.931	0.527	R 🔴	🟡 Y	5.65 E-2	33.159	32.644	33.924	0.489	R 🔴
	Pyrrolo-quinoline quinone [Methylobacillus flagellatus KT]637938963 YP_546152												
MFLA2045	3.9 E-2	5.130	4.705	5.933	0.414	Y 🟡	🟡 Y	1.87 E-1	23.308	22.974	24.151	0.479	Y 🟡
	NAD-dependent epimerase/dehydratase [Methylobacillus flagellatus KT]637938964 YP_546153												
MFLA2046		4.974	4.850	5.914	0.126	Y 🟡	🟡 Y	1.76 E-1	24.202	23.860	25.041	0.490	Y 🟡
	NUDIX hydrolase [Methylobacillus flagellatus KT]637938965 YP_546154												
MFLA2047		0.000	0.000			⬛	⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637938966 YP_546155												
MFLA2048		0.000	0.000			⬛	⬛		0.000	0.000			⬛
	" Proton-translocating NADH-quinone oxidoreductase, chain N [Methylobacillus flagellatus KT]637938967 YP_546156 """												
MFLA2049		0.000	0.000			⬛	⬛		0.000	0.000			⬛
	" proton-translocating NADH-quinone oxidoreductase, chain M [Methylobacillus flagellatus KT]637938968 YP_546157 """												
MFLA2050		0.000	0.000			⬛	⬛		0.000	0.000			⬛
	" proton-translocating NADH-quinone oxidoreductase, chain L [Methylobacillus flagellatus KT]637938969 YP_546158 """												
MFLA2051		0.000	0.000			⬛	⬛		0.000	0.000			⬛
	" NADH-ubiquinone oxidoreductase, chain 4L [Methylobacillus flagellatus KT]637938970 YP_546159 """												
MFLA2052		1.843		1.843		Y 🟡	🟡 Y		18.958		18.958		Y 🟡
	" NADH-ubiquinone/plastoquinone oxidoreductase, chain 6 [Methylobacillus flagellatus KT]637938971 YP_546160 """												
MFLA2053		4.435	2.226	4.717	2.294	Y 🟡	🟡 Y	2.52 E-2	23.237	20.011	23.383	3.199	Y 🟡
	" NADH-quinone oxidoreductase, chain I [Methylobacillus flagellatus KT]637938972 YP_546161 """												
MFLA2054		0.000	0.000			⬛	⬛		0.000	0.000			⬛
	" respiratory-chain NADH dehydrogenase, subunit 1 [Methylobacillus flagellatus KT]637938973 YP_546162 """												
MFLA2055	0	7.877	4.895	8.049	2.818	R 🔴	🟡 Y	2.67 E-2	27.204	23.252	27.294	3.842	R 🔴
	" NADH-quinone oxidoreductase, chain G [Methylobacillus flagellatus KT]637938974 YP_546163 """												
MFLA2056	0	6.870	3.453	6.999	3.443	R 🔴	🔴 R	7.97 E-3	25.675	21.748	25.766	4.013	R 🔴
	" NADH-quinone oxidoreductase, F subunit [Methylobacillus flagellatus KT]637938975 YP_546164 """												
MFLA2057		4.053	1.000	4.218	1.863	Y 🟡	🟡 Y	5.84 E-2	24.090	20.077	24.177	2.992	Y 🟡
	" NADH-quinone oxidoreductase, E subunit [Methylobacillus flagellatus KT]637938976 YP_546165 """												
MFLA2058	0	6.312	2.372	6.403	3.964	R 🔴	🔴 R	4.7 E-4	25.915	21.202	25.969	4.751	R 🔴
	" NADH dehydrogenase I, D subunit [Methylobacillus flagellatus KT]637938977 YP_546166 """												



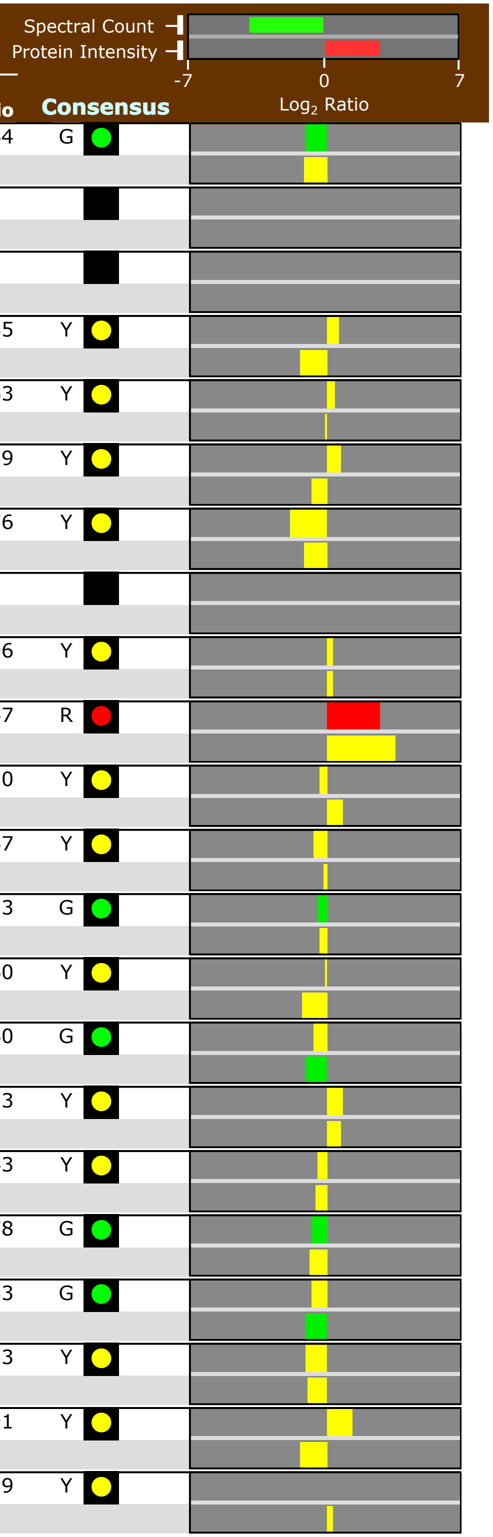
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	**Consensus**	
MFLA2059		4.682		4.682		Y	🟡	🟡	Y		23.772		23.772		Y	🟡
	" NADH (or F420H2) dehydrogenase, subunit C [Methylobacillus flagellatus KT]637938978 YP_546167 """															
MFLA2060		4.120	2.871	4.627	1.251	Y	🟡	🟡	Y	2.61 E-2	23.320	21.081	23.597	2.380	Y	🟡
	" NADH-quinone oxidoreductase, B subunit [Methylobacillus flagellatus KT]637938979 YP_546168 """															
MFLA2061		0.000	0.000				■	■			0.000	0.000				■
	" NADH-ubiquinone/plastoquinone oxidoreductase, chain 3 [Methylobacillus flagellatus KT]637938980 YP_546169 """															
MFLA2062		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938981 YP_546170															
MFLA2063		0.000	0.000				■	■			0.000	0.000				■
	" preprotein translocase, SecG subunit [Methylobacillus flagellatus KT]637938983 YP_546171 """															
MFLA2064		2.983	3.140	4.064	0.857	Y	🟡	🟡	Y	2.28 E-2	22.747	22.993	23.875	0.754	Y	🟡
	Triosephosphate isomerase [Methylobacillus flagellatus KT]637938984 YP_546172															
MFLA2065		2.980	2.459	3.743	0.521	Y	🟡	🟡	Y		20.050	20.351	21.208	-0.301	Y	🟡
	single-stranded-DNA-specific exonuclease RecJ [Methylobacillus flagellatus KT]637938985 YP_546173															
MFLA2066		1.843		1.843		Y	🟡	🟡	Y		18.925		18.925		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938986 YP_546174															
MFLA2067			0.000	0.000		Y	🟡	🟡	Y			19.484	19.484		Y	🟡
	" phosphohistidine phosphatase, SixA [Methylobacillus flagellatus KT]637938987 YP_546175 """															
MFLA2068		5.004	3.871	5.546	1.118	Y	🟡	🟡	Y	7.7 E-2	23.143	22.645	23.916	0.517	Y	🟡
	putative partition-related protein [Methylobacillus flagellatus KT]637938988 YP_546176															
MFLA2069		4.872	3.517	5.348	1.391	Y	🟡	🟡	Y	2.74 E-2	23.585	22.168	24.044	1.377	Y	🟡
	adenylate cyclase [Methylobacillus flagellatus KT]637938989 YP_546177															
MFLA2070		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938990 YP_546178															
MFLA2071		3.341	3.505	4.425	-0.167	Y	🟡	🟡	Y	5.51 E-2	21.709	22.346	23.062	-0.698	Y	🟡
	TrkA-N [Methylobacillus flagellatus KT]637938991 YP_546179															
MFLA2072		1.106		1.106		Y	🟡	🟡	Y		19.198		19.198		Y	🟡
	Class I peptide chain release factor [Methylobacillus flagellatus KT]637938992 YP_546180															
MFLA2073		4.714	3.866	5.352	0.914	Y	🟡	🔴	R	1.97 E-3	23.242	22.622	23.965	0.620	R	🔴
	Leucyl aminopeptidase [Methylobacillus flagellatus KT]637938993 YP_546181															
MFLA2074	6.75 E-9	8.345	8.800	9.590	-0.461	Y	🟡	🟡	Y	1.16 E-1	27.734	28.099	28.928	-0.475	Y	🟡
	" 2-oxo-acid dehydrogenase E1 component, homodimeric type [Methylobacillus flagellatus KT]637938994 YP_546182 """															
MFLA2075	2.99 E-2	6.954	7.117	8.038	-0.189	Y	🟡	🟡	Y	2.7 E-2	26.405	26.819	27.627	-0.425	Y	🟡
	catalytic domain of components of various dehydrogenase complexes [Methylobacillus flagellatus KT]637938995 YP_546183															
MFLA2076	4.82 E-2	6.483	6.471	7.477	0.018	Y	🟡	🟡	Y	6.73 E-2	26.014	26.379	27.208	-0.354	Y	🟡
	Dihydrolipoamide dehydrogenase [Methylobacillus flagellatus KT]637938996 YP_546184															
MFLA2077		3.106	4.520	4.980	-0.076	Y	🟡	🟡	Y	1.57 E-1	21.259	23.990	24.193	-0.959	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938997 YP_546185															
MFLA2078		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637938998 YP_546186															
MFLA2079		2.906	3.254	4.091	-0.410	Y	🟡	🟡	Y	2.54 E-2	21.297	23.977	24.186	-2.605	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637938999 YP_546187															
MFLA2080		1.813	2.700	3.324	-0.887	Y	🟡	🟡	Y		19.337	20.762	21.219	-1.425	Y	🟡
	" putative transcriptional acitvator, Baf [Methylobacillus flagellatus KT]637939000 YP_546188 """															



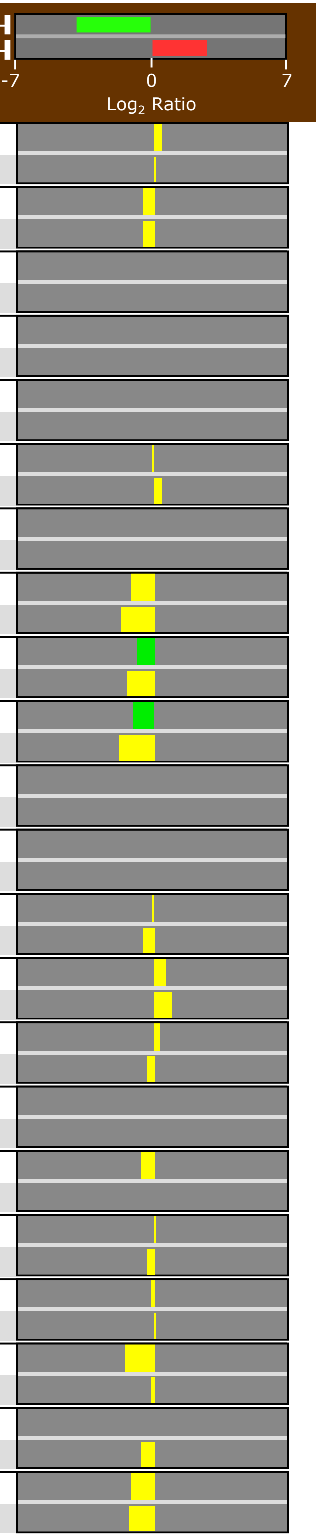


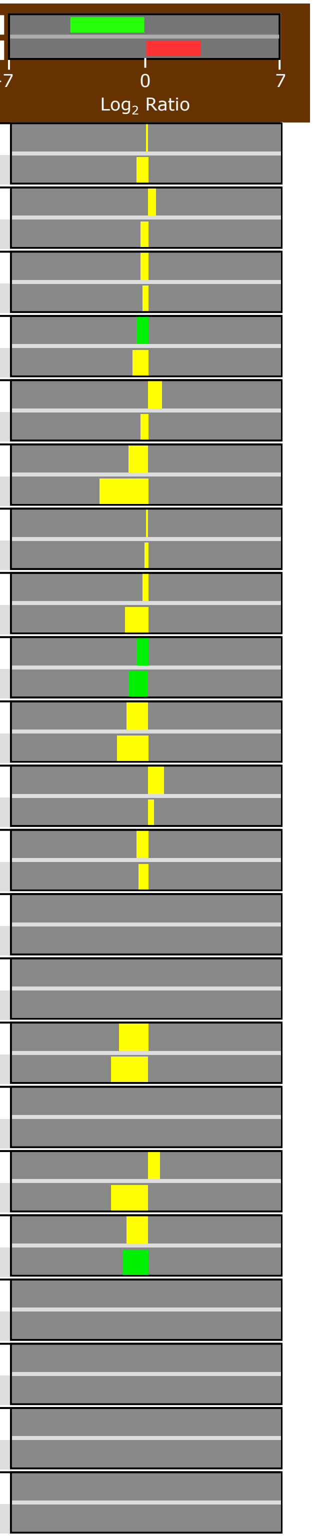
ORF	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity						
	q-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation		*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus
MFLA2081		3.106		3.106		Y ●	● Y		20.435		20.435		Y ●
	Biotin--acetyl-CoA-carboxylase ligase [Methylobacillus flagellatus KT]637939001 YP_546189												
MFLA2082	3.33 E-2	7.133	7.331	8.235	-0.214	Y ●	● Y	2.06 E-2	26.102	27.015	27.630	-0.974	Y ●
	glutaminyl-tRNA synthetase [Methylobacillus flagellatus KT]637939002 YP_546190												
MFLA2083		2.906	0.931	3.233	0.736	Y ●	● Y	6.85 E-2	19.934	20.172	21.058	-1.329	Y ●
	" flavin reductase-like, FMN-binding [Methylobacillus flagellatus KT]637939003 YP_546191 """												
MFLA2084		0.000	0.000			■	■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939004 YP_546192												
MFLA2085			1.807	1.807		Y ●	● Y			18.942	18.942		Y ●
	peptide methionine sulfoxide reductase [Methylobacillus flagellatus KT]637939005 YP_546193												
MFLA2086		1.521	0.000	1.952	1.521	Y ●	● Y		19.060	20.827	21.199	-1.767	Y ●
	" Cobyrinic acid a,c-diamide synthase [Methylobacillus flagellatus KT]637939006 YP_546194 """												
MFLA2087		1.967	1.585	2.788	-0.626	Y ●	● Y	9.64 E-2	21.731	18.808	21.910	1.832	Y ●
	3-deoxy-D-manno-octulosonate cytidylyltransferase [Methylobacillus flagellatus KT]637939013 YP_546195												
MFLA2088		4.060	5.196	5.737	-1.136	Y ●	● Y	1.96 E-1	25.294	25.228	26.261	0.068	Y ●
	protein of unknown function DUF343 [Methylobacillus flagellatus KT]637939014 YP_546196												
MFLA2089		4.370	4.679	5.533	-0.454	Y ●	● Y	9.18 E-2	22.549	23.132	23.870	-0.610	Y ●
	tetraacyldisaccharide 4'-kinase [Methylobacillus flagellatus KT]637939015 YP_546197												
MFLA2090		3.899	5.145	5.653	-1.241	Y ●	● Y	1.89 E-2	22.593	23.495	24.113	-0.922	Y ●
	Lipid A export ATP-binding/permease protein MsbA [Methylobacillus flagellatus KT]637939016 YP_546198												
MFLA2091	2.35 E-6	5.672	4.098	6.090	1.579	R ●	● Y	1.53 E-2	24.688	23.889	25.343	0.799	R ●
	Biopolymer transport protein ExbD/TolR [Methylobacillus flagellatus KT]637939017 YP_546199												
MFLA2092	1.21 E-2	6.402	6.459	7.431	-0.092	Y ●	● Y	1.34 E-1	25.701	25.853	26.779	-0.174	Y ●
	MotA/TolQ/ExbB proton channel [Methylobacillus flagellatus KT]637939018 YP_546200												
MFLA2093		0.000	0.000			■	■		0.000	0.000			■
	DNA internalization-related competence protein ComEC/Rec2 [Methylobacillus flagellatus KT]637939019 YP_546201												
MFLA2094		4.413	2.871	4.839	1.544	Y ●	● Y	2.42 E-1	22.492	22.390	23.442	-0.051	Y ●
	" Lipoprotein releasing system, ATP-binding protein [Methylobacillus flagellatus KT]637939020 YP_546202 """												
MFLA2095		3.159	2.941	4.054	-0.091	Y ●	● R	7.12 E-3	21.644	21.131	22.410	0.512	Y ●
	" Lipoprotein releasing system, transmembrane protein, LolC/E family [Methylobacillus flagellatus KT]637939021 YP_546203 """												
MFLA2096		2.521	4.086	4.506	-0.175	Y ●	● Y	1.46 E-1	19.724	23.629	23.722	-1.871	Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637939022 YP_546204												
MFLA2097		2.691	2.668	3.679	0.022	Y ●	● Y		21.040	20.974	22.007	0.066	Y ●
	" riboflavin synthase, alpha subunit [Methylobacillus flagellatus KT]637939023 YP_546205 """												
MFLA2098	1.27 E-4	6.067	6.598	7.357	-0.616	G ●	● Y	4.78 E-2	24.896	25.493	26.225	-0.639	G ●
	" 3,4-dihydroxy-2-butanone 4-phosphate synthase [Methylobacillus flagellatus KT]637939024 YP_546206 """												
MFLA2099		3.718	4.548	5.192	-0.817	Y ●	● Y	5.77 E-2	22.869	24.192	24.677	-2.146	Y ●
	protein of unknown function DUF179 [Methylobacillus flagellatus KT]637939025 YP_546207												
MFLA2100			1.322	1.322		Y ●	● Y			21.053	21.053		Y ●
	Holliday junction resolvase YqgF [Methylobacillus flagellatus KT]637939026 YP_546208												
MFLA2101		5.405	5.975	6.718	-0.533	Y ●	● G	4.7 E-4	24.174	25.237	25.801	-1.064	G ●
	phosphoribosyltransferase [Methylobacillus flagellatus KT]637939027 YP_546209												
MFLA2102	1.06 E-3	6.547	7.012	7.798	-0.466	Y ●	● Y	9.62 E-2	25.414	25.711	26.570	-0.309	Y ●
	aspartate carbamoyltransferase [Methylobacillus flagellatus KT]637939028 YP_546210												

	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**				**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**	
MFLA2103	1.77 E-7	5.367	6.408	6.980	-1.066	G	🟢	🟡	Y	2.06 E-2	24.442	25.539	26.093	-1.164	G	🟢
	" dihydroorotase, multifunctional complex type [Methylobacillus flagellatus KT]637939029 YP_546211 """															
MFLA2104		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	Twin-arginine translocation pathway signal [Methylobacillus flagellatus KT]637939030 YP_546212															
MFLA2105		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	Integral membrane protein TerC [Methylobacillus flagellatus KT]637939031 YP_546213															
MFLA2106		4.246	2.923	4.731	0.625	Y	🟡	🟡	Y	2.07 E-1	22.032	22.473	23.269	-1.385	Y	🟡
	twitching motility protein [Methylobacillus flagellatus KT]637939032 YP_546214															
MFLA2107		5.966	5.510	6.756	0.422	Y	🟡	🟡	Y	2.48 E-1	24.703	24.758	25.731	-0.063	Y	🟡
	twitching motility protein [Methylobacillus flagellatus KT]637939033 YP_546215															
MFLA2108		4.922	4.251	5.625	0.664	Y	🟡	🟡	Y	1.5 E-2	22.851	23.587	24.265	-0.759	Y	🟡
	Protein of unknown function UPF0001 [Methylobacillus flagellatus KT]637939034 YP_546216															
MFLA2109		1.106	4.071	4.245	-1.904	Y	🟡	🟡	Y	2.76 E-2	22.003	24.179	24.468	-1.176	Y	🟡
	pyrroline-5-carboxylate reductase [Methylobacillus flagellatus KT]637939035 YP_546217															
MFLA2110		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	protein of unknown function YGGT [Methylobacillus flagellatus KT]637939036 YP_546218															
MFLA2111	3.34 E-2	5.535	5.156	6.358	0.317	Y	🟡	🟡	Y	1.33 E-1	25.461	25.116	26.299	0.296	Y	🟡
	" NADP oxidoreductase, coenzyme F420-dependent [Methylobacillus flagellatus KT]637939037 YP_546219 """															
MFLA2112	5.91 E-11	5.826	3.162	6.037	2.655	R	🔴	🟡	Y	1.03 E-2	25.167	21.597	25.284	3.547	R	🔴
	" ribonuclease, Rne/Rng family [Methylobacillus flagellatus KT]637939038 YP_546220 """															
MFLA2113		0.521	0.931	1.741	-0.411	Y	🟡	🟡	Y		20.795	19.965	21.439	0.830	Y	🟡
	maf protein [Methylobacillus flagellatus KT]637939039 YP_546221															
MFLA2114	1.12 E-1	4.660	5.271	5.998	-0.671	Y	🟡	🟡	Y	2.41 E-1	24.635	24.712	25.674	-0.167	Y	🟡
	NUDIX hydrolase [Methylobacillus flagellatus KT]637939040 YP_546222															
MFLA2115	4.95 E-3	5.717	6.211	6.985	-0.527	G	🟢	🟡	Y	3.7 E-2	24.489	24.908	25.714	-0.433	G	🟢
	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Methylobacillus flagellatus KT]637939041 YP_546223															
MFLA2116		4.888	5.019	5.955	-0.130	Y	🟡	🟡	Y	1.18 E-2	24.062	25.305	25.814	-1.260	Y	🟡
	glutathione S-transferase-like protein [Methylobacillus flagellatus KT]637939042 YP_546224															
MFLA2117		2.923	3.240	4.090	-0.667	Y	🟡	🟢	G	8.83 E-3	21.852	22.981	23.524	-1.140	G	🟢
	nicotinate-nucleotide pyrophosphorylase [Methylobacillus flagellatus KT]637939043 YP_546225															
MFLA2118		4.126	3.162	4.723	0.841	Y	🟡	🟡	Y	7.07 E-2	22.747	22.116	23.466	0.733	Y	🟡
	type II secretion system protein E [Methylobacillus flagellatus KT]637939044 YP_546226															
MFLA2119		8.830	9.293	10.080	-0.491	Y	🟡	🟡	Y	1.19 E-1	27.740	28.188	28.981	-0.643	Y	🟡
	" acetolactate synthase, large subunit, biosynthetic type [Methylobacillus flagellatus KT]637939045 YP_546227 """															
MFLA2120	4.53 E-11	6.832	7.412	8.151	-0.751	G	🟢	🟡	Y	3.17 E-2	26.181	27.046	27.678	-0.878	G	🟢
	" acetolactate synthase, small subunit [Methylobacillus flagellatus KT]637939046 YP_546228 """															
MFLA2121		9.853	10.467	11.193	-0.847	Y	🟡	🟢	G	4.58 E-3	28.889	29.963	30.524	-1.083	G	🟢
	ketol-acid reductoisomerase [Methylobacillus flagellatus KT]637939047 YP_546229															
MFLA2122		4.115	5.139	5.716	-1.114	Y	🟡	🟡	Y	3.09 E-2	22.418	23.297	23.923	-0.953	Y	🟡
	Phosphatidylserine decarboxylase [Methylobacillus flagellatus KT]637939048 YP_546230															
MFLA2123		3.038	1.471	3.457	1.286	Y	🟡	🟡	Y	8.19 E-2	20.902	21.980	22.539	-1.391	Y	🟡
	NUDIX hydrolase [Methylobacillus flagellatus KT]637939049 YP_546231															
MFLA2124	7.38 E-2	5.060	5.139	6.100	-0.030	Y	🟡	🟡	Y	1.41 E-1	24.790	24.428	25.620	0.259	Y	🟡
	40-residue YVTN beta-propeller repeat [Methylobacillus flagellatus KT]637939050 YP_546232															



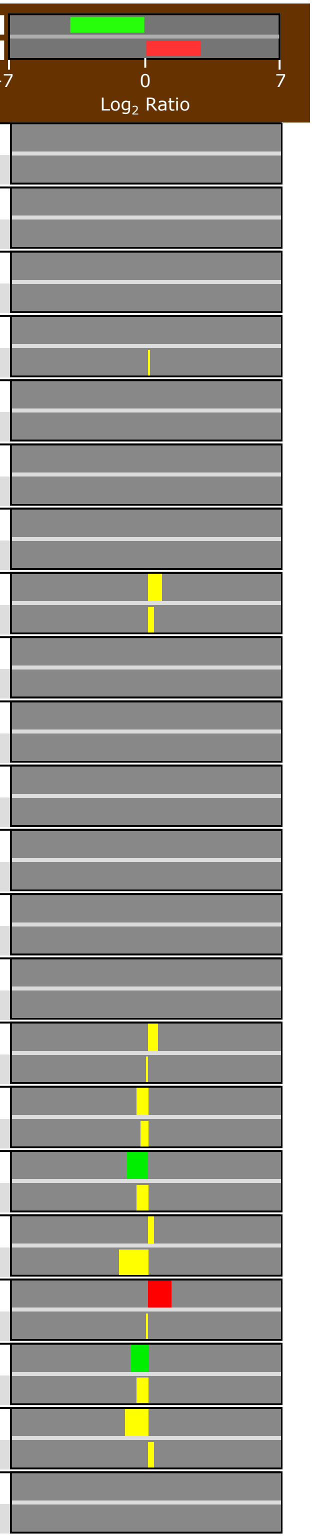
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA2125		6.300	5.844	7.090	0.430	Y	🟡	🟡	Y	1.69 E-1	26.285	26.205	27.245	0.090	Y	🟡
	MxaD gene product [Methylobacillus flagellatus KT]637939051 YP_546233															
MFLA2126		5.981	6.239	7.116	-0.597	Y	🟡	🟡	Y	9.25 E-2	26.952	27.425	28.208	-0.553	Y	🟡
	methylation [Methylobacillus flagellatus KT]637939052 YP_546234															
MFLA2127		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637939053 YP_546235															
MFLA2128		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	beta-lactamase-like protein [Methylobacillus flagellatus KT]637939054 YP_546236															
MFLA2129		3.259		3.259		Y	🟡	🟡	Y		20.411		20.411		Y	🟡
	adenylate/guanylate cyclase [Methylobacillus flagellatus KT]637939055 YP_546237															
MFLA2130		3.600	2.585	4.180	-0.126	Y	🟡	🟡	Y	9.14 E-2	23.308	21.857	23.758	0.442	Y	🟡
	Carboxylesterase [Methylobacillus flagellatus KT]637939056 YP_546238															
MFLA2131		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" exodeoxyribonuclease VII, small subunit [Methylobacillus flagellatus KT]637939057 YP_546239 """															
MFLA2132	1.84 E-2	4.347	5.479	6.022	-1.197	Y	🟡	🟡	Y	1.69 E-2	23.674	25.412	25.790	-1.712	Y	🟡
	Polyprenyl synthetase [Methylobacillus flagellatus KT]637939058 YP_546240															
MFLA2133	1.54 E-6	5.534	6.349	6.999	-0.919	G	🟢	🟡	Y	4.7 E-2	24.561	25.728	26.260	-1.377	G	🟢
	deoxyxylulose-5-phosphate synthase [Methylobacillus flagellatus KT]637939059 YP_546241															
MFLA2134	0	6.765	7.792	8.368	-1.094	G	🟢	🟡	Y	1.34 E-2	26.369	27.963	28.376	-1.796	G	🟢
	protein of unknown function DUF198 [Methylobacillus flagellatus KT]637939060 YP_546242															
MFLA2135		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" conserved hypothetical protein, predicted peptidase aspartic family [Methylobacillus flagellatus KT]637939061 YP_546243 """															
MFLA2136		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	major facilitator superfamily MFS_1 [Methylobacillus flagellatus KT]637939062 YP_546244															
MFLA2137	6.65 E-2	6.564	6.652	7.609	-0.093	Y	🟡	🟡	Y	2.88 E-2	24.922	25.556	26.274	-0.649	Y	🟡
	Chorismate synthase [Methylobacillus flagellatus KT]637939063 YP_546245															
MFLA2138		1.521	2.095	2.836	0.555	Y	🟡	🟡	Y	1.34 E-1	20.910	21.219	22.073	0.921	Y	🟡
	" Pseudouridine synthase, Rsu [Methylobacillus flagellatus KT]637939064 YP_546246 """															
MFLA2139	4.39 E-5	8.670	8.328	9.509	0.345	Y	🟡	🟡	Y	1.57 E-1	26.858	27.137	28.005	-0.400	Y	🟡
	isocitrate/isopropylmalate dehydrogenase [Methylobacillus flagellatus KT]637939065 YP_546247															
MFLA2140		10.894	10.644	11.774	0.044	Y	🟡	🟡	Y	2.54 E-1	28.327	28.400	29.364	-0.036	Y	🟡
	cold-shock DNA-binding domain protein [Methylobacillus flagellatus KT]637939066 YP_546248															
MFLA2141		4.556	5.143	5.879	-0.698	Y	🟡	🟡	Y	2.06 E-1	23.611	23.585	24.598	0.024	Y	🟡
	type II secretion system protein E [Methylobacillus flagellatus KT]637939067 YP_546249															
MFLA2142		4.066	3.962	5.015	0.090	Y	🟡	🟡	Y	2.04 E-1	22.197	22.451	23.330	-0.439	Y	🟡
	type II secretion system protein [Methylobacillus flagellatus KT]637939068 YP_546250															
MFLA2143	3.52 E-2	6.478	6.698	7.592	-0.191	Y	🟡	🟡	Y	9.14 E-2	26.450	26.381	27.416	0.071	Y	🟡
	putative thiol:disulphide interchange protein [Methylobacillus flagellatus KT]637939069 YP_546251															
MFLA2144		2.761	4.044	4.540	-1.456	Y	🟡	🟡	Y	2.67 E-1	23.114	23.070	24.092	-0.224	Y	🟡
	" Ubiquinone biosynthesis hydroxylase, UbiH/UbiF/VisC/COQ6 family [Methylobacillus flagellatus KT]637939070 YP_546252 """															
MFLA2145		4.888	4.886	5.887	0.014	Y	🟡	🟡	Y	1.76 E-1	22.496	22.880	23.701	-0.734	Y	🟡
	" Ubiquinone biosynthesis hydroxylase, UbiH/UbiF/VisC/COQ6 family [Methylobacillus flagellatus KT]637939071 YP_546253 """															
MFLA2146		3.353	4.067	4.754	-1.239	Y	🟡	🟡	Y	9.93 E-2	22.026	23.246	23.761	-1.337	Y	🟡
	peptidase M24 [Methylobacillus flagellatus KT]637939072 YP_546254															



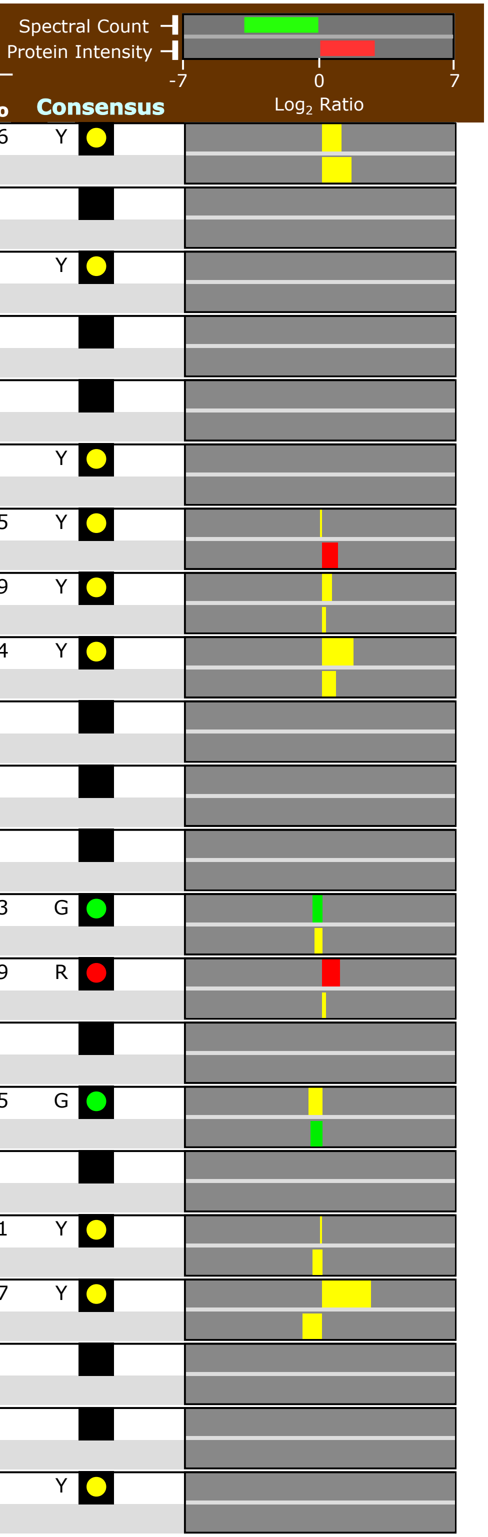


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**				**q-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**	
MFLA2147		4.864	4.979	5.922	-0.114	Y	🟡	🟡	Y	1.16 E-1	23.885	24.334	25.127	-0.636	Y	🟡
	Nucleotidyl transferase [Methylobacillus flagellatus KT]637939073 YP_546255															
MFLA2148		4.804	4.268	5.561	0.436	Y	🟡	🟡	Y	1.98 E-1	24.007	24.350	25.189	-0.363	Y	🟡
	aminoglycoside phosphotransferase [Methylobacillus flagellatus KT]637939074 YP_546256															
MFLA2149	9.87 E-3	6.224	6.668	7.463	-0.434	Y	🟡	🟡	Y	1.01 E-1	25.191	25.455	26.329	-0.294	Y	🟡
	Organic solvent tolerance protein [Methylobacillus flagellatus KT]637939075 YP_546257															
MFLA2150	6.31 E-7	6.937	7.547	8.274	-0.633	G	🟢	🟡	Y	2.7 E-2	25.493	26.274	26.936	-0.841	G	🟢
	PpiC-type peptidyl-prolyl cis-trans isomerase [Methylobacillus flagellatus KT]637939076 YP_546258															
MFLA2151		2.937	2.226	3.625	0.736	Y	🟡	🟡	Y	1.12 E-1	21.204	21.655	22.447	-0.424	Y	🟡
	4-hydroxythreonine-4-phosphate dehydrogenase [Methylobacillus flagellatus KT]637939077 YP_546259															
MFLA2152		2.106	4.129	4.446	-0.994	Y	🟡	🟡	Y	1.3 E-1	20.555	24.580	24.666	-2.528	Y	🟡
	dimethyladenosine transferase [Methylobacillus flagellatus KT]637939078 YP_546260															
MFLA2153	1.05 E-1	7.008	7.147	8.079	-0.133	Y	🟡	🟡	Y	6.9 E-2	27.646	27.831	28.742	-0.188	Y	🟡
	adenylate kinases [Methylobacillus flagellatus KT]637939079 YP_546261															
MFLA2154		4.461	4.835	5.660	-0.291	Y	🟡	🟡	Y	1.39 E-2	22.529	23.775	24.283	-1.231	Y	🟡
	methyl-accepting chemotaxis sensory transducer [Methylobacillus flagellatus KT]637939080 YP_546262															
MFLA2155	1.21 E-7	7.373	7.926	8.676	-0.555	G	🟢	🟢	G	9.92 E-3	26.314	27.336	27.914	-1.047	G	🟢
	leucyl-tRNA synthetase [Methylobacillus flagellatus KT]637939081 YP_546263															
MFLA2156		3.106	5.194	5.499	-1.065	Y	🟡	🟡	Y	6.85 E-2	21.668	24.317	24.530	-1.627	Y	🟡
	Rare lipoprotein B [Methylobacillus flagellatus KT]637939082 YP_546264															
MFLA2157		3.364	2.595	4.030	0.786	Y	🟡	🟡	Y	2.28 E-1	21.565	21.433	22.501	0.271	Y	🟡
	" DNA polymerase III, delta subunit [Methylobacillus flagellatus KT]637939083 YP_546265 """															
MFLA2158		7.884	8.351	9.136	-0.558	Y	🟡	🟡	Y	1.04 E-1	25.922	26.318	27.134	-0.489	Y	🟡
	gamma-glutamyl phosphate reductase [Methylobacillus flagellatus KT]637939084 YP_546266															
MFLA2159		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	putative nicotinate-nucleotide adenylyltransferase [Methylobacillus flagellatus KT]637939085 YP_546267															
MFLA2160		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	dethiobiotin synthase [Methylobacillus flagellatus KT]637939086 YP_546268															
MFLA2161		3.066	4.479	4.939	-1.519	Y	🟡	🟡	Y	1.9 E-2	20.600	22.554	22.885	-1.912	Y	🟡
	Biotin biosynthesis protein BioC [Methylobacillus flagellatus KT]637939087 YP_546269															
MFLA2162			3.523	3.523		Y	🟡	🟡	Y			23.022	23.022		Y	🟡
	bioH protein [Methylobacillus flagellatus KT]637939088 YP_546270															
MFLA2163		2.328	2.816	3.593	0.570	Y	🟡	🟡	Y	4.59 E-2	18.919	21.848	22.026	-1.922	Y	🟡
	8-amino-7-oxononanoate synthase [Methylobacillus flagellatus KT]637939089 YP_546271															
MFLA2164		3.761	4.702	5.307	-1.078	Y	🟡	🟢	G	8.9 E-3	22.523	23.772	24.279	-1.269	G	🟢
	biotin synthase [Methylobacillus flagellatus KT]637939090 YP_546272															
MFLA2165		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637939091 YP_546273															
MFLA2166		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	putative lipoprotein [Methylobacillus flagellatus KT]637939092 YP_546274															
MFLA2167		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	protein of unknown function DUF81 [Methylobacillus flagellatus KT]637939093 YP_546275															
MFLA2168		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	beta-lactamase-like protein [Methylobacillus flagellatus KT]637939094 YP_546276															

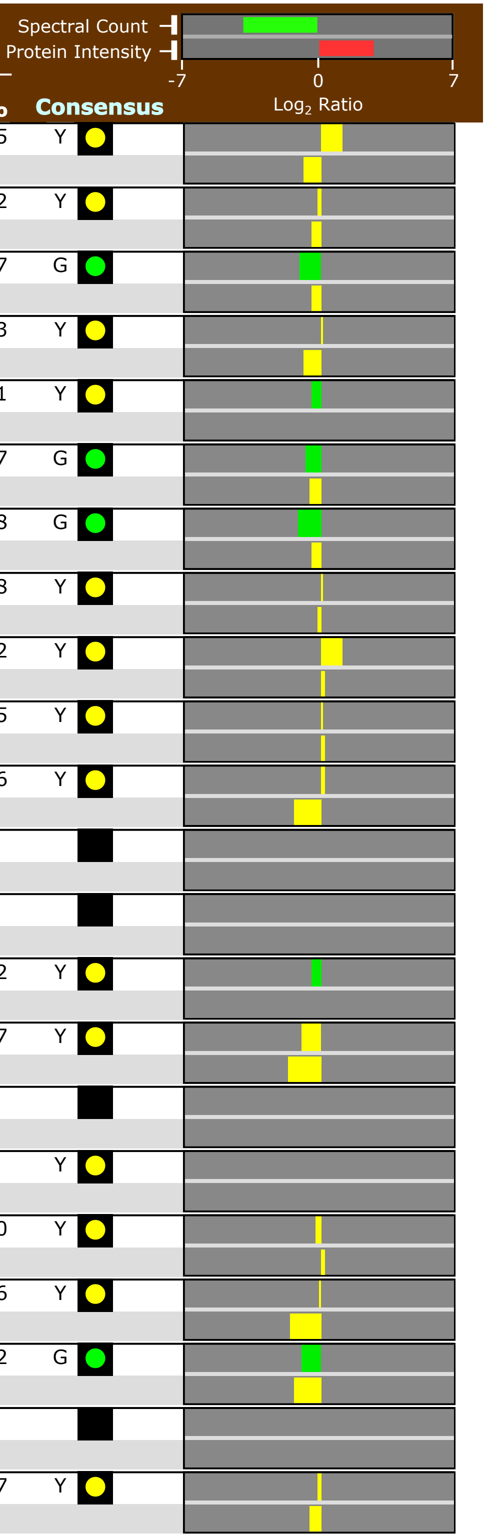
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	**Consensus**	
MFLA2169			2.816	2.816		Y	🟡	🟡	Y			22.304	22.304		Y	🟡
	cyanate lyase [Methylobacillus flagellatus KT]637939095 YP_546277															
MFLA2170		0.813		0.813		Y	🟡	🟡	Y		18.483		18.483		Y	🟡
	nitrate transport ATP-binding subunits C and D [Methylobacillus flagellatus KT]637939096 YP_546278															
MFLA2171		0.000	0.000				■	■			0.000	0.000				■
	nitrate transport permease [Methylobacillus flagellatus KT]637939097 YP_546279															
MFLA2172		3.341	3.315	4.328	0.021	Y	🟡	🟡	Y	2.74 E-1	21.463	21.476	22.469	0.108	Y	🟡
	" putative nitrate transporter component, nrtA [Methylobacillus flagellatus KT]637939098 YP_546280 """															
MFLA2173		0.000	0.000				■	■			0.000	0.000				■
	Rubredoxin-type Fe(Cys)4 protein [Methylobacillus flagellatus KT]637939099 YP_546281															
MFLA2174		0.000	0.000				■	■			0.000	0.000				■
	putative acyl-CoA dehydrogenase [Methylobacillus flagellatus KT]637939100 YP_546282															
MFLA2175		0.000	0.000				■	■			0.000	0.000				■
	OsmC-like protein [Methylobacillus flagellatus KT]637939101 YP_546283															
MFLA2176		3.294	2.562	3.974	0.655	Y	🟡	🟡	Y	2.2 E-1	21.223	21.074	22.150	0.314	Y	🟡
	" transcriptional regulator, NifA subfamily, Fis Family [Methylobacillus flagellatus KT]637939102 YP_546284 """															
MFLA2177		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939103 YP_546285															
MFLA2178		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939104 YP_546286															
MFLA2179		4.762		4.762		Y	🟡	🟡	Y		21.416		21.416		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939105 YP_546287															
MFLA2180		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939106 YP_546288															
MFLA2181		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939107 YP_546289															
MFLA2182		0.000	0.000				■	■			0.000	0.000				■
	" RNA methyltransferase TrmH, group 2 [Methylobacillus flagellatus KT]637939108 YP_546290 """															
MFLA2183	1.67 E-2	6.378	5.916	7.165	0.451	Y	🟡	🟡	Y	2.42 E-1	25.099	25.160	26.130	-0.052	Y	🟡
	Glycerol-3-phosphate dehydrogenase (NAD(P)+) [Methylobacillus flagellatus KT]637939109 YP_546291															
MFLA2184		3.430	3.893	4.680	-0.626	Y	🟡	🟡	Y	2.66 E-1	23.559	23.610	24.585	-0.354	Y	🟡
	protein of unknown function DUF1058 [Methylobacillus flagellatus KT]637939110 YP_546292															
MFLA2185	0	7.224	8.243	8.821	-1.051	G	🟢	🟡	Y	8.4 E-2	28.958	29.575	30.299	-0.591	G	🟢
	protein-export protein SecB [Methylobacillus flagellatus KT]637939111 YP_546293															
MFLA2186		3.674	3.404	4.546	0.264	Y	🟡	🟡	Y	5.47 E-2	21.923	23.532	23.941	-1.533	Y	🟡
	" Glutaredoxin, GrxC [Methylobacillus flagellatus KT]637939112 YP_546294 """															
MFLA2187	2.52 E-11	6.901	5.797	7.452	1.158	R	🔴	🟡	Y	1.91 E-1	24.646	24.815	25.733	-0.104	Y	🟡
	Rhodanese-like protein [Methylobacillus flagellatus KT]637939113 YP_546295															
MFLA2188	3.87 E-15	7.108	7.994	8.618	-0.889	G	🟢	🟡	Y	8.26 E-2	26.440	26.925	27.703	-0.585	G	🟢
	" phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent [Methylobacillus flagellatus KT]637939114 YP_546296 """															
MFLA2189		2.674	3.857	4.384	-1.189	Y	🟡	🟡	Y	1.16 E-1	21.948	21.625	22.796	0.274	Y	🟡
	peptidase M23B [Methylobacillus flagellatus KT]637939115 YP_546297															
MFLA2190		3.081		3.081		Y	🟡	🟡	Y		17.037		17.037		Y	🟡
	protein of unknown function UPF0047 [Methylobacillus flagellatus KT]637939116 YP_546298															



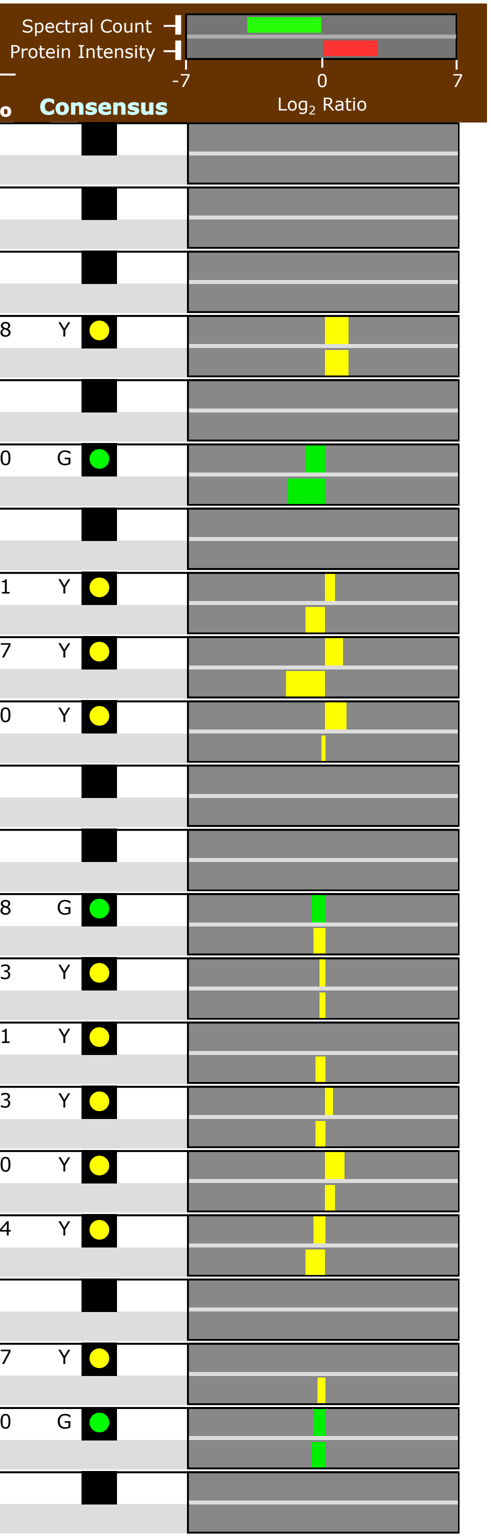
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA2191		3.532	2.505	4.108	0.994	Y	🟡	🟡	Y	3.82 E-2	23.458	21.848	23.867	1.546	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939117 YP_546299															
MFLA2192		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939118 YP_546300															
MFLA2193		1.843		1.843		Y	🟡	🟡	Y		21.607		21.607		Y	🟡
	TonB-dependent receptor [Methylobacillus flagellatus KT]637939119 YP_546301															
MFLA2194		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637939120 YP_546302															
MFLA2195		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637939121 YP_546303															
MFLA2196		2.691		2.691		Y	🟡	🟡	Y		19.534		19.534		Y	🟡
	" cytochrome c, class I [Methylobacillus flagellatus KT]637939122 YP_546304 """															
MFLA2197	3.03 E-2	6.317	6.407	7.363	-0.088	Y	🟡	🔴	R	6.19 E-3	26.744	25.908	27.386	0.835	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939123 YP_546305															
MFLA2198	7.21 E-10	9.065	8.601	9.852	0.464	Y	🟡	🟡	Y	1.39 E-1	28.743	28.570	29.659	0.159	Y	🟡
	ATPase AAA-2 [Methylobacillus flagellatus KT]637939124 YP_546306															
MFLA2199		3.025	0.346	3.235	1.613	Y	🟡	🟡	Y	1.08 E-1	22.610	20.898	22.994	0.674	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939125 YP_546307															
MFLA2200		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939126 YP_546308															
MFLA2201		0.000	0.000				■	■			0.000	0.000				■
	periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637939127 YP_546309															
MFLA2202		0.000	0.000				■	■			0.000	0.000				■
	response regulator receiver domain protein (CheY-like) [Methylobacillus flagellatus KT]637939128 YP_546310															
MFLA2203	0	9.495	10.002	10.770	-0.522	G	🟢	🟡	Y	1.01 E-2	29.497	29.911	30.719	-0.413	G	🟢
	phosphoenolpyruvate synthase [Methylobacillus flagellatus KT]637939129 YP_546311															
MFLA2204	3.53 E-5	6.240	5.328	6.855	0.924	R	🔴	🟡	Y	1.99 E-1	25.080	24.920	26.003	0.229	R	🔴
	protein of unknown function DUF299 [Methylobacillus flagellatus KT]637939130 YP_546312															
MFLA2205		0.000	0.000				■	■			0.000	0.000				■
	DoxX [Methylobacillus flagellatus KT]637939131 YP_546313															
MFLA2206		8.074	8.756	9.455	-0.748	Y	🟡	🟢	G	6.19 E-3	29.230	29.835	30.564	-0.605	G	🟢
	" Alcohol dehydrogenase, zinc-binding [Methylobacillus flagellatus KT]637939132 YP_546314 """															
MFLA2207		0.000	0.000				■	■			0.000	0.000				■
	lipoprotein signal peptidase [Methylobacillus flagellatus KT]637939133 YP_546315															
MFLA2208	1 E-1	7.514	7.591	8.553	-0.084	Y	🟡	🟡	Y	1.53 E-2	26.132	26.611	27.391	-0.481	Y	🟡
	isoleucyl-tRNA synthetase [Methylobacillus flagellatus KT]637939134 YP_546316															
MFLA2209		2.521	0.000	2.752	2.521	Y	🟡	🟡	Y		21.035	22.073	22.645	-1.037	Y	🟡
	riboflavin biosynthesis protein RibF [Methylobacillus flagellatus KT]637939135 YP_546317															
MFLA2210		0.000	0.000				■	■			0.000	0.000				■
	integral membrane protein MviN [Methylobacillus flagellatus KT]637939136 YP_546318															
MFLA2211		0.000	0.000				■	■			0.000	0.000				■
	ribosomal protein S20 [Methylobacillus flagellatus KT]637939137 YP_546319															
MFLA2212		4.240		4.240		Y	🟡	🟡	Y		22.869		22.869		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939138 YP_546320															

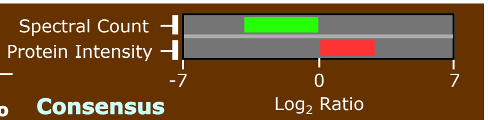


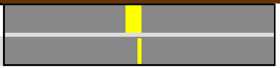
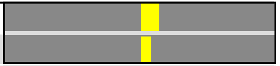
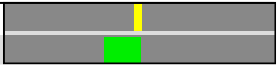
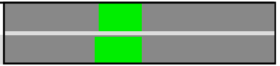
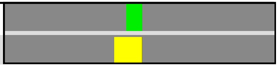
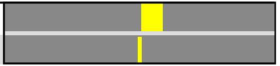
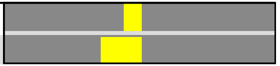
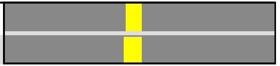
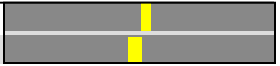
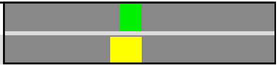
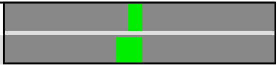
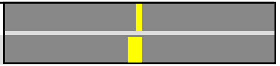
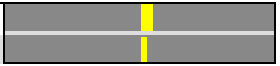
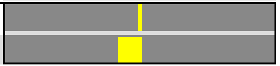
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		Consensus
MFLA2213		3.552	2.759	4.209	1.142	Y	🟡	🟡	Y	1.02 E-1	23.793	24.926	25.468	-0.905	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939139 YP_546321															
MFLA2214	2.35 E-2	7.219	7.428	8.327	-0.215	Y	🟡	🟡	Y	1.09 E-1	26.206	26.592	27.412	-0.492	Y	🟡
	" phosphoribosylaminoimidazole carboxylase, ATPase subunit [Methylobacillus flagellatus KT]637939140 YP_546322 """															
MFLA2215	1.65 E-5	4.547	5.702	6.238	-1.132	G	🟢	🟡	Y	6.87 E-2	24.559	25.069	25.837	-0.507	G	🟢
	" phosphoribosylaminoimidazole carboxylase, catalytic subunit [Methylobacillus flagellatus KT]637939141 YP_546323 """															
MFLA2216	8.77 E-2	5.050	4.960	6.005	0.057	Y	🟡	🟡	Y	3.12 E-2	23.263	24.109	24.747	-0.943	Y	🟡
	glutamate 5-kinase [Methylobacillus flagellatus KT]637939142 YP_546324															
MFLA2217	6.94 E-3	5.619	6.081	6.868	-0.523	G	🟢	🟡	Y	2.42 E-1	25.455	25.401	26.428	0.011	Y	🟡
	Small GTP-binding protein domain [Methylobacillus flagellatus KT]637939143 YP_546325															
MFLA2218	8.81 E-17	7.695	8.474	9.136	-0.787	G	🟢	🟡	Y	1.99 E-2	25.803	26.376	27.118	-0.567	G	🟢
	ribosomal protein L27 [Methylobacillus flagellatus KT]637939144 YP_546326															
MFLA2219	0	6.699	7.905	8.424	-1.202	G	🟢	🟡	Y	3.04 E-2	28.097	28.620	29.382	-0.528	G	🟢
	ribosomal protein L21 [Methylobacillus flagellatus KT]637939145 YP_546327															
MFLA2220	1.42 E-2	6.038	5.908	6.975	0.059	Y	🟡	🟡	Y	1.61 E-1	24.592	24.826	25.713	-0.208	Y	🟡
	Trans-hexaprenyltranstransferase [Methylobacillus flagellatus KT]637939146 YP_546328															
MFLA2221		4.706	3.261	5.158	1.105	Y	🟡	🟡	Y	1.59 E-1	23.177	22.682	23.950	0.202	Y	🟡
	outer membrane efflux protein [Methylobacillus flagellatus KT]637939147 YP_546329															
MFLA2222	1.15 E-2	5.681	5.555	6.620	0.124	Y	🟡	🟡	Y	1.71 E-1	25.295	24.939	26.128	0.245	Y	🟡
	secretion protein HlyD [Methylobacillus flagellatus KT]637939148 YP_546330															
MFLA2223		4.991	4.385	5.720	0.195	Y	🟡	🟡	Y	2.38 E-1	22.722	22.942	23.836	-1.446	Y	🟡
	ABC transporter related [Methylobacillus flagellatus KT]637939149 YP_546331															
MFLA2224		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939150 YP_546332															
MFLA2225		0.000	0.000				■	■			0.000	0.000				■
	Prepilin peptidase [Methylobacillus flagellatus KT]637939151 YP_546333															
MFLA2226	6.51 E-3	6.016	6.523	7.292	-0.513	G	🟢	🟡	Y	2.48 E-1	26.468	26.415	27.442	-0.012	Y	🟡
	Dephospho-CoA kinase [Methylobacillus flagellatus KT]637939152 YP_546334															
MFLA2227		4.011	5.018	5.600	-1.036	Y	🟡	🟡	Y	1.02 E-2	23.336	25.075	25.453	-1.727	Y	🟡
	protein of unknown function DUF1342 [Methylobacillus flagellatus KT]637939153 YP_546335															
MFLA2228		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF329 [Methylobacillus flagellatus KT]637939154 YP_546336															
MFLA2229			0.931	0.931		Y	🟡	🟡	Y			19.602	19.602		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939155 YP_546337															
MFLA2230		2.106	3.441	3.922	-0.314	Y	🟡	🟡	Y	7.27 E-2	20.190	21.021	21.665	0.170	Y	🟡
	mutator mutT protein [Methylobacillus flagellatus KT]637939156 YP_546338															
MFLA2231		4.352	4.505	5.431	-0.145	Y	🟡	🟡	Y	1.77 E-2	22.491	23.928	24.381	-1.616	Y	🟡
	protein of unknown function DUF815 [Methylobacillus flagellatus KT]637939157 YP_546339															
MFLA2232	8.65 E-7	5.610	6.507	7.127	-0.958	G	🟢	🟡	Y	2.9 E-2	24.244	25.492	25.999	-1.422	G	🟢
	arginine biosynthesis bifunctional protein ArgJ [Methylobacillus flagellatus KT]637939158 YP_546340															
MFLA2233		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF1289 [Methylobacillus flagellatus KT]637939159 YP_546341															
MFLA2234	3.19 E-3	8.738	8.935	9.840	-0.199	Y	🟡	🟡	Y	9.79 E-2	27.619	28.083	28.870	-0.577	Y	🟡
	" preprotein translocase, SecA subunit [Methylobacillus flagellatus KT]637939160 YP_546342 """															

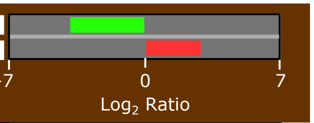


ORF	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		Consensus
MFLA2235		0.000	0.000				■	■			0.000	0.000				■
	peptidase M23B [Methylobacillus flagellatus KT]637939161 YP_546343															
MFLA2236		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939162 YP_546344															
MFLA2237		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF81 [Methylobacillus flagellatus KT]637939163 YP_546345															
MFLA2238		3.235	1.000	3.513	1.232	Y	🟡	🟡	Y	1.3 E-1	21.759	19.318	22.003	1.228	Y	🟡
	ABC transporter related [Methylobacillus flagellatus KT]637939164 YP_546346															
MFLA2239		0.000	0.000				■	■			0.000	0.000				■
	ABC-2 [Methylobacillus flagellatus KT]637939165 YP_546347															
MFLA2240	3.4 E-16	6.761	7.757	8.343	-1.022	G	🟢	🟢	G	5.35 E-3	26.102	27.961	28.312	-1.920	G	🟢
	Inorganic diphosphatase [Methylobacillus flagellatus KT]637939166 YP_546348															
MFLA2241		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF1232 [Methylobacillus flagellatus KT]637939167 YP_546349															
MFLA2242	1.29 E-2	6.139	5.614	6.900	0.539	Y	🟡	🟡	Y	1.12 E-2	24.947	25.876	26.485	-0.951	Y	🟡
	phosphoribosylaminoimidazole-succinocarboxamide synthase [Methylobacillus flagellatus KT]637939168 YP_546350															
MFLA2243		4.766	3.866	5.385	0.950	Y	🟡	🟡	Y	4.84 E-2	23.622	25.765	26.059	-1.967	Y	🟡
	" Fructose-bisphosphate aldolase, class II, Calvin cycle subtype [Methylobacillus flagellatus KT]637939169 YP_546351 """															
MFLA2244	1.49 E-2	5.540	4.444	6.093	1.139	Y	🟡	🟡	Y	1.63 E-1	23.289	23.882	24.616	-0.180	Y	🟡
	Pyruvate kinase [Methylobacillus flagellatus KT]637939170 YP_546352															
MFLA2245		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939171 YP_546353															
MFLA2246		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939172 YP_546354															
MFLA2247	1.45 E-6	6.380	7.098	7.783	-0.716	G	🟢	🟡	Y	5.47 E-2	25.532	26.034	26.805	-0.558	G	🟢
	Phosphoglycerate kinase [Methylobacillus flagellatus KT]637939173 YP_546355															
MFLA2248	3.1 E-2	7.414	7.675	8.550	-0.262	Y	🟡	🟡	Y	6.11 E-2	27.398	27.657	28.533	-0.273	Y	🟡
	" glyceraldehyde-3-phosphate dehydrogenase, type I [Methylobacillus flagellatus KT]637939174 YP_546356 """															
MFLA2249		11.651	11.663	12.657	-0.044	Y	🟡	🟡	Y	5.03 E-2	30.795	31.272	32.053	-0.521	Y	🟡
	transketolase [Methylobacillus flagellatus KT]637939175 YP_546357															
MFLA2250		6.027	5.504	6.789	0.377	Y	🟡	🟡	Y	1.66 E-2	25.143	25.661	26.425	-0.513	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939176 YP_546358															
MFLA2251		4.211	2.871	4.691	1.002	Y	🟡	🟡	Y	6.17 E-2	22.684	22.147	23.441	0.540	Y	🟡
	protein of unknown function DUF558 [Methylobacillus flagellatus KT]637939177 YP_546359															
MFLA2252		3.945	4.488	5.242	-0.591	Y	🟡	🟡	Y	5.13 E-2	21.430	22.501	23.062	-1.024	Y	🟡
	" transcriptional regulator, XRE family [Methylobacillus flagellatus KT]637939178 YP_546360 """															
MFLA2253		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939179 YP_546361															
MFLA2254		3.753	3.830	4.792	-0.050	Y	🟡	🟡	Y	8.43 E-2	21.247	21.705	22.494	-0.417	Y	🟡
	Formate--tetrahydrofolate ligase [Methylobacillus flagellatus KT]637939180 YP_546362															
MFLA2255	1.54 E-6	6.943	7.584	8.298	-0.640	G	🟢	🟢	G	1.69 E-3	27.125	27.854	28.535	-0.730	G	🟢
	acetylglutamate kinase [Methylobacillus flagellatus KT]637939181 YP_546363															
MFLA2256		0.000	0.000				■	■			0.000	0.000				■
	Pyrimidine 5-nucleotidase [Methylobacillus flagellatus KT]637939182 YP_546364															

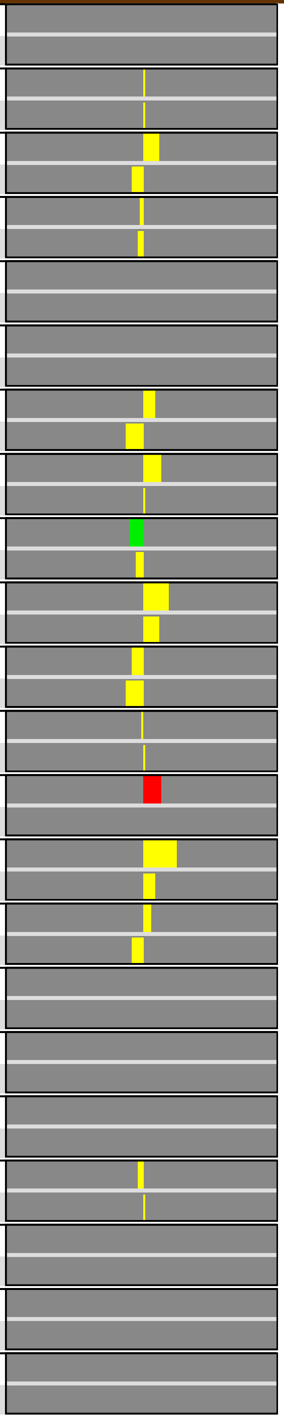




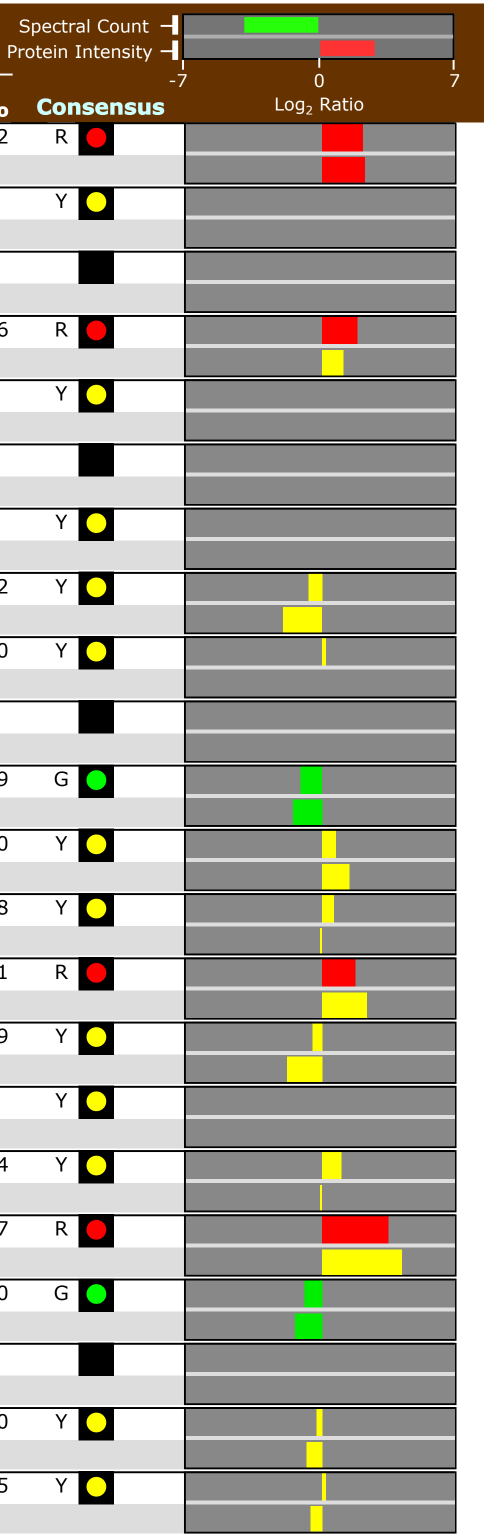
ORF	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity					Consensus		
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio			
MFLA2257		4.093	4.895	5.549	-0.824	Y	🟡	🟡	Y	1.59 E-1	25.243	25.387	26.317	-0.175	Y	🟡	
	" transcriptional regulator, TetR family [Methylobacillus flagellatus KT]637939183 YP_546365 """																
MFLA2258		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637939184 YP_546366																
MFLA2259			0.346	0.346		Y	🟡	🟡	Y			21.842	21.842		Y	🟡	
	metal dependent phosphohydrolase [Methylobacillus flagellatus KT]637939185 YP_546367																
MFLA2260		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	NAD-dependent epimerase/dehydratase [Methylobacillus flagellatus KT]637939186 YP_546368																
MFLA2261		5.448	4.444	6.032	0.916	Y	🟡	🟡	Y	8.8 E-2	23.573	22.971	24.304	0.521	Y	🟡	
	" Lytic transglycosylase, catalytic [Methylobacillus flagellatus KT]637939187 YP_546369 """																
MFLA2262	1.93 E-2	5.028	5.286	6.163	-0.373	Y	🟡	🟢	G	4.58 E-3	22.706	24.521	24.882	-1.864	G	🟢	
	UDP-3-0-acyl N-acetylglucosamine deacetylase [Methylobacillus flagellatus KT]637939188 YP_546370																
MFLA2263	0	4.783	6.981	7.265	-2.192	G	🟢	🟢	G	4.58 E-3	24.812	27.133	27.396	-2.448	G	🟢	
	cell division protein FtsZ [Methylobacillus flagellatus KT]637939189 YP_546371																
MFLA2264	0	6.227	7.502	8.001	-1.249	G	🟢	🟡	Y	3.74 E-2	24.886	26.094	26.613	-1.243	G	🟢	
	cell division protein FtsA [Methylobacillus flagellatus KT]637939190 YP_546372																
MFLA2265		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	cell division protein FtsQ [Methylobacillus flagellatus KT]637939191 YP_546373																
MFLA2266	3.38 E-3	4.899	5.706	6.358	-0.809	G	🟢	🟡	Y	1.29 E-2	23.715	24.979	25.481	-1.355	G	🟢	
	D-alanine--D-alanine ligase [Methylobacillus flagellatus KT]637939192 YP_546374																
MFLA2267		4.714	3.627	5.271	1.084	Y	🟡	🟡	Y	7.77 E-2	22.980	23.237	24.114	-0.244	Y	🟡	
	UDP-N-acetylenolpyruvoylglucosamine reductase [Methylobacillus flagellatus KT]637939193 YP_546375																
MFLA2268		4.120	5.022	5.640	-0.887	Y	🟡	🟡	Y	1.08 E-2	21.517	23.667	23.960	-2.137	Y	🟡	
	UDP-N-acetylmuramate--alanine ligase [Methylobacillus flagellatus KT]637939194 YP_546376																
MFLA2269		4.391	5.130	5.808	-0.756	Y	🟡	🟡	Y	9.8 E-2	23.338	23.991	24.701	-0.915	Y	🟡	
	UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase [Methylobacillus flagellatus KT]637939195																
MFLA2270		0.521	0.000	1.284	0.521	Y	🟡	🟡	Y		19.251	19.902	20.613	-0.651	Y	🟡	
	cell cycle protein [Methylobacillus flagellatus KT]637939196 YP_546378																
MFLA2271	4.93 E-5	4.709	5.764	6.331	-1.105	G	🟢	🟡	Y	1.13 E-2	22.652	24.240	24.655	-1.613	G	🟢	
	UDP-N-acetylmuramoylalanine--D-glutamate ligase [Methylobacillus flagellatus KT]637939197 YP_546379																
MFLA2272			0.346	0.346		Y	🟡	🟡	Y			16.861	16.861		Y	🟡	
	phospho-N-acetylmuramoyl-pentapeptide- transferase [Methylobacillus flagellatus KT]637939198 YP_546380																
MFLA2273	2.12 E-3	5.402	6.113	6.801	-0.715	G	🟢	🟢	G	4.29 E-3	23.956	25.243	25.738	-1.291	G	🟢	
	" UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate--D-alanyl-D-alanyl ligase [Methylobacillus flagellatus KT]637939199 YP_546381 """																
MFLA2274		1.843	3.140	3.632	-0.284	Y	🟡	🟡	Y	8.56 E-2	21.185	22.862	23.255	-0.662	Y	🟡	
	UDP-N-acetylmuramyl-tripeptide synthetases [Methylobacillus flagellatus KT]637939200 YP_546382																
MFLA2275		3.386	2.739	4.099	0.625	Y	🟡	🟡	Y	1.78 E-1	21.774	21.264	22.541	0.309	Y	🟡	
	Peptidoglycan glycosyltransferase [Methylobacillus flagellatus KT]637939201 YP_546383																
MFLA2276		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	" Cell division protein, FtsL -like protein [Methylobacillus flagellatus KT]637939202 YP_546384 """																
MFLA2277		3.259	3.453	4.359	-0.175	Y	🟡	🟡	Y	2.52 E-2	22.082	23.181	23.734	-1.236	Y	🟡	
	methyltransferase [Methylobacillus flagellatus KT]637939203 YP_546385																
MFLA2278			4.548	4.548		Y	🟡	🟡	Y			24.358	24.358		Y	🟡	
	protein of unknown function UPF0040 [Methylobacillus flagellatus KT]637939204 YP_546386																

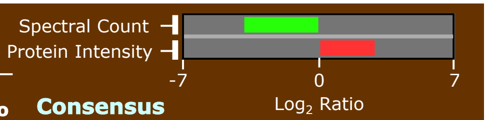


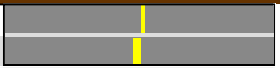
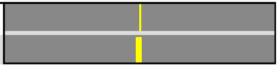
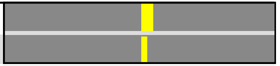
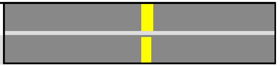
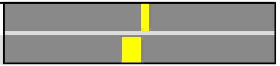
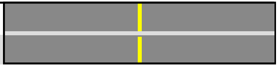
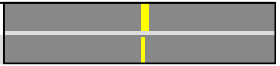
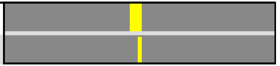
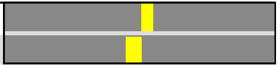
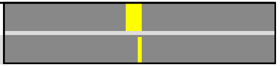
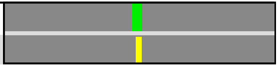
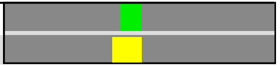
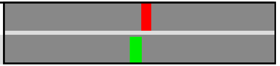
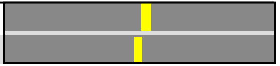
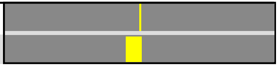
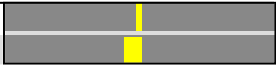
	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	***q*-value**	**log$_2$ Methylamine**	**log$_2$ Methanol**	**log$_2$ Sc Sum**	**log$_2$Ratio**	**Regulation**	***q*-value**	**log$_2$ Methylamine**	**log$_2$ Methanol**	**log$_2$ Pi Sum**	**log$_2$Ratio**	**Consensus**
MFLA2279		0.000	0.000			■ ■		0.000	0.000			■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637939205 YP_546387											
MFLA2280		4.614	4.471	5.544	0.149	Y ● ● Y	1.86 E-1	23.881	23.529	24.716	0.116	Y ●
	" dihydroorotase, homodimeric type [Methylobacillus flagellatus KT]637939206 YP_546388 """											
MFLA2281		4.140	3.347	4.797	0.833	Y ● ● Y	2.45 E-1	21.935	22.076	23.007	-0.566	Y ●
	Protein of unknown function UPF0011 [Methylobacillus flagellatus KT]637939207 YP_546389											
MFLA2282	1.19 E-1	5.530	5.771	6.655	-0.245	Y ● ● Y	7.38 E-2	24.094	24.372	25.240	-0.277	Y ●
	Putative lipoprotein-like protein [Methylobacillus flagellatus KT]637939208 YP_546390											
MFLA2283		0.521		0.521		Y ● ● Y		20.209		20.209		Y ●
	protein of unknown function UPF0102 [Methylobacillus flagellatus KT]637939209 YP_546391											
MFLA2284		0.000	0.000			■ ■		0.000	0.000			■
	phosphoheptose isomerase [Methylobacillus flagellatus KT]637939210 YP_546392											
MFLA2285		6.980	6.415	7.725	0.638	Y ● ● Y	4.01 E-2	26.347	27.320	27.914	-0.934	Y ●
	transport-associated [Methylobacillus flagellatus KT]637939211 YP_546393											
MFLA2286		4.067	2.871	4.590	0.912	Y ● ● Y	2.34 E-1	24.109	23.989	25.050	0.103	Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637939212 YP_546394											
MFLA2287	3.73 E-6	6.332	6.996	7.702	-0.666	G ● ● Y	2.04 E-1	25.144	25.336	26.243	-0.357	G ●
	hypothetical protein [Methylobacillus flagellatus KT]637939213 YP_546395											
MFLA2288		3.408	1.000	3.657	1.328	Y ● ● Y	1.55 E-1	20.801	18.543	21.075	0.842	Y ●
	diguanylate phosphodiesterase (EAL domain) [Methylobacillus flagellatus KT]637939214 YP_546396											
MFLA2289		6.652	7.119	7.904	-0.599	Y ● ● Y	1.66 E-2	27.319	28.261	28.865	-0.931	Y ●
	thioredoxin [Methylobacillus flagellatus KT]637939215 YP_546397											
MFLA2290	4.72 E-2	8.815	8.937	9.878	-0.122	Y ● ● Y	2.36 E-1	27.139	27.088	28.113	0.070	Y ●
	transcription termination factor Rho [Methylobacillus flagellatus KT]637939216 YP_546398											
MFLA2291	0	8.296	7.446	8.933	0.859	R ● ● Y	2.11 E-1	26.702	26.522	27.615	0.044	Y ●
	ribosomal protein L31 [Methylobacillus flagellatus KT]637939217 YP_546399											
MFLA2292		2.983	1.322	3.380	1.661	Y ● ● Y		20.230	19.656	20.972	0.574	Y ●
	" glycosyl transferase, family 39 [Methylobacillus flagellatus KT]637939218 YP_546400 """											
MFLA2293		5.157	4.545	5.883	0.440	Y ● ● Y	1.77 E-2	23.535	24.135	24.866	-0.614	Y ●
	" putative transcriptional regulator, ModE family [Methylobacillus flagellatus KT]637939219 YP_546401 """											
MFLA2294		0.000	0.000			■ ■		0.000	0.000			■
	molybdenum cofactor synthesis-like protein [Methylobacillus flagellatus KT]637939220 YP_546402											
MFLA2295		0.000	0.000			■ ■		0.000	0.000			■
	molybdopterin-guanine dinucleotide biosynthesis protein A [Methylobacillus flagellatus KT]637939221 YP_546403											
MFLA2296		0.000	0.000			■ ■		0.000	0.000			■
	molybdopterin-guanine dinucleotide biosynthesis protein B [Methylobacillus flagellatus KT]637939222 YP_546404											
MFLA2297	6.11 E-2	5.101	5.321	6.215	-0.302	Y ● ● Y	2.02 E-1	25.239	24.940	26.097	0.066	Y ●
	" MoeA-like, domain I and II [Methylobacillus flagellatus KT]637939223 YP_546405 """											
MFLA2298		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939224 YP_546406											
MFLA2299		1.674		1.674		Y ● ● Y		21.511		21.511		Y ●
	" transcriptional regulator, GntR family [Methylobacillus flagellatus KT]637939225 YP_546407 """											
MFLA2300		1.521		1.521		Y ● ● Y		20.306		20.306		Y ●
	PfkB [Methylobacillus flagellatus KT]637939226 YP_546408											



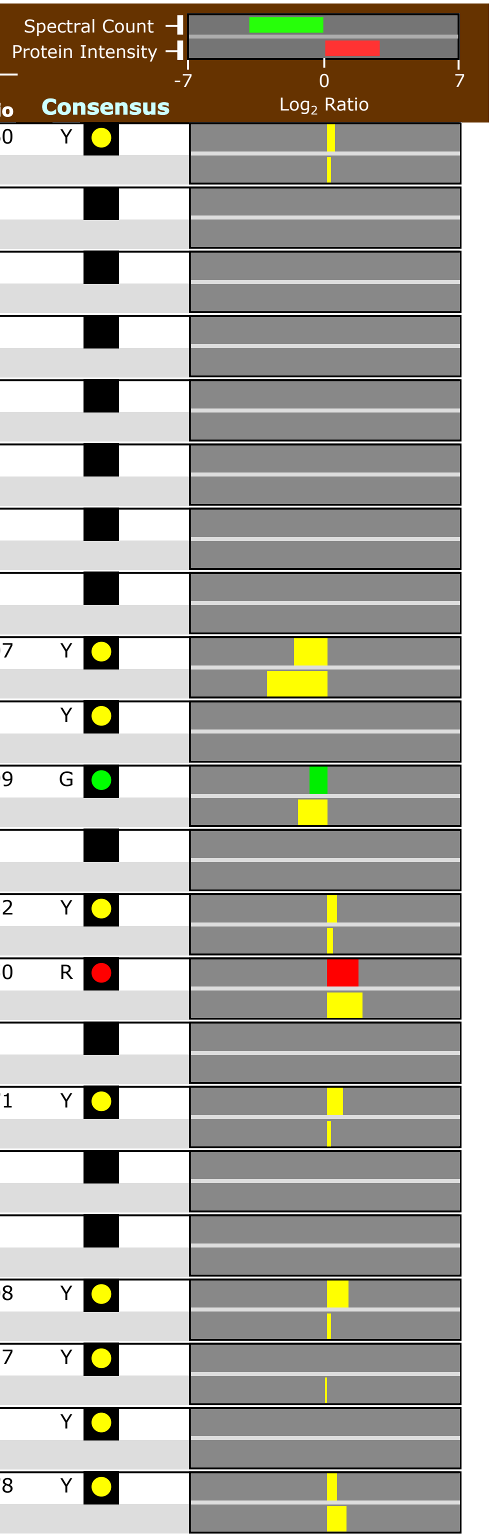
	AM/OH *M Flagellatus* Spectral Count							AM/OH *M Flagellatus* Protein Intensity								
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA2301	0	6.727	4.611	7.026	2.057	R	🔴	🔴	R	4.58 E-3	26.238	24.066	26.527	2.182	R	🔴
	TonB-dependent receptor [Methylobacillus flagellatus KT]637939227 YP_546409															
MFLA2302		2.983		2.983		Y	🟡	🟡	Y		17.144		17.144		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939228 YP_546410															
MFLA2303		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	cytochrome B561 [Methylobacillus flagellatus KT]637939229 YP_546411															
MFLA2304	0	7.906	6.088	8.266	1.796	R	🔴	🟡	Y	6.03 E-2	26.807	25.705	27.359	1.136	R	🔴
	40-residue YVTN beta-propeller repeat [Methylobacillus flagellatus KT]637939230 YP_546412															
MFLA2305		2.843		2.843		Y	🟡	🟡	Y		21.398		21.398		Y	🟡
	beta-lactamase-like protein [Methylobacillus flagellatus KT]637939231 YP_546413															
MFLA2306		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	TonB-like protein [Methylobacillus flagellatus KT]637939232 YP_546414															
MFLA2307		1.106		1.106		Y	🟡	🟡	Y		20.001		20.001		Y	🟡
	periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637939233 YP_546415															
MFLA2308		4.451	4.807	5.640	-0.686	Y	🟡	🟡	Y	3.28 E-2	22.873	24.834	25.163	-2.032	Y	🟡
	alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen [Methylobacillus flagellatus KT]637939234 YP_546416															
MFLA2309	7.93 E-2	7.524	7.345	8.437	0.183	Y	🟡	🟡	Y	2.21 E-1	27.096	27.114	28.105	-0.020	Y	🟡
	PhoH-like protein [Methylobacillus flagellatus KT]637939235 YP_546417															
MFLA2310		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	major facilitator superfamily MFS_1 [Methylobacillus flagellatus KT]637939236 YP_546418															
MFLA2311	0	7.491	8.556	9.120	-1.069	G	🟢	🟢	G	4.1 E-3	26.482	27.989	28.424	-1.509	G	🟢
	FAD-dependent pyridine nucleotide-disulphide oxidoreductase [Methylobacillus flagellatus KT]637939237 YP_546419															
MFLA2312		4.324	3.773	5.075	0.733	Y	🟡	🟡	Y	7.36 E-2	24.762	23.591	25.292	1.350	Y	🟡
	" cytochrome c, class I [Methylobacillus flagellatus KT]637939238 YP_546420 """															
MFLA2313	6.08 E-2	5.274	4.641	5.992	0.639	Y	🟡	🟡	Y	2.7 E-1	24.204	24.223	25.214	-0.078	Y	🟡
	" extracellular solute-binding protein, family 3 [Methylobacillus flagellatus KT]637939239 YP_546421 """															
MFLA2314	2.35 E-13	5.995	4.129	6.345	1.724	R	🔴	🟡	Y	4.54 E-2	25.291	22.888	25.541	2.311	R	🔴
	Pyrrolo-quinoline quinone [Methylobacillus flagellatus KT]637939240 YP_546422															
MFLA2315		4.126	4.528	5.341	-0.524	Y	🟡	🟡	Y	1.02 E-1	23.134	24.003	24.633	-1.779	Y	🟡
	proline iminopeptidase [Methylobacillus flagellatus KT]637939241 YP_546423															
MFLA2316		2.828		2.828		Y	🟡	🟡	Y		19.273		19.273		Y	🟡
	cyclic nucleotide-binding domain (cNMP-BD) protein [Methylobacillus flagellatus KT]637939242 YP_546424															
MFLA2317		4.576	3.551	5.153	0.973	Y	🟡	🟡	Y	1.26 E-1	23.190	23.256	24.223	-0.064	Y	🟡
	2OG-Fe(II) oxygenase [Methylobacillus flagellatus KT]637939243 YP_546425															
MFLA2318	0	8.370	5.041	8.507	3.417	R	🔴	🟡	Y	3.18 E-2	27.367	23.389	27.456	4.057	R	🔴
	TonB-dependent siderophore receptor [Methylobacillus flagellatus KT]637939244 YP_546426															
MFLA2319	1.1 E-8	6.341	7.155	7.805	-0.861	G	🟢	🟢	G	3.72 E-3	25.929	27.306	27.776	-1.380	G	🟢
	Rhodanese-like protein [Methylobacillus flagellatus KT]637939245 YP_546427															
MFLA2320		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637939246 YP_546428															
MFLA2321		6.352	6.583	7.472	-0.348	Y	🟡	🟡	Y	2.02 E-1	24.442	24.739	25.598	-0.830	Y	🟡
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637939247 YP_546429 """															
MFLA2322	1.19 E-1	6.799	6.641	7.722	0.155	Y	🟡	🟡	Y	6.48 E-2	26.411	26.958	27.710	-0.625	Y	🟡
	sigma 70 (RpoD) [Methylobacillus flagellatus KT]637939249 YP_546430															

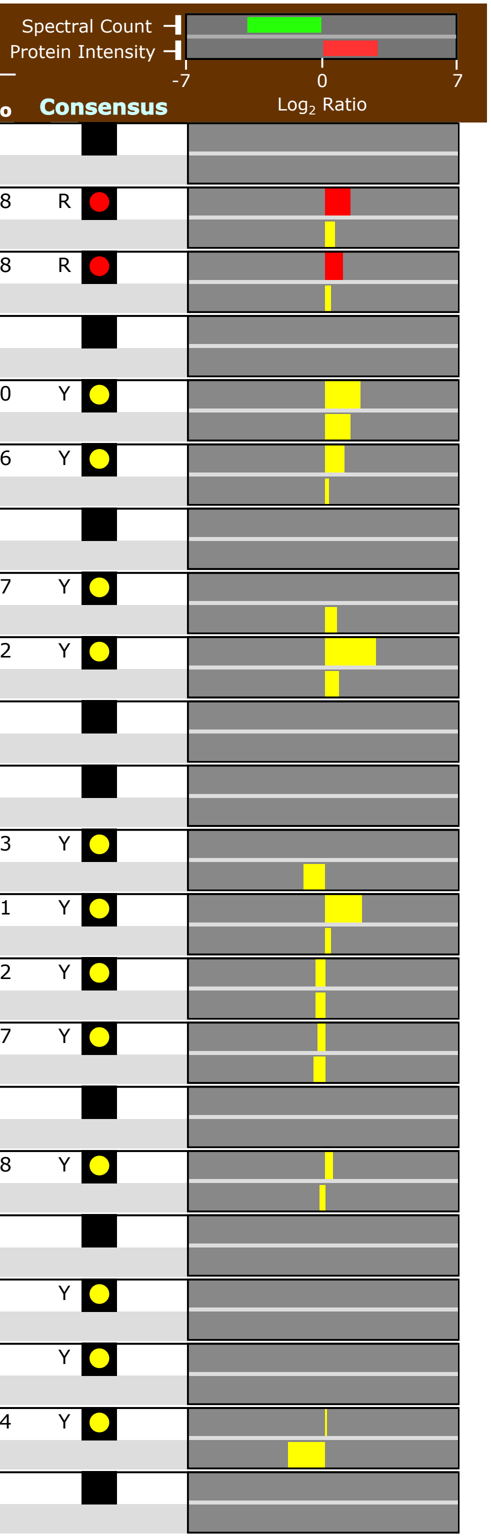




	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity							
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus		$\log_2$ Ratio
MFLA2323	1.13 E-1	5.120	4.991	6.057	0.207	Y	🟡	🟡	Y	2.19 E-1	22.634	22.826	23.734	-0.363	Y	🟡	
	DNA primase [Methylobacillus flagellatus KT]637939250 YP_546431																
MFLA2324		6.708	6.712	7.710	-0.092	Y	🟡	🟡	Y	1.5 E-1	25.289	25.541	26.421	-0.303	Y	🟡	
	GatB/Yqey [Methylobacillus flagellatus KT]637939251 YP_546432																
MFLA2325		4.741	4.079	5.447	0.618	Y	🟡	🟡	Y	8.7 E-2	25.763	25.487	26.632	0.306	Y	🟡	
	ribosomal protein S21 [Methylobacillus flagellatus KT]637939252 YP_546433																
MFLA2326		4.796	4.098	5.489	0.624	Y	🟡	🟡	Y	5.97 E-2	23.367	22.878	24.143	0.484	Y	🟡	
	" metalloendopeptidase, putative, glycoprotease family [Methylobacillus flagellatus KT]637939253 YP_546434 """																
MFLA2327		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	protein of unknown function DUF205 [Methylobacillus flagellatus KT]637939254 YP_546435																
MFLA2328			0.585	0.585		Y	🟡	🟡	Y			20.782	20.782		Y	🟡	
	dihydroneopterin aldolase [Methylobacillus flagellatus KT]637939255 YP_546436																
MFLA2329		0.521		0.521		Y	🟡	🟡	Y		19.527		19.527		Y	🟡	
	Tyrosine recombinase XerD [Methylobacillus flagellatus KT]637939256 YP_546437																
MFLA2330		2.813	3.476	4.182	0.444	Y	🟡	🟡	Y	1.37 E-1	19.438	21.661	21.941	-1.008	Y	🟡	
	methylated-DNA--protein-cysteine methyltransferase [Methylobacillus flagellatus KT]637939257 YP_546438																
MFLA2331		8.141	8.296	9.221	-0.196	Y	🟡	🟡	Y	2.28 E-1	27.783	27.880	28.832	-0.179	Y	🟡	
	ribosomal protein L19 [Methylobacillus flagellatus KT]637939258 YP_546439																
MFLA2332		3.851	3.435	4.658	0.362	Y	🟡	🟡	Y	2.02 E-1	22.587	22.312	23.456	0.236	Y	🟡	
	tRNA (guanine-N1)-methyltransferase [Methylobacillus flagellatus KT]637939259 YP_546440																
MFLA2333		3.610	4.173	4.919	-0.626	Y	🟡	🟡	Y	8.15 E-2	23.147	23.408	24.283	-0.245	Y	🟡	
	16S rRNA processing protein RimM [Methylobacillus flagellatus KT]637939260 YP_546441																
MFLA2334	2.94 E-12	5.298	6.539	7.048	-1.087	G	🟢	🟡	Y	1.08 E-1	27.466	27.845	28.668	-0.479	G	🟢	
	ribosomal protein S16 [Methylobacillus flagellatus KT]637939261 YP_546442																
MFLA2335		2.621	2.000	3.343	0.621	Y	🟡	🟡	Y		21.037	21.827	22.485	-0.789	Y	🟡	
	ExsB [Methylobacillus flagellatus KT]637939262 YP_546443																
MFLA2336		4.342	4.795	5.586	-0.836	Y	🟡	🟡	Y	1.9 E-1	23.570	23.806	24.693	-0.209	Y	🟡	
	Radical SAM [Methylobacillus flagellatus KT]637939263 YP_546444																
MFLA2337	2.74 E-6	7.375	7.924	8.675	-0.549	G	🟢	🟡	Y	1.23 E-1	27.455	27.780	28.627	-0.291	G	🟢	
	Tetratricopeptide region [Methylobacillus flagellatus KT]637939264 YP_546445																
MFLA2338	0	10.317	11.276	11.875	-1.075	G	🟢	🟡	Y	1.38 E-2	29.643	31.015	31.487	-1.491	G	🟢	
	OmpA/MotB [Methylobacillus flagellatus KT]637939265 YP_546446																
MFLA2339	9.29 E-5	7.371	6.842	8.131	0.537	R	🔴	🟢	G	4.85 E-3	26.636	27.231	27.964	-0.594	Y	🟡	
	TolB-like protein [Methylobacillus flagellatus KT]637939266 YP_546447																
MFLA2340		3.844	3.385	4.633	0.468	Y	🟡	🟡	Y	1.74 E-1	22.904	23.214	24.067	-0.400	Y	🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637939267 YP_546448																
MFLA2341			1.807	1.807		Y	🟡	🟡	Y			21.856	21.856		Y	🟡	
	Biopolymer transport protein ExbD/TolR [Methylobacillus flagellatus KT]637939268 YP_546449																
MFLA2342		5.925	5.883	6.904	-0.078	Y	🟡	🟡	Y	1.06 E-2	24.931	25.671	26.348	-0.753	Y	🟡	
	MotA/TolQ/ExbB proton channel [Methylobacillus flagellatus KT]637939269 YP_546450																
MFLA2343			0.000	0.000		Y	🟡	🟡	Y			20.099	20.099		Y	🟡	
	4-hydroxybenzoyl-CoA thioesterase [Methylobacillus flagellatus KT]637939270 YP_546451																
MFLA2344		4.439	4.697	5.574	-0.274	Y	🟡	🟡	Y	1.33 E-1	22.612	23.294	23.993	-0.924	Y	🟡	
	Holliday junction DNA helicase RuvB [Methylobacillus flagellatus KT]637939271 YP_546452																

ORF	AM/OH *M Flagellatus* Spectral Count					Regulation	AM/OH *M Flagellatus* Protein Intensity					Consensus
	q-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio		*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	
MFLA2345		4.970	4.462	5.738	0.440	Y ● ● Y	1.71 E-1	23.508	23.233	24.377	0.160	Y ●
	aldo/keto reductase [Methylobacillus flagellatus KT]637939272 YP_546453											
MFLA2346		0.000	0.000			■ ■		0.000	0.000			■
	" transcriptional regulator, LacI family [Methylobacillus flagellatus KT]637939273 YP_546454 """											
MFLA2347		0.000	0.000			■ ■		0.000	0.000			■
	ABC transporter related [Methylobacillus flagellatus KT]637939274 YP_546455											
MFLA2348		0.000	0.000			■ ■		0.000	0.000			■
	" extracellular solute-binding protein, family 1 [Methylobacillus flagellatus KT]637939275 YP_546456 """											
MFLA2349		0.000	0.000			■ ■		0.000	0.000			■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637939276 YP_546457											
MFLA2350		0.000	0.000			■ ■		0.000	0.000			■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637939277 YP_546458											
MFLA2351		0.000	0.000			■ ■		0.000	0.000			■
	TonB-dependent receptor [Methylobacillus flagellatus KT]637939278 YP_546459											
MFLA2352		0.000	0.000			■ ■		0.000	0.000			■
	" nitrilotriacetate monooxygenase, A subunit, putative [Methylobacillus flagellatus KT]637939279 YP_546460 """											
MFLA2353		0.813	3.579	3.777	-1.717	Y ● ● Y	3.86 E-2	19.029	23.142	23.223	-3.107	Y ●
	Holliday junction DNA helicase RuvA [Methylobacillus flagellatus KT]637939280 YP_546461											
MFLA2354			1.769	1.769		Y ● ● Y			20.490	20.490		Y ●
	crossover junction endodeoxyribonuclease RuvC [Methylobacillus flagellatus KT]637939281 YP_546462											
MFLA2355	9.68 E-6	5.364	6.146	6.807	-0.893	G ● ● Y	1.17 E-2	24.209	25.712	26.148	-1.499	G ●
	protein of unknown function DUF28 [Methylobacillus flagellatus KT]637939282 YP_546463											
MFLA2356		0.000	0.000			■ ■		0.000	0.000			■
	" protein of unknown function DUF6, transmembrane [Methylobacillus flagellatus KT]637939283 YP_546464 """											
MFLA2357		7.419	6.880	8.174	0.528	Y ● ● Y	6.58 E-3	26.876	26.544	27.719	0.332	Y ●
	conserved hypothetical signal peptide protein [Methylobacillus flagellatus KT]637939284 YP_546465											
MFLA2358	0	6.881	4.980	7.223	1.596	R ● ● Y	2.05 E-2	26.138	24.351	26.505	1.750	R ●
	conserved hypothetical signal peptide protein [Methylobacillus flagellatus KT]637939285 YP_546466											
MFLA2359		0.000	0.000			■ ■		0.000	0.000			■
	" transcriptional regulator, MarR family [Methylobacillus flagellatus KT]637939286 YP_546467 """											
MFLA2360		3.860	2.991	4.490	0.847	Y ● ● Y	1.96 E-1	23.341	23.210	24.277	0.171	Y ●
	putative signal-transduction protein with CBS domains [Methylobacillus flagellatus KT]637939287 YP_546468											
MFLA2361		0.000	0.000			■ ■		0.000	0.000			■
	Potassium efflux system protein [Methylobacillus flagellatus KT]637939288 YP_546469											
MFLA2362		0.000	0.000			■ ■		0.000	0.000			■
	NAD(P)H dehydrogenase (quinone) [Methylobacillus flagellatus KT]637939289 YP_546470											
MFLA2363		1.843	1.769	2.806	1.084	Y ● ● Y	1.98 E-1	21.770	22.605	23.247	0.208	Y ●
	protein of unknown function UPF0047 [Methylobacillus flagellatus KT]637939290 YP_546471											
MFLA2364		7.352	7.290	8.321	-0.028	Y ● ● Y	2.41 E-1	26.734	26.809	27.772	-0.117	Y ●
	conserved hypothetical protein-putative formaldehyde-activating enzyme [Methylobacillus flagellatus KT]637939291 YP_546472											
MFLA2365		2.691		2.691		Y ● ● Y		19.916		19.916		Y ●
	protein of unknown function DUF140 [Methylobacillus flagellatus KT]637939292 YP_546473											
MFLA2366		3.159	2.573	3.895	0.459	Y ● ● Y	1.1 E-1	21.230	19.914	21.717	0.978	Y ●
	ABC transporter related [Methylobacillus flagellatus KT]637939293 YP_546474											



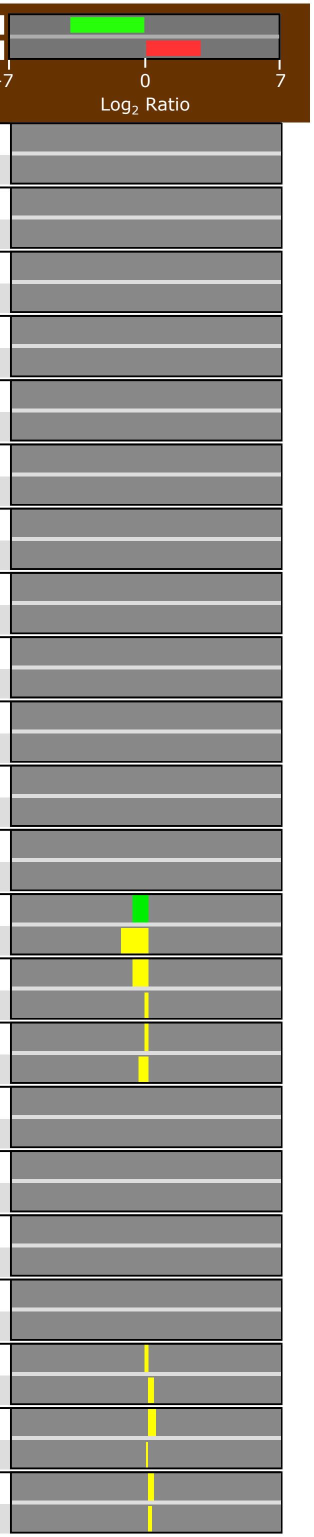


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	**Consensus**	
MFLA2367		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939294 YP_546475															
MFLA2368	6.08 E-12	6.515	5.136	6.984	1.299	R	🔴	🟡	Y	1.06 E-1	25.522	24.957	26.267	0.488	R	🔴
	Mammalian cell entry related [Methylobacillus flagellatus KT]637939295 YP_546476															
MFLA2369	4.28 E-6	5.603	4.573	6.178	0.903	R	🔴	🟡	Y	5.38 E-2	24.815	24.485	25.660	0.318	R	🔴
	putative lipoprotein [Methylobacillus flagellatus KT]637939296 YP_546477															
MFLA2370		0.000	0.000				■	■			0.000	0.000				■
	" transcriptional regulator, AraC family [Methylobacillus flagellatus KT]637939297 YP_546478 """															
MFLA2371		3.221	2.862	4.053	1.755	Y	🟡	🟡	Y	2.11 E-2	21.703	21.415	22.566	1.290	Y	🟡
	" RND efflux system, outer membrane lipoprotein, NodT [Methylobacillus flagellatus KT]637939298 YP_546479 """															
MFLA2372		4.032	2.000	4.347	1.017	Y	🟡	🟡	Y	1.17 E-1	22.304	21.092	22.821	0.206	Y	🟡
	secretion protein HlyD [Methylobacillus flagellatus KT]637939299 YP_546480															
MFLA2373		0.000	0.000				■	■			0.000	0.000				■
	[Methylobacillus flagellatus KT]639329603															
MFLA2375	1.05 E-2	5.964	5.854	6.910	0.000	Y	🟡	🟡	Y	1.12 E-1	26.343	25.353	26.931	0.647	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939300 YP_546481															
MFLA2376		2.621	0.000	2.838	2.621	Y	🟡	🟡	Y		18.785	18.132	19.495	0.652	Y	🟡
	putative redox protein [Methylobacillus flagellatus KT]637939301 YP_546482															
MFLA2377		0.000	0.000				■	■			0.000	0.000				■
	Catalase [Methylobacillus flagellatus KT]637939302 YP_546483															
MFLA2378		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939304 YP_546484															
MFLA2379		2.967	1.931	3.540	0.028	Y	🟡	🟡	Y	8.91 E-2	20.626	20.609	21.618	-1.103	Y	🟡
	phospholipase D/Transphosphatidylase [Methylobacillus flagellatus KT]637939305 YP_546485															
MFLA2380		2.691	1.915	3.354	1.856	Y	🟡	🟡	Y	2.7 E-1	19.330	20.288	20.887	0.321	Y	🟡
	Endonuclease/exonuclease/phosphatase [Methylobacillus flagellatus KT]637939306 YP_546486															
MFLA2381		6.616	7.145	7.905	-0.548	Y	🟡	🟡	Y	6.21 E-2	25.481	25.968	26.745	-0.532	Y	🟡
	" quinolinate synthetase complex, A subunit [Methylobacillus flagellatus KT]637939307 YP_546487 """															
MFLA2382		2.106	3.600	4.038	-0.445	Y	🟡	🟡	Y	1.33 E-1	20.577	22.284	22.670	-0.627	Y	🟡
	NUDIX hydrolase [Methylobacillus flagellatus KT]637939308 YP_546488															
MFLA2383		0.000	0.000				■	■			0.000	0.000				■
	adenine phosphoribosyltransferase [Methylobacillus flagellatus KT]637939309 YP_546489															
MFLA2384	2.89 E-5	7.813	7.402	8.622	0.385	Y	🟡	🟡	Y	1.08 E-1	26.914	27.195	28.061	-0.328	Y	🟡
	aspartyl-tRNA synthetase [Methylobacillus flagellatus KT]637939310 YP_546490															
MFLA2385		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF502 [Methylobacillus flagellatus KT]637939311 YP_546491															
MFLA2386			4.769	4.769		Y	🟡	🟡	Y			22.918	22.918		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939312 YP_546492															
MFLA2387		0.521		0.521		Y	🟡	🟡	Y		17.752		17.752		Y	🟡
	TonB-dependent siderophore receptor [Methylobacillus flagellatus KT]637939313 YP_546493															
MFLA2388		1.106	1.000	2.054	0.106	Y	🟡	🟡	Y		19.316	21.190	21.538	-1.874	Y	🟡
	" extracellular solute-binding protein, family 5 [Methylobacillus flagellatus KT]637939314 YP_546494 """															
MFLA2389		0.000	0.000				■	■			0.000	0.000				■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637939315 YP_546495															

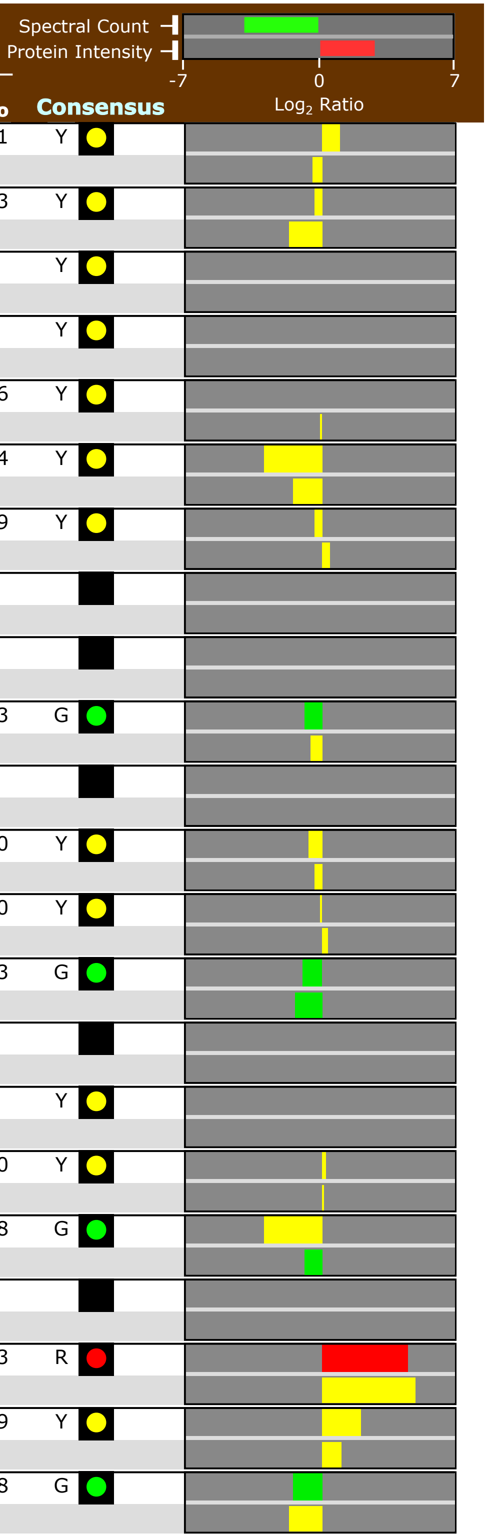
Spectral Count 🟩
Protein Intensity 🟥
-7 0 7
$\log_2$ Ratio

	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA2390		0.000	0.000			■ ■		0.000	0.000			■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637939316 YP_546496											
MFLA2391			0.000	0.000		Y ● ● Y			18.641	18.641		Y ●
	ABC transporter related [Methylobacillus flagellatus KT]637939317 YP_546497											
MFLA2392		0.000	0.000			■ ■		0.000	0.000			■
	OmpA/MotB [Methylobacillus flagellatus KT]637939318 YP_546498											
MFLA2393		0.000	0.000			■ ■		0.000	0.000			■
	protein of unknown function DUF11 [Methylobacillus flagellatus KT]637939319 YP_546499											
MFLA2394		0.521		0.521		Y ● ● Y		19.146		19.146		Y ●
	" two component transcriptional regulator, winged helix family [Methylobacillus flagellatus KT]637939320 YP_546500 """											
MFLA2395		0.000	0.000			■ ■		0.000	0.000			■
	periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637939321 YP_546501											
MFLA2396		0.000	0.000			■ ■		0.000	0.000			■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637939322 YP_546502											
MFLA2397		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939323 YP_546503											
MFLA2398		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939324 YP_546504											
MFLA2399		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939325 YP_546505											
MFLA2400		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939326 YP_546506											
MFLA2401		0.000	0.000			■ ■		0.000	0.000			■
	" TonB-dependent receptor, putative [Methylobacillus flagellatus KT]637939327 YP_546507 """											
MFLA2402		0.000	0.000			■ ■		0.000	0.000			■
	Biopolymer transport protein ExbD/TolR [Methylobacillus flagellatus KT]637939328 YP_546508											
MFLA2403		0.000	0.000			■ ■		0.000	0.000			■
	Biopolymer transport protein ExbD/TolR [Methylobacillus flagellatus KT]637939329 YP_546509											
MFLA2404		0.000	0.000			■ ■		0.000	0.000			■
	MotA/TolQ/ExbB proton channel [Methylobacillus flagellatus KT]637939330 YP_546510											
MFLA2405			2.154	2.154		Y ● ● Y			19.329	19.329		Y ●
	Filamentous haemagglutinin-like protein [Methylobacillus flagellatus KT]637939331 YP_546511											
MFLA2406		0.000	0.000			■ ■		0.000	0.000			■
	hemolysin activation/secretion protein [Methylobacillus flagellatus KT]637939332 YP_546512											
MFLA2407		5.430	4.435	6.016	0.883	Y ● ● Y	1.04 E-1	23.547	22.777	24.213	0.614	Y ●
	hypothetical protein [Methylobacillus flagellatus KT]637939333 YP_546513											
MFLA2408		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939334 YP_546514											
MFLA2409		0.000	0.000			■ ■		0.000	0.000			■
	" transcriptional regulator, LuxR family [Methylobacillus flagellatus KT]637939335 YP_546515 """											
MFLA2410		0.000	0.000			■ ■		0.000	0.000			■
	" Lytic transglycosylase, catalytic [Methylobacillus flagellatus KT]637939336 YP_546516 """											
MFLA2411		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939337 YP_546517											

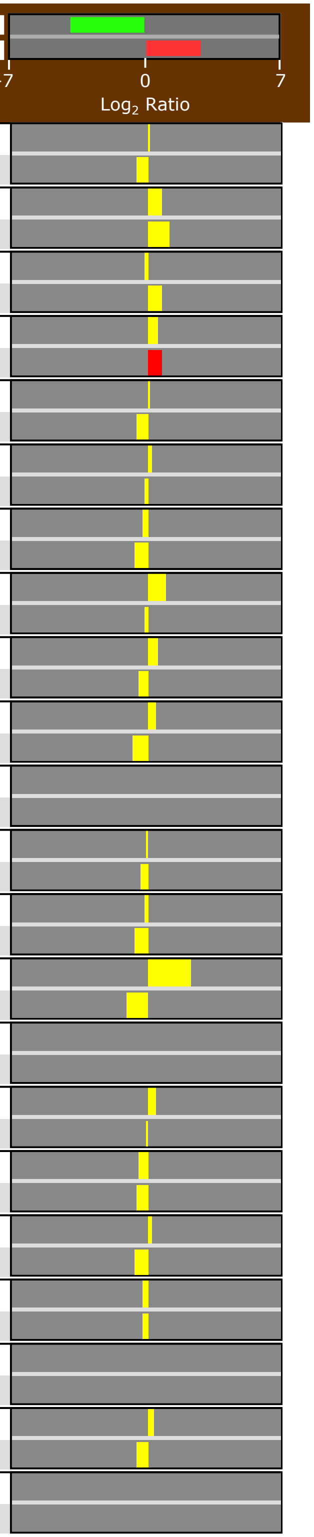
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA2412		0.000	0.000				■	■			0.000	0.000				■
	methylation [Methylobacillus flagellatus KT]637939338 YP_546518															
MFLA2413		0.000	0.000				■	■			0.000	0.000				■
	methylation [Methylobacillus flagellatus KT]637939339 YP_546519															
MFLA2414			1.322	1.322		Y	🟡	🟡	Y			18.263	18.263		Y	🟡
	type II and III secretion system protein [Methylobacillus flagellatus KT]637939340 YP_546520															
MFLA2415		0.000	0.000				■	■			0.000	0.000				■
	putative prolin-rich transmembrane protein [Methylobacillus flagellatus KT]637939341 YP_546521															
MFLA2416		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939342 YP_546522															
MFLA2417		0.000	0.000				■	■			0.000	0.000				■
	Fimbrial assembly [Methylobacillus flagellatus KT]637939343 YP_546523															
MFLA2418		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939344 YP_546524															
MFLA2419		0.000	0.000				■	■			0.000	0.000				■
	type II secretion system protein E [Methylobacillus flagellatus KT]637939345 YP_546525															
MFLA2420		0.000	0.000				■	■			0.000	0.000				■
	type II secretion system protein [Methylobacillus flagellatus KT]637939346 YP_546526															
MFLA2421		0.000	0.000				■	■			0.000	0.000				■
	General secretion pathway protein G [Methylobacillus flagellatus KT]637939347 YP_546527															
MFLA2422		0.000	0.000				■	■			0.000	0.000				■
	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) [Methylobacillus flagellatus KT]637939348 YP_546528															
MFLA2423			4.773	4.773		Y	🟡	🟡	Y			25.070	25.070		Y	🟡
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637939349 YP_546529															
MFLA2424	4.38 E-5	5.699	6.509	7.160	-0.817	G	🟢	🟡	Y	3.67 E-2	25.044	26.455	26.916	-1.412	G	🟢
	single-strand binding protein [Methylobacillus flagellatus KT]637939350 YP_546530															
MFLA2425		0.813	1.585	2.250	-0.772	Y	🟡	🟡	Y		19.820	20.042	20.935	-0.222	Y	🟡
	major facilitator superfamily MFS_1 [Methylobacillus flagellatus KT]637939351 YP_546531															
MFLA2426	1.95 E-2	6.840	7.071	7.960	-0.210	Y	🟡	🟡	Y	2.4 E-2	25.686	26.204	26.968	-0.528	Y	🟡
	" excinuclease ABC, A subunit [Methylobacillus flagellatus KT]637939352 YP_546532 """															
MFLA2427		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939353 YP_546533															
MFLA2428		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939354 YP_546534															
MFLA2429		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939355 YP_546535															
MFLA2430		0.000	0.000				■	■			0.000	0.000				■
	DoxX [Methylobacillus flagellatus KT]637939356 YP_546536															
MFLA2431		5.661	5.873	6.771	-0.238	Y	🟡	🟡	Y	1.15 E-1	24.857	24.602	25.735	0.300	Y	🟡
	hydroxymethylbutenyl pyrophosphate reductase [Methylobacillus flagellatus KT]637939357 YP_546537															
MFLA2432		2.328	1.931	3.143	0.397	Y	🟡	🟡	Y		20.647	20.758	21.704	-0.111	Y	🟡
	cobalamin biosynthesis protein CbiB [Methylobacillus flagellatus KT]637939358 YP_546538															
MFLA2433		5.107	4.788	5.956	0.317	Y	🟡	🟡	Y	1.43 E-1	23.913	23.771	24.844	0.162	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939359 YP_546539															

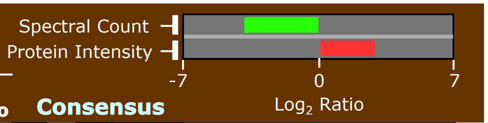


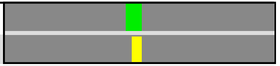
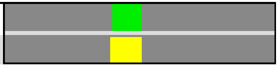
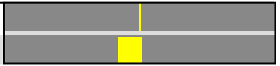
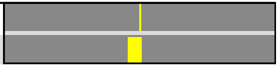
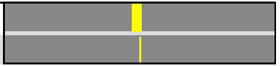
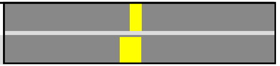
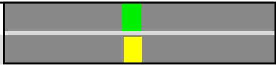
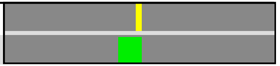
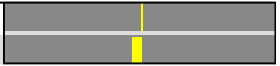
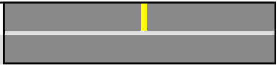
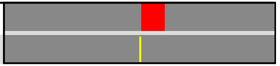
ORF	AM/OH *M Flagellatus* Spectral Count					Regulation				AM/OH *M Flagellatus* Protein Intensity					Consensus	
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio					*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		
MFLA2434		7.572	6.530	8.143	0.867	Y	🟡	🟡	Y	1.11 E-1	25.417	25.807	26.625	-0.471	Y	🟡
	formyltetrahydrofolate deformylase [Methylobacillus flagellatus KT]637939360 YP_546540															
MFLA2435		4.413	4.862	5.655	-0.428	Y	🟡	🟡	Y	1.83 E-1	23.112	23.560	24.354	-1.673	Y	🟡
	outer membrane efflux protein [Methylobacillus flagellatus KT]637939361 YP_546541															
MFLA2436		0.521		0.521		Y	🟡	🟡	Y		20.494		20.494		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939362 YP_546542															
MFLA2437		1.843		1.843		Y	🟡	🟡	Y		20.273		20.273		Y	🟡
	" Type I secretion membrane fusion protein, HlyD [Methylobacillus flagellatus KT]637939363 YP_546543 """															
MFLA2438	1.32 E-1	5.502	5.550	6.526	-0.044	Y	🟡	🟡	Y	2.7 E-1	25.200	25.225	26.212	-0.106	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939364 YP_546544															
MFLA2439		2.025	5.042	5.210	-3.012	Y	🟡	🟡	Y	6.34 E-2	22.011	23.725	24.109	-1.524	Y	🟡
	Hemolysin-type calcium-binding region [Methylobacillus flagellatus KT]637939365 YP_546545															
MFLA2440		2.543	2.739	3.645	-0.410	Y	🟡	🟡	Y	1.14 E-1	22.315	21.853	23.103	0.419	Y	🟡
	ABC transporter related [Methylobacillus flagellatus KT]637939366 YP_546546															
MFLA2441		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	Chromate transporter [Methylobacillus flagellatus KT]637939367 YP_546547															
MFLA2442		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637939368 YP_546548															
MFLA2443	1.46 E-8	5.463	6.457	7.044	-0.913	G	🟢	🟡	Y	6.49 E-2	25.282	25.864	26.602	-0.643	G	🟢
	diaminopimelate decarboxylase [Methylobacillus flagellatus KT]637939369 YP_546549															
MFLA2444		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	Monofunctional biosynthetic peptidoglycan transglycosylase [Methylobacillus flagellatus KT]637939370 YP_546550															
MFLA2445		4.277	4.999	5.683	-0.736	Y	🟡	🟡	Y	1.17 E-1	22.381	22.733	23.568	-0.380	Y	🟡
	shikimate 5-dehydrogenase [Methylobacillus flagellatus KT]637939371 YP_546551															
MFLA2446		7.641	7.747	8.695	-0.127	Y	🟡	🟡	Y	3.53 E-2	26.538	26.237	27.395	0.310	Y	🟡
	Rhodanese-like protein [Methylobacillus flagellatus KT]637939372 YP_546552															
MFLA2447	0	9.180	10.195	10.775	-1.036	G	🟢	🟢	G	8.9 E-3	28.192	29.561	30.033	-1.363	G	🟢
	" glutamine synthetase, type I [Methylobacillus flagellatus KT]637939373 YP_546553 """															
MFLA2448		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637939374 YP_546554															
MFLA2449			0.000	0.000		Y	🟡	🟡	Y			19.601	19.601		Y	🟡
	" signal transduction histidine kinase, nitrogen specific, NtrB [Methylobacillus flagellatus KT]637939375 YP_546555 """															
MFLA2450		4.522	4.288	5.410	0.160	Y	🟡	🟡	Y	1.04 E-1	22.883	22.742	23.814	0.140	Y	🟡
	" nitrogen metabolism transcriptional regulator, NtrC, Fis Family [Methylobacillus flagellatus KT]637939376 YP_546556 """															
MFLA2451		2.637	5.631	5.802	-3.009	Y	🟡	🟢	G	8.35 E-3	22.759	23.626	24.257	-0.878	G	🟢
	protein of unknown function DUF86 [Methylobacillus flagellatus KT]637939377 YP_546557															
MFLA2452		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" DNA polymerase, beta-like region [Methylobacillus flagellatus KT]637939378 YP_546558 """															
MFLA2453	0	13.800	9.662	13.880	4.446	R	🔴	🟡	Y	1.18 E-2	34.023	29.425	34.081	4.833	R	🔴
	hypothetical protein [Methylobacillus flagellatus KT]637939379 YP_546559															
MFLA2454		3.461	1.471	3.785	1.994	Y	🟡	🟡	Y	1.04 E-1	22.323	20.123	22.608	1.019	Y	🟡
	Deoxyguanosinetriphosphate triphosphohydrolase [Methylobacillus flagellatus KT]637939380 YP_546560															
MFLA2455	0	5.476	6.973	7.411	-1.539	G	🟢	🟡	Y	1.22 E-2	25.126	26.694	27.114	-1.698	G	🟢
	3-dehydroquinate synthase [Methylobacillus flagellatus KT]637939381 YP_546561															



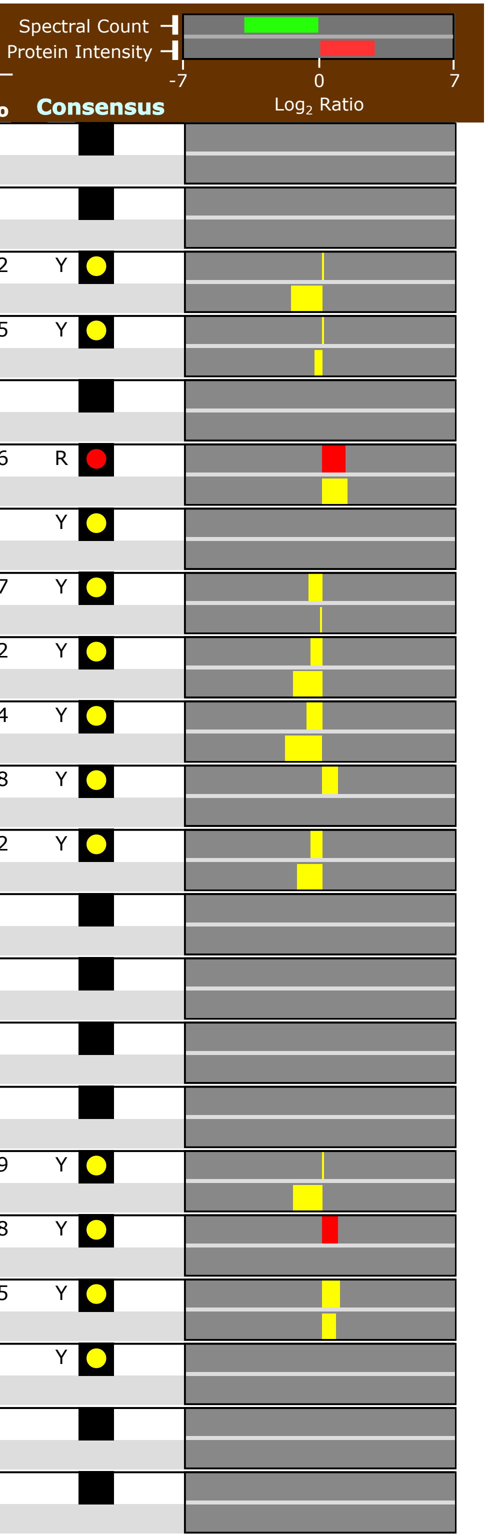
	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity						
ORF	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation		q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA2456	1.42 E-1	5.814	5.703	6.760	0.117	Y 🟡	🟡 Y	9.25 E-2	23.556	24.120	24.865	-0.611	Y 🟡
	Shikimate kinase [Methylobacillus flagellatus KT]637939382 YP_546562												
MFLA2457		7.032	6.503	7.792	0.655	Y 🟡	🟡 Y	2.27 E-2	26.654	25.635	27.232	1.053	Y 🟡
	type II and III secretion system protein [Methylobacillus flagellatus KT]637939383 YP_546563												
MFLA2458		4.419	4.844	5.647	-0.224	Y 🟡	🟡 Y	8.3 E-2	24.335	23.706	25.055	0.707	Y 🟡
	type IV pilus assembly protein PilP [Methylobacillus flagellatus KT]637939384 YP_546564												
MFLA2459		4.397	3.893	5.167	0.472	Y 🟡	🔴 R	8.91 E-3	23.851	23.148	24.542	0.700	R 🔴
	" Pilus assembly protein, PilO [Methylobacillus flagellatus KT]637939385 YP_546565 """												
MFLA2460		3.482	3.422	4.452	0.055	Y 🟡	🟡 Y	4.33 E-2	22.839	23.450	24.177	-0.628	Y 🟡
	Fimbrial assembly [Methylobacillus flagellatus KT]637939386 YP_546566												
MFLA2461	1.06 E-1	5.515	5.278	6.401	0.225	Y 🟡	🟡 Y	1.75 E-1	24.027	24.326	25.184	-0.157	Y 🟡
	type IV pilus assembly protein PilM [Methylobacillus flagellatus KT]637939387 YP_546567												
MFLA2462	1.1 E-2	6.504	6.840	7.682	-0.347	Y 🟡	🟡 Y	1.1 E-2	26.304	26.972	27.677	-0.679	Y 🟡
	Penicillin-binding protein 1A [Methylobacillus flagellatus KT]637939388 YP_546568												
MFLA2463		3.120	2.184	3.727	0.947	Y 🟡	🟡 Y	2.03 E-1	21.048	21.320	22.190	-0.166	Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939389 YP_546569												
MFLA2464	2.03 E-2	5.964	5.442	6.726	0.511	Y 🟡	🟡 Y	3.86 E-2	24.367	24.825	25.614	-0.466	Y 🟡
	Porphobilinogen synthase [Methylobacillus flagellatus KT]637939390 YP_546570												
MFLA2465	1.75 E-2	5.874	5.448	6.677	0.439	Y 🟡	🟡 Y	6.18 E-2	23.683	24.460	25.123	-0.816	Y 🟡
	Indole-3-glycerol-phosphate synthase [Methylobacillus flagellatus KT]637939391 YP_546571												
MFLA2466		0.000	0.000			■	■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939392 YP_546572												
MFLA2467	1.14 E-1	5.265	5.363	6.315	-0.092	Y 🟡	🟡 Y	8.56 E-2	23.870	24.300	25.101	-0.425	Y 🟡
	anthranilate phosphoribosyltransferase [Methylobacillus flagellatus KT]637939393 YP_546573												
MFLA2468		7.214	7.403	8.312	-0.248	Y 🟡	🟡 Y	6.15 E-2	24.791	25.562	26.227	-0.742	Y 🟡
	glutamine amidotransferase of anthranilate synthase or para-aminobenzoate synthase [Methylobacillus flagellatus KT]637939394 YP_546574												
MFLA2469		3.427	2.295	3.970	2.169	Y 🟡	🟡 Y	2.1 E-2	17.984	20.105	20.403	-1.121	Y 🟡
	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) [Methylobacillus flagellatus KT]637939395 YP_546575												
MFLA2470		0.000	0.000			■	■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939396 YP_546576												
MFLA2471		8.420	7.968	9.212	0.384	Y 🟡	🟡 Y	2.5 E-1	27.504	27.561	28.533	-0.137	Y 🟡
	anthranilate synthase component I [Methylobacillus flagellatus KT]637939397 YP_546577												
MFLA2472	5.7 E-11	8.704	9.176	9.959	-0.472	Y 🟡	🟡 Y	1.01 E-2	28.031	28.630	29.362	-0.604	Y 🟡
	Ribulose-phosphate 3-epimerase [Methylobacillus flagellatus KT]637939398 YP_546578												
MFLA2473		4.429	4.151	5.296	0.229	Y 🟡	🟡 Y	9.93 E-2	22.387	22.955	23.699	-0.736	Y 🟡
	Shikimate/quinate 5-dehydrogenase [Methylobacillus flagellatus KT]637939399 YP_546579												
MFLA2474		5.389	5.656	6.529	-0.328	Y 🟡	🟡 Y	1.47 E-1	25.258	25.602	26.440	-0.263	Y 🟡
	peptide chain release factor 1 [Methylobacillus flagellatus KT]637939400 YP_546580												
MFLA2475		0.000	0.000			■	■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939401 YP_546581												
MFLA2476		3.753	3.523	4.643	0.264	Y 🟡	🟡 Y	1.41 E-1	22.077	22.740	23.447	-0.637	Y 🟡
	" modification methylase, HemK family [Methylobacillus flagellatus KT]637939402 YP_546582 """												
MFLA2477		0.521		0.521		Y 🟡	🟡 Y		19.623		19.623		Y 🟡
	Beta-lactamase [Methylobacillus flagellatus KT]637939403 YP_546583												



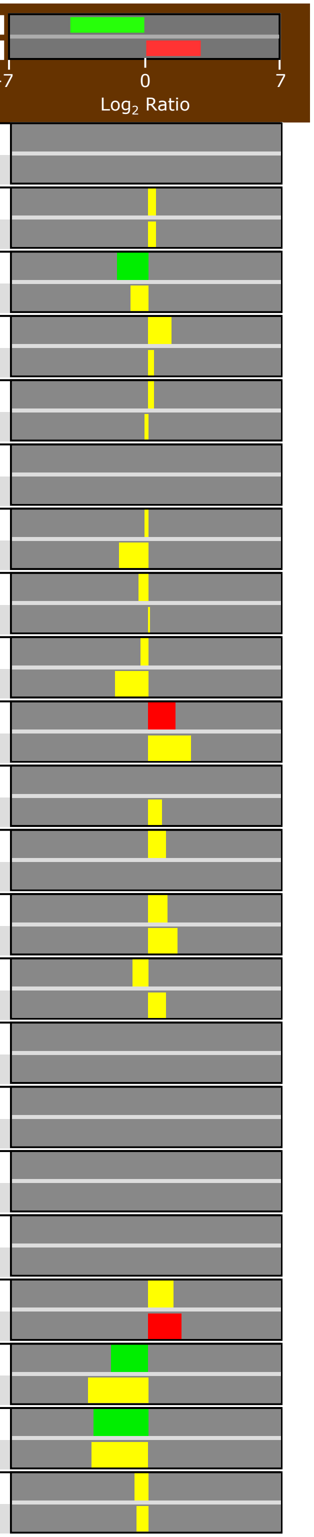


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity							
ORF	***q*-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Sc Sum**	**$\log_2$Ratio**	**Regulation**				***q*-value**	**$\log_2$ Methylamine**	**$\log_2$ Methanol**	**$\log_2$ Pi Sum**	**$\log_2$Ratio**	**Consensus**		Log₂ Ratio
MFLA2478		0.000	0.000				■	■			0.000	0.000				■	
	" protein of unknown function DUF6, transmembrane [Methylobacillus flagellatus KT]637939404 YP_546584 """																
MFLA2479		0.000	0.000				■	■			0.000	0.000				■	
	" putative carbonic anhydrase, family 3 [Methylobacillus flagellatus KT]637939405 YP_546585 """																
MFLA2480	5.62 E-3	4.705	5.524	6.172	-0.818	G	🟢	🟡	Y	8.11 E-2	24.427	24.880	25.672	-0.523	G	🟢	
	homoserine O-acetyltransferase [Methylobacillus flagellatus KT]637939406 YP_546586																
MFLA2481	1.06 E-7	4.126	5.601	6.044	-1.520	G	🟢	🟡	Y	4.64 E-2	22.610	23.784	24.314	-1.566	G	🟢	
	Methionine biosynthesis MetW [Methylobacillus flagellatus KT]637939407 YP_546587																
MFLA2482		0.000	0.000				■	■			0.000	0.000				■	
	hypothetical protein [Methylobacillus flagellatus KT]637939408 YP_546588																
MFLA2483		0.000	0.000				■	■			0.000	0.000				■	
	major facilitator superfamily MFS_1 [Methylobacillus flagellatus KT]637939409 YP_546589																
MFLA2484		4.003	3.999	5.001	-0.075	Y	🟡	🟡	Y	4.29 E-2	21.631	22.771	23.311	-1.166	Y	🟡	
	exodeoxyribonuclease III (xth) [Methylobacillus flagellatus KT]637939410 YP_546590																
MFLA2485	4.31 E-2	6.080	6.159	7.120	-0.135	Y	🟡	🟡	Y	4.29 E-2	25.164	25.813	26.525	-0.724	Y	🟡	
	orotate phosphoribosyltransferase [Methylobacillus flagellatus KT]637939411 YP_546591																
MFLA2486			0.346	0.346		Y	🟡	🟡	Y			17.766	17.766		Y	🟡	
	T/U mismatch-specific DNA glycosylase [Methylobacillus flagellatus KT]637939412 YP_546592																
MFLA2487			2.562	2.562		Y	🟡	🟡	Y			26.354	26.354		Y	🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637939413 YP_546593																
MFLA2488	5.04 E-7	7.844	8.297	9.088	-0.461	Y	🟡	🟡	Y	1.97 E-1	27.097	27.183	28.140	-0.109	Y	🟡	
	" glutamyl-tRNA(Gln) amidotransferase, B subunit [Methylobacillus flagellatus KT]637939414 YP_546594 """																
MFLA2489		5.620	6.167	6.919	-0.626	Y	🟡	🟡	Y	4.11 E-2	25.406	26.555	27.092	-1.149	Y	🟡	
	" glutamyl-tRNA(Gln) amidotransferase, A subunit [Methylobacillus flagellatus KT]637939415 YP_546595 """																
MFLA2490	4.67 E-8	5.810	6.810	7.395	-1.000	G	🟢	🟡	Y	1.32 E-2	24.675	25.548	26.177	-0.902	G	🟢	
	" glutamyl-tRNA(Gln) amidotransferase, C subunit [Methylobacillus flagellatus KT]637939416 YP_546596 """																
MFLA2491	1.54 E-3	8.047	8.307	9.183	-0.269	Y	🟡	🟢	G	4.58 E-3	27.566	28.758	29.282	-1.196	G	🟢	
	" cell shape determining protein, MreB/Mrl family [Methylobacillus flagellatus KT]637939417 YP_546597 """																
MFLA2492		4.628	4.494	5.563	0.116	Y	🟡	🟡	Y	1.26 E-1	22.949	23.408	24.197	-0.480	Y	🟡	
	rod shape-determining protein MreC [Methylobacillus flagellatus KT]637939418 YP_546598																
MFLA2493		0.000	0.000				■	■			0.000	0.000				■	
	Rod shape-determining protein MreD [Methylobacillus flagellatus KT]637939419 YP_546599																
MFLA2494		4.025	3.715	4.878	0.264	Y	🟡	🟡	Y	2.7 E-1	22.076	22.061	23.068	0.046	Y	🟡	
	Peptidoglycan glycosyltransferase [Methylobacillus flagellatus KT]637939420 YP_546600																
MFLA2495		0.000	0.000				■	■			0.000	0.000				■	
	Rod shape-determining protein RodA [Methylobacillus flagellatus KT]637939421 YP_546601																
MFLA2496	2.19 E-5	5.696	4.523	6.226	1.207	R	🔴	🟡	Y	1.1 E-2	24.849	23.928	25.461	0.932	R	🔴	
	rare lipoprotein A [Methylobacillus flagellatus KT]637939422 YP_546602																
MFLA2497	0	7.546	6.255	8.040	1.231	R	🔴	🟡	Y	2.05 E-1	26.220	26.338	27.280	-0.068	Y	🟡	
	Serine-type D-Ala-D-Ala carboxypeptidase [Methylobacillus flagellatus KT]637939423 YP_546603																
MFLA2498			1.540	1.540		Y	🟡	🟡	Y			21.733	21.733		Y	🟡	
	" aminotransferase, class IV [Methylobacillus flagellatus KT]637939424 YP_546604 """																
MFLA2499		0.000	0.000				■	■			0.000	0.000				■	
	protein of unknown function DUF493 [Methylobacillus flagellatus KT]637939425 YP_546605																

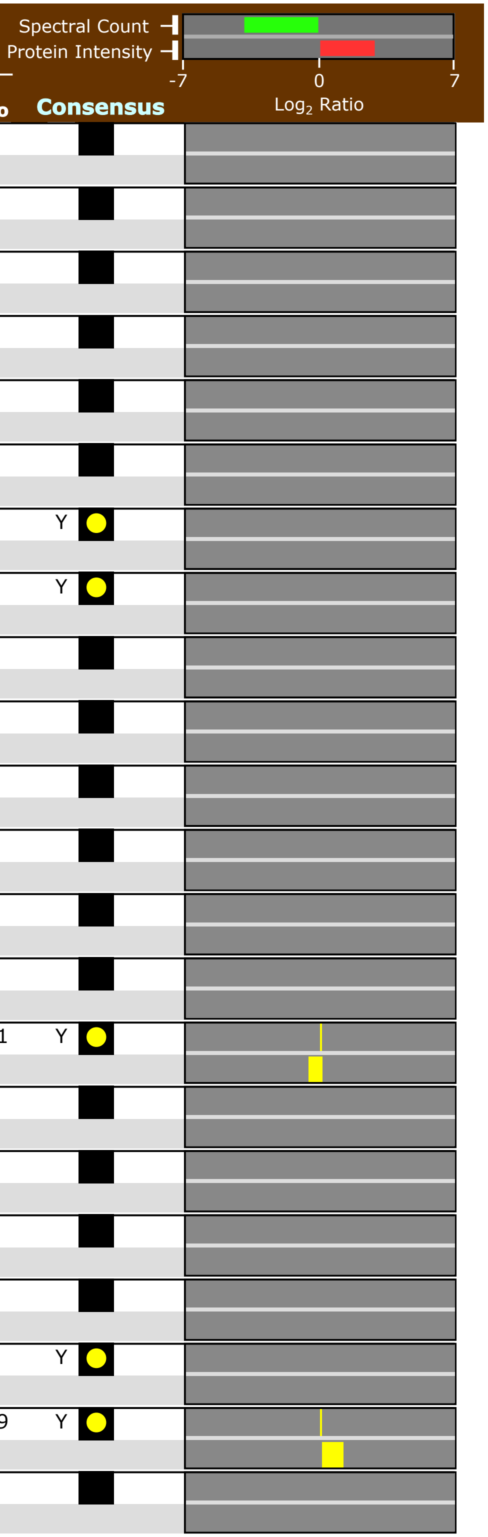
	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA2500		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	lipoate-protein ligase B [Methylobacillus flagellatus KT]637939426 YP_546606											
MFLA2501		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	lipoic acid synthetase [Methylobacillus flagellatus KT]637939427 YP_546607											
MFLA2502		3.619	3.505	4.563	0.063	Y 🟡 🟡 Y	6.47 E-2	21.055	22.420	22.893	-1.562	Y 🟡
	protein of unknown function DUF21 [Methylobacillus flagellatus KT]637939428 YP_546608											
MFLA2503		4.933	4.800	5.868	0.130	Y 🟡 🟡 Y	9.14 E-2	23.720	24.087	24.915	-0.425	Y 🟡
	" Ubiquinone biosynthesis hydroxylase, UbiH/UbiF/VisC/COQ6 family [Methylobacillus flagellatus KT]637939429 YP_546609 """											
MFLA2504		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	" pyridoxamine 5'-phosphate oxidase-related, FMN-binding [Methylobacillus flagellatus KT]637939430 YP_546610 """											
MFLA2505	6.96 E-6	5.820	4.635	6.346	1.156	R 🔴 🟡 Y	2.93 E-2	25.262	23.940	25.748	1.296	R 🔴
	NADPH-dependent FMN reductase [Methylobacillus flagellatus KT]637939431 YP_546611											
MFLA2506		1.521		1.521		Y 🟡 🟡 Y		18.032		18.032		Y 🟡
	histidine triad (HIT) protein [Methylobacillus flagellatus KT]637939432 YP_546612											
MFLA2507		3.996	4.722	5.404	-0.702	Y 🟡 🟡 Y	8.56 E-2	22.659	22.759	23.710	-0.097	Y 🟡
	TonB-like protein [Methylobacillus flagellatus KT]637939433 YP_546613											
MFLA2508		3.692	4.271	5.011	-0.605	Y 🟡 🟡 Y	5.48 E-2	21.612	22.678	23.241	-1.522	Y 🟡
	UDP-N-acetylmuramate [Methylobacillus flagellatus KT]637939434 YP_546614											
MFLA2509		5.786	6.409	7.131	-0.837	Y 🟡 🟡 Y	7.45 E-2	24.339	25.558	26.073	-1.884	Y 🟡
	5-methyltetrahydrofolate--homocysteine methyltransferase [Methylobacillus flagellatus KT]637939435 YP_546615											
MFLA2510		4.860	4.125	5.539	0.847	Y 🟡 🟡 Y	2.02 E-1	22.586	22.909	23.756	0.028	Y 🟡
	Mg chelatase-related protein [Methylobacillus flagellatus KT]637939436 YP_546616											
MFLA2511		3.093	3.669	4.410	-0.591	Y 🟡 🟡 Y	1.71 E-1	22.667	23.334	24.038	-1.332	Y 🟡
	protein of unknown function DUF526 [Methylobacillus flagellatus KT]637939437 YP_546617											
MFLA2512		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637939438 YP_546618											
MFLA2513		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	" nitrogen regulatory protein P-II (GlnB, GlnK) [Methylobacillus flagellatus KT]637939439 YP_546619 """											
MFLA2514		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	ammonium transporter [Methylobacillus flagellatus KT]637939440 YP_546620											
MFLA2515		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637939441 YP_546621											
MFLA2516		4.832	4.656	5.747	0.125	Y 🟡 🟡 Y	2.51 E-2	22.878	24.200	24.685	-1.549	Y 🟡
	Glutamate--cysteine ligase GshA [Methylobacillus flagellatus KT]637939442 YP_546622											
MFLA2517	4.55 E-3	5.783	5.034	6.456	0.751	R 🔴 🟡 Y	2.7 E-1	23.883	23.894	24.889	-0.008	Y 🟡
	glutathione synthetase [Methylobacillus flagellatus KT]637939443 YP_546623											
MFLA2518		7.696	6.563	8.238	0.873	Y 🟡 🟡 Y	1.13 E-1	26.984	25.955	27.559	0.655	Y 🟡
	Tfp pilus assembly protein tip-associated adhesin PilY1-like protein [Methylobacillus flagellatus KT]637939444 YP_546624											
MFLA2519		2.398		2.398		Y 🟡 🟡 Y		19.488		19.488		Y 🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939445 YP_546625											
MFLA2520		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637939446 YP_546626											
MFLA2521		0.000	0.000			⬛ ⬛		0.000	0.000			⬛
	hypothetical protein [Methylobacillus flagellatus KT]637939447 YP_546627											

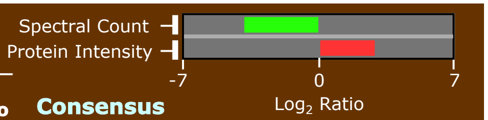


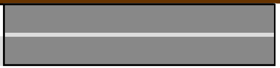
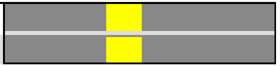
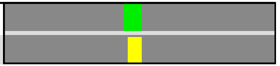
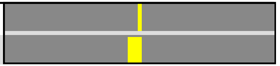
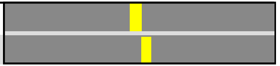
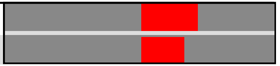
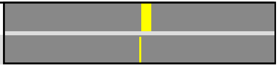
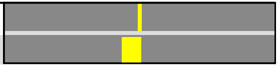
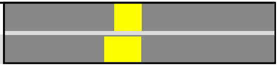
ORF	AM/OH *M Flagellatus* Spectral Count					Regulation				AM/OH *M Flagellatus* Protein Intensity					Consensus	
	q-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio					*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio		
MFLA2522			0.000	0.000		Y	🟡	🟡	Y			25.444	25.444		Y	🟡
	methylation [Methylobacillus flagellatus KT]637939448 YP_546628															
MFLA2523		2.813	3.422	4.150	0.394	Y	🟡	🟡	Y	1.43 E-2	23.604	24.156	24.906	0.448	Y	🟡
	methylation [Methylobacillus flagellatus KT]637939449 YP_546629															
MFLA2524	0	8.169	9.723	10.146	-1.629	G	🟢	🟡	Y	1.11 E-2	28.687	29.527	30.167	-0.861	G	🟢
	conserved hypothetical protein-putative formaldehyde-activating enzyme [Methylobacillus flagellatus KT]637939450 YP_546630															
MFLA2525		1.521	0.346	2.050	1.174	Y	🟡	🟡	Y		19.918	19.646	20.788	0.272	Y	🟡
	A/G-specific adenine glycosylase [Methylobacillus flagellatus KT]637939451 YP_546631															
MFLA2526	4.11 E-2	7.258	6.978	8.125	0.280	Y	🟡	🟡	Y	1.26 E-1	25.870	26.117	26.999	-0.237	Y	🟡
	AsmA [Methylobacillus flagellatus KT]637939452 YP_546632															
MFLA2527		0.000	0.000				■	■			0.000	0.000				■
	" undecaprenol kinase, putative [Methylobacillus flagellatus KT]637939453 YP_546633 """															
MFLA2528		3.482	3.729	4.611	-0.210	Y	🟡	🟡	Y	4.79 E-2	23.165	24.785	25.191	-1.495	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939454 YP_546634															
MFLA2529		3.408	3.962	4.712	-0.541	Y	🟡	🟡	Y	2.42 E-1	22.503	22.361	23.434	0.128	Y	🟡
	" Pseudouridine synthase, Rsu [Methylobacillus flagellatus KT]637939455 YP_546635 """															
MFLA2530		7.597	7.791	8.697	-0.417	Y	🟡	🟡	Y	1.89 E-2	26.363	28.030	28.425	-1.715	Y	🟡
	thiamine biosynthesis protein ThiC [Methylobacillus flagellatus KT]637939456 YP_546636															
MFLA2531	5.42 E-8	5.905	4.509	6.369	1.436	R	🔴	🟡	Y	4.98 E-2	24.918	22.533	25.171	2.211	R	🔴
	protein-L-isoaspartate(D-aspartate) O-methyltransferase [Methylobacillus flagellatus KT]637939457 YP_546637															
MFLA2532		3.235	3.295	4.265	-0.027	Y	🟡	🟡	Y	1.28 E-1	21.519	20.936	22.257	0.664	Y	🟡
	secretion protein HlyD [Methylobacillus flagellatus KT]637939458 YP_546638															
MFLA2533		3.952	3.032	4.564	0.926	Y	🟡	🟡	Y	2.34 E-1	22.081	22.224	23.154	0.019	Y	🟡
	acriflavin resistance protein [Methylobacillus flagellatus KT]637939459 YP_546639															
MFLA2534		4.186	3.032	4.721	1.029	Y	🟡	🟡	Y	6.44 E-2	23.734	22.168	24.154	1.512	Y	🟡
	" Type I secretion outer membrane protein, TolC [Methylobacillus flagellatus KT]637939460 YP_546640 """															
MFLA2535		0.813	1.585	2.250	-0.772	Y	🟡	🟡	Y		21.390	20.508	22.015	0.882	Y	🟡
	isochorismatase hydrolase [Methylobacillus flagellatus KT]637939461 YP_546641															
MFLA2536			2.897	2.897		Y	🟡	🟡	Y			20.825	20.825		Y	🟡
	Three-deoxy-D-manno-octulosonic-acid transferase-like protein [Methylobacillus flagellatus KT]637939462 YP_546642															
MFLA2537			0.346	0.346		Y	🟡	🟡	Y			20.241	20.241		Y	🟡
	periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637939463 YP_546643															
MFLA2538		0.000	0.000				■	■			0.000	0.000				■
	" two component transcriptional regulator, winged helix family [Methylobacillus flagellatus KT]637939464 YP_546644 """															
MFLA2539		0.000	0.000				■	■			0.000	0.000				■
	Outer membrane autotransporter barrel [Methylobacillus flagellatus KT]637939465 YP_546645															
MFLA2540		4.587	3.254	5.069	1.336	Y	🟡	🔴	R	7.12 E-3	23.885	22.240	24.285	1.671	R	🔴
	isochorismatase hydrolase [Methylobacillus flagellatus KT]637939466 YP_546646															
MFLA2541	0	5.927	7.806	8.153	-1.920	G	🟢	🟡	Y	1.53 E-2	24.111	27.078	27.252	-3.112	G	🟢
	Ribonucleoside-diphosphate reductase [Methylobacillus flagellatus KT]637939467 YP_546647															
MFLA2542	0	4.299	6.283	6.608	-2.792	G	🟢	🟡	Y	2.54 E-2	23.463	25.996	26.226	-2.912	G	🟢
	hypothetical protein [Methylobacillus flagellatus KT]637939468 YP_546648															
MFLA2543		3.461	4.191	4.872	-0.725	Y	🟡	🟡	Y	1.05 E-1	22.864	23.294	24.095	-0.557	Y	🟡
	formaldehyde-activating enzyme [Methylobacillus flagellatus KT]637939469 YP_546649															

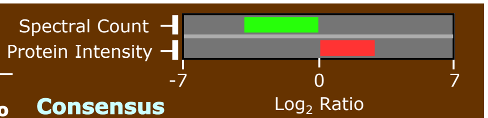
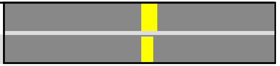
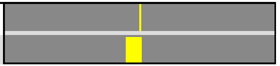
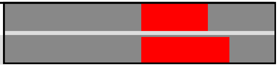
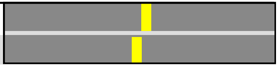
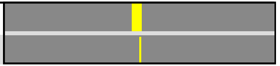
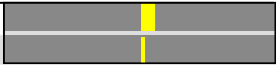
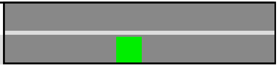
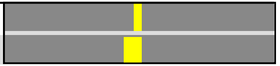
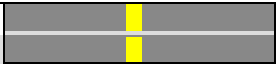
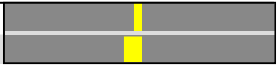


	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	**Consensus**
MFLA2544		0.000	0.000			■ ■		0.000	0.000			■
	" RND efflux system, outer membrane lipoprotein, NodT [Methylobacillus flagellatus KT]637939470 YP_546650 """											
MFLA2545		0.000	0.000			■ ■		0.000	0.000			■
	RND multidrug efflux transporter MexB [Methylobacillus flagellatus KT]637939471 YP_546651											
MFLA2546		0.000	0.000			■ ■		0.000	0.000			■
	Cation/multidrug efflux pump-like protein [Methylobacillus flagellatus KT]637939472 YP_546652											
MFLA2547		0.000	0.000			■ ■		0.000	0.000			■
	IstB-like ATP-binding protein [Methylobacillus flagellatus KT]637939473 YP_546653											
MFLA2548		0.000	0.000			■ ■		0.000	0.000			■
	" Integrase, catalytic region [Methylobacillus flagellatus KT]637939474 YP_546654 """											
MFLA2549		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939475 YP_546655											
MFLA2550			0.585	0.585		Y ● ● Y			18.431	18.431		Y ●
	Heavy metal translocating P-type ATPase [Methylobacillus flagellatus KT]637939476 YP_546656											
MFLA2551		2.746		2.746		Y ● ● Y		21.040		21.040		Y ●
	Heavy metal efflux pump CzcA [Methylobacillus flagellatus KT]637939477 YP_546657											
MFLA2552		0.000	0.000			■ ■		0.000	0.000			■
	secretion protein HlyD [Methylobacillus flagellatus KT]637939478 YP_546658											
MFLA2553		0.000	0.000			■ ■		0.000	0.000			■
	outer membrane efflux protein [Methylobacillus flagellatus KT]637939479 YP_546659											
MFLA2554		0.000	0.000			■ ■		0.000	0.000			■
	protein of unknown function UPF0060 [Methylobacillus flagellatus KT]637939480 YP_546660											
MFLA2555		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939481 YP_546661											
MFLA2556		0.000	0.000			■ ■		0.000	0.000			■
	RND multidrug efflux transporter MexB [Methylobacillus flagellatus KT]637939482 YP_546662											
MFLA2557		0.000	0.000			■ ■		0.000	0.000			■
	secretion protein HlyD [Methylobacillus flagellatus KT]637939483 YP_546663											
MFLA2558		3.700	3.754	4.728	-0.133	Y ● ● Y	7.54 E-2	22.640	23.231	23.966	-0.711	Y ●
	" transcriptional regulator, IclR family [Methylobacillus flagellatus KT]637939484 YP_546664 """											
MFLA2559		0.000	0.000			■ ■		0.000	0.000			■
	binding-protein-dependent transport systems inner membrane component [Methylobacillus flagellatus KT]637939485 YP_546665											
MFLA2560		0.000	0.000			■ ■		0.000	0.000			■
	ABC transporter related [Methylobacillus flagellatus KT]637939486 YP_546666											
MFLA2561		0.000	0.000			■ ■		0.000	0.000			■
	NLPA lipoprotein [Methylobacillus flagellatus KT]637939487 YP_546667											
MFLA2562		0.000	0.000			■ ■		0.000	0.000			■
	Glutamate--ammonia ligase [Methylobacillus flagellatus KT]637939488 YP_546668											
MFLA2563			1.184	1.184		Y ● ● Y			19.966	19.966		Y ●
	Homoserine O-acetyltransferase [Methylobacillus flagellatus KT]637939489 YP_546669											
MFLA2564		2.259	2.649	3.467	-0.082	Y ● ● Y	5.48 E-2	22.200	20.950	22.707	1.139	Y ●
	" transcriptional regulator, TetR family [Methylobacillus flagellatus KT]637939490 YP_546670 """											
MFLA2565		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939491 YP_546671											

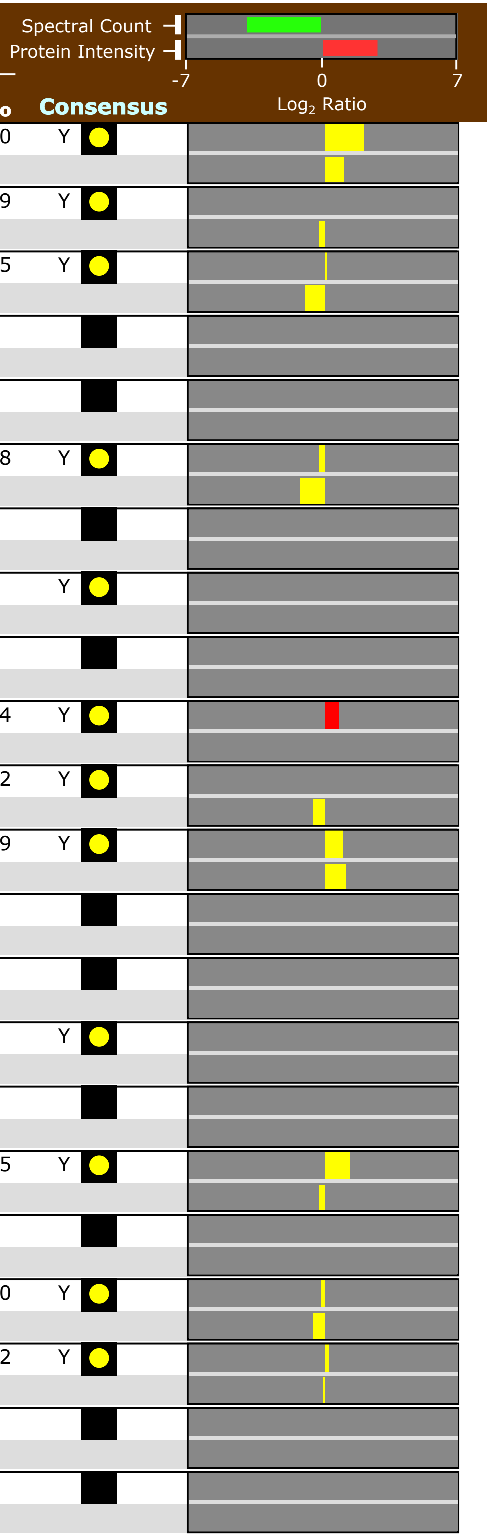


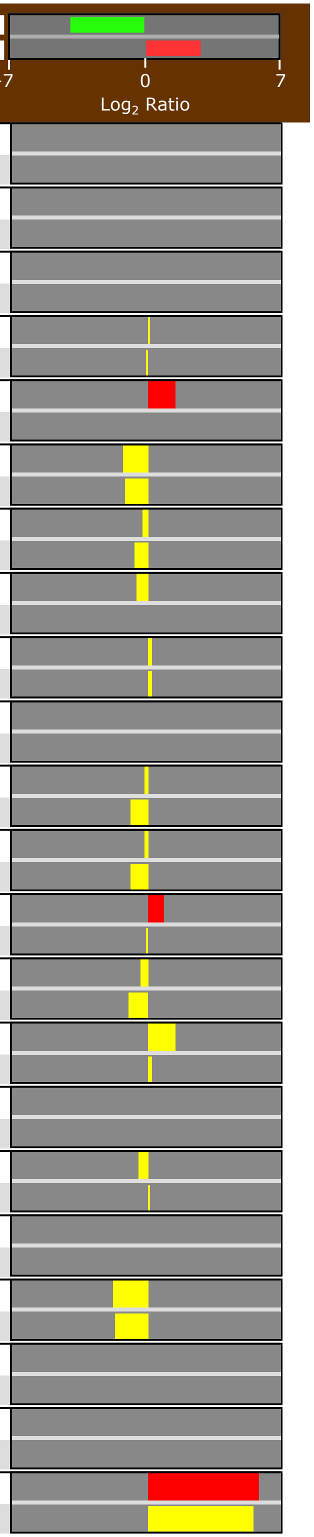


	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity							
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus		$\log_2$ Ratio
MFLA2566		1.521		1.521		Y	🟡	🟡	Y		19.530		19.530		Y	🟡	
	Heavy metal efflux pump CzcA [Methylobacillus flagellatus KT]637939492 YP_546672																
MFLA2567		0.521	2.322	2.686	-1.801	Y	🟡	🟡	Y		18.839	20.601	20.974	-1.762	Y	🟡	
	secretion protein HlyD [Methylobacillus flagellatus KT]637939493 YP_546673																
MFLA2568		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	outer membrane efflux protein [Methylobacillus flagellatus KT]637939494 YP_546674																
MFLA2569		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637939495 YP_546675																
MFLA2570		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637939496 YP_546676 """																
MFLA2571	0	9.587	10.324	11.002	-0.938	G	🟢	🟡	Y	1.96 E-1	30.319	30.617	31.476	-0.705	G	🟢	
	5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase [Methylobacillus flagellatus KT]637939497 YP_546677																
MFLA2572		3.744	2.889	4.379	0.718	Y	🟡	🔴	R	9.69 E-3	22.773	20.239	23.003	3.012	R	🔴	
	Catalase-like protein [Methylobacillus flagellatus KT]637939498 YP_546678																
MFLA2573		4.633	4.947	5.799	-0.249	Y	🟡	🟡	Y	5.38 E-2	22.229	22.961	23.641	-0.689	Y	🟡	
	isochorismatase hydrolase [Methylobacillus flagellatus KT]637939499 YP_546679																
MFLA2574		1.106	2.739	3.142	-0.632	Y	🟡	🟡	Y	7.24 E-2	20.079	20.625	21.377	0.462	Y	🟡	
	Pirin-like protein [Methylobacillus flagellatus KT]637939500 YP_546680																
MFLA2575			0.000	0.000		Y	🟡	🟡	Y			18.440	18.440		Y	🟡	
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637939501 YP_546681 """																
MFLA2576		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	" protein of unknown function DUF6, transmembrane [Methylobacillus flagellatus KT]637939502 YP_546682 """																
MFLA2577		1.521		1.521		Y	🟡	🟡	Y		18.994		18.994		Y	🟡	
	FAD-dependent pyridine nucleotide-disulphide oxidoreductase [Methylobacillus flagellatus KT]637939503 YP_546683																
MFLA2578		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637939504 YP_546684																
MFLA2579	0	6.568	3.654	6.748	2.935	R	🔴	🔴	R	7.71 E-3	24.644	22.551	24.948	2.211	R	🔴	
	hypothetical protein [Methylobacillus flagellatus KT]637939505 YP_546685																
MFLA2580		2.328	1.807	3.091	0.521	Y	🟡	🟡	Y		19.186	19.309	20.249	-0.122	Y	🟡	
	" transcriptional regulator, TetR family [Methylobacillus flagellatus KT]637939506 YP_546686 """																
MFLA2581		2.328	2.516	3.425	-0.188	Y	🟡	🟡	Y		21.304	22.345	22.917	-1.042	Y	🟡	
	" transcriptional regulator, MarR family [Methylobacillus flagellatus KT]637939507 YP_546687 """																
MFLA2582		1.106		1.106		Y	🟡	🟡	Y		18.410		18.410		Y	🟡	
	" RND efflux system, outer membrane lipoprotein, NodT [Methylobacillus flagellatus KT]637939508 YP_546688 """																
MFLA2583		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	Fusaric acid resistance protein conserved region [Methylobacillus flagellatus KT]637939509 YP_546689																
MFLA2584		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	protein of unknown function DUF1656 [Methylobacillus flagellatus KT]637939510 YP_546690																
MFLA2585		1.521	3.919	4.170	-1.399	Y	🟡	🟡	Y	9.64 E-2	19.169	22.183	22.352	-1.920	Y	🟡	
	secretion protein HlyD [Methylobacillus flagellatus KT]637939511 YP_546691																
MFLA2586		0.000	0.000				⬛	⬛			0.000	0.000				⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637939512 YP_546692																
MFLA2587	5.31 E-2	5.820	5.384	6.618	0.436	Y	🟡	🟡	Y	2.26 E-1	24.748	24.714	25.731	0.026	Y	🟡	
	multi-sensor hybrid histidine kinase [Methylobacillus flagellatus KT]637939513 YP_546693																

	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA2588		0.000	0.000			⬛ ⬛		0.000	0.000			⬛	
	" MCP methyltransferase, CheR-type [Methylobacillus flagellatus KT]637939514 YP_546694 """												
MFLA2589		0.000	0.000			⬛ ⬛		0.000	0.000			⬛	
	CheB methylesterase [Methylobacillus flagellatus KT]637939515 YP_546695												
MFLA2590		3.106	3.391	4.255	0.799	Y 🟡 🟡 Y	7.63 E-2	21.044	21.477	22.277	0.583	Y 🟡	
	response regulator receiver sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637939516 YP_546696												
MFLA2591	5.82 E-2	6.366	6.510	7.440	-0.145	Y 🟡 🟡 Y	4.29 E-2	25.858	26.755	27.375	-0.849	Y 🟡	
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637939517 YP_546697												
MFLA2592		0.000	0.000			⬛ ⬛		0.000	0.000			⬛	
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637939518 YP_546698 """												
MFLA2593		0.000	0.000			⬛ ⬛		0.000	0.000			⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637939519 YP_546699												
MFLA2594		3.930	1.540	4.182	2.447	Y 🟡 🟡 Y	7.09 E-2	22.377	21.096	22.874	1.100	Y 🟡	
	Uracil-DNA glycosylase superfamily [Methylobacillus flagellatus KT]637939520 YP_546700												
MFLA2595		0.000	0.000			⬛ ⬛		0.000	0.000			⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637939521 YP_546701												
MFLA2596		0.000	0.000			⬛ ⬛		0.000	0.000			⬛	
	proline-rich region [Methylobacillus flagellatus KT]637939522 YP_546702												
MFLA2597		0.000	0.000			⬛ ⬛		0.000	0.000			⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637939523 YP_546703												
MFLA2598		0.000	0.000			⬛ ⬛		0.000	0.000			⬛	
	hypothetical protein [Methylobacillus flagellatus KT]637939524 YP_546704												
MFLA2599	0	7.004	3.523	7.128	3.393	R 🔴 🔴 R	8.35 E-3	25.735	21.215	25.796	4.504	R 🔴	
	" 6-phosphogluconate dehydrogenase, decarboxylating [Methylobacillus flagellatus KT]637939525 YP_546705 """												
MFLA2600			3.540	3.540		Y 🟡 🟡 Y			22.592	22.592		Y 🟡	
	hypothetical protein [Methylobacillus flagellatus KT]637939526 YP_546706												
MFLA2601	4.18 E-2	4.621	5.073	5.865	0.548	Y 🟡 🟡 Y	1.73 E-1	22.446	24.179	24.559	-0.457	Y 🟡	
	PsiF [Methylobacillus flagellatus KT]637939527 YP_546707												
MFLA2602		6.464	6.816	7.651	-0.525	Y 🟡 🟡 Y	2.3 E-1	25.641	25.744	26.694	-0.089	Y 🟡	
	Carboxymethylenebutenolidase [Methylobacillus flagellatus KT]637939528 YP_546708												
MFLA2603		4.748	4.064	5.446	0.701	Y 🟡 🟡 Y	2.48 E-1	22.695	22.576	23.637	0.233	Y 🟡	
	restriction endonuclease [Methylobacillus flagellatus KT]637939529 YP_546709												
MFLA2604	1.16 E-1	5.642	5.643	6.643	0.007	Y 🟡 🟢 G	9.49 E-3	23.552	24.824	25.324	-1.277	Y 🟡	
	N-6 DNA methylase [Methylobacillus flagellatus KT]637939530 YP_546710												
MFLA2605		3.173	3.488	4.339	-0.417	Y 🟡 🟡 Y	2.07 E-2	21.527	22.423	23.043	-0.905	Y 🟡	
	virulence protein [Methylobacillus flagellatus KT]637939531 YP_546711												
MFLA2606		2.967	3.764	4.420	-0.757	Y 🟡 🟡 Y	1.28 E-1	21.522	22.197	22.899	-0.799	Y 🟡	
	restriction modification system DNA specificity domain [Methylobacillus flagellatus KT]637939532 YP_546712												
MFLA2607		6.080	6.515	7.314	-0.395	Y 🟡 🟡 Y	2.59 E-2	24.417	25.302	25.926	-0.867	Y 🟡	
	protein of unknown function DUF450 [Methylobacillus flagellatus KT]637939533 YP_546713												
MFLA2608		0.000	0.000			⬛ ⬛		0.000	0.000			⬛	
	[Methylobacillus flagellatus KT]639329604												
MFLA2609		4.949	4.098	5.585	0.858	Y 🟡 🟡 Y	2.25 E-1	23.671	23.546	24.610	0.075	Y 🟡	
	PfkB [Methylobacillus flagellatus KT]637939534 YP_546714												

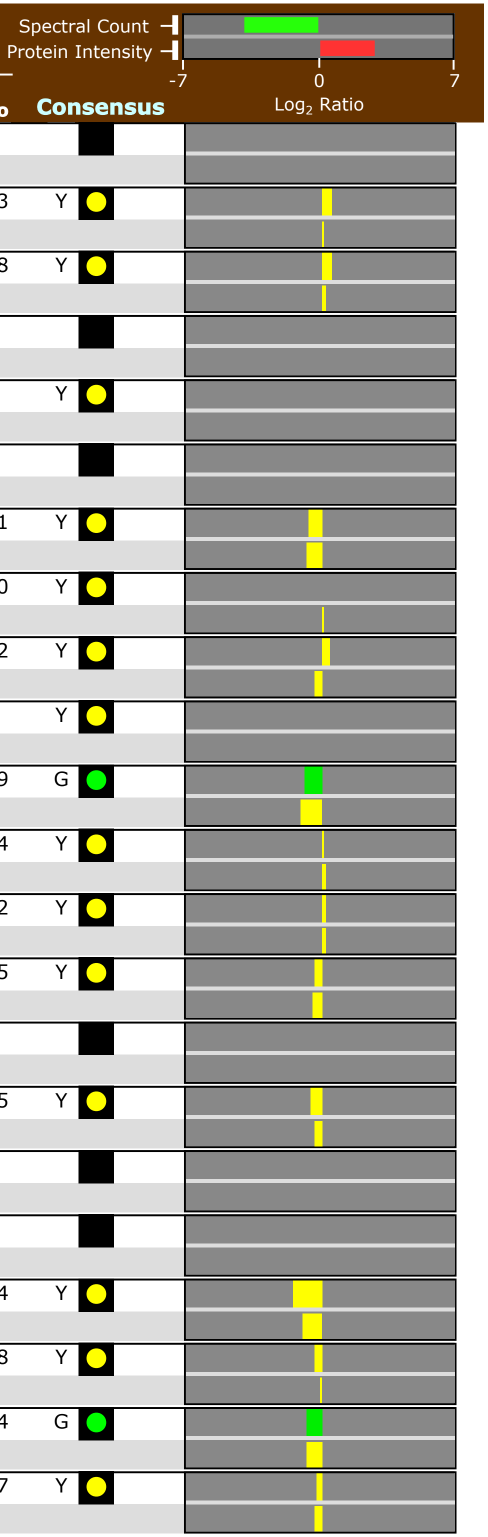
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA2610		4.294	2.226	4.603	1.994	Y	🟡	🟡	Y	9.64 E-2	21.637	20.262	22.108	1.000	Y	🟡
	" Sucrose-phosphate synthase, glycosyltransferase region [Methylobacillus flagellatus KT]637939535 YP_546715 """															
MFLA2611	4.16 E-2	4.929	4.880	5.905	-0.017	Y	🟡	🟡	Y	1.95 E-1	23.556	23.874	24.724	-0.309	Y	🟡
	" alpha amylase, catalytic region [Methylobacillus flagellatus KT]637939536 YP_546716 """															
MFLA2612		2.923	2.540	3.744	0.105	Y	🟡	🟡	Y	1.02 E-1	19.717	22.552	22.741	-0.955	Y	🟡
	MscS Mechanosensitive ion channel [Methylobacillus flagellatus KT]637939537 YP_546717															
MFLA2613		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939538 YP_546718															
MFLA2614		0.000	0.000				■	■			0.000	0.000				■
	" transcriptional regulator, ArsR family [Methylobacillus flagellatus KT]637939539 YP_546719 """															
MFLA2615		4.017	4.308	5.170	-0.328	Y	🟡	🟡	Y	3.03 E-2	23.468	24.662	25.185	-1.268	Y	🟡
	ProQ activator of osmoprotectant transporter ProP [Methylobacillus flagellatus KT]637939540 YP_546720															
MFLA2616		0.000	0.000				■	■			0.000	0.000				■
	NUDIX hydrolase [Methylobacillus flagellatus KT]637939541 YP_546721															
MFLA2617			1.825	1.825		Y	🟡	🟡	Y			21.436	21.436		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939542 YP_546722															
MFLA2618		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF182 [Methylobacillus flagellatus KT]637939543 YP_546723															
MFLA2619	7.57 E-13	8.198	7.447	8.871	0.749	R	🔴	🟡	Y	2.53 E-1	27.153	27.114	28.134	0.024	Y	🟡
	Twin-arginine translocation pathway signal [Methylobacillus flagellatus KT]637939544 YP_546724															
MFLA2620	1.81 E-2	5.777	5.721	6.749	-0.018	Y	🟡	🟡	Y	1.05 E-1	24.547	25.081	25.839	-0.612	Y	🟡
	(2Fe-2S)-binding [Methylobacillus flagellatus KT]637939545 YP_546725															
MFLA2621		3.294	2.410	3.919	0.862	Y	🟡	🟡	Y	9.62 E-2	22.271	20.584	22.661	1.139	Y	🟡
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637939546 YP_546726 """															
MFLA2622		0.000	0.000				■	■			0.000	0.000				■
	major facilitator superfamily MFS_1 [Methylobacillus flagellatus KT]637939547 YP_546727															
MFLA2623		0.000	0.000				■	■			0.000	0.000				■
	VanZ like protein [Methylobacillus flagellatus KT]637939548 YP_546728															
MFLA2624			0.000	0.000		Y	🟡	🟡	Y			18.058	18.058		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939549 YP_546729															
MFLA2625		0.000	0.000				■	■			0.000	0.000				■
	[Methylobacillus flagellatus KT]639329605															
MFLA2626		4.665	3.385	5.163	1.295	Y	🟡	🟡	Y	1.46 E-1	22.089	22.811	23.495	-0.265	Y	🟡
	diguanylate cyclase (GGDEF domain) [Methylobacillus flagellatus KT]637939550 YP_546730															
MFLA2627		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939551 YP_546731															
MFLA2628		4.774	5.012	5.898	-0.243	Y	🟡	🟡	Y	1.13 E-1	22.659	23.122	23.909	-0.610	Y	🟡
	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC and GAF sensor(s) [Methylobacillus flagellatus KT]637939552 YP_546732															
MFLA2629	1.98 E-2	5.167	4.891	6.035	0.216	Y	🟡	🟡	Y	1.77 E-1	24.096	24.244	25.172	-0.132	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939553 YP_546733															
MFLA2630		0.000	0.000				■	■			0.000	0.000				■
	major facilitator superfamily MFS_1 [Methylobacillus flagellatus KT]637939554 YP_546734															
MFLA2631		0.000	0.000				■	■			0.000	0.000				■
	Entericidin EcnAB [Methylobacillus flagellatus KT]637939555 YP_546735															





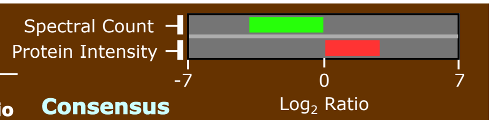
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA2632		0.521		0.521		Y	🟡	🟡	Y		18.491		18.491		Y	🟡
	" transcriptional regulator, LysR family [Methylobacillus flagellatus KT]637939556 YP_546736 """															
MFLA2633		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	DoxX [Methylobacillus flagellatus KT]637939557 YP_546737															
MFLA2634		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	" Extradiol ring-cleavage dioxygenase, class III enzyme, subunit B [Methylobacillus flagellatus KT]637939558 YP_546738 """															
MFLA2635		4.547	4.462	5.505	0.069	Y	🟡	🟡	Y	1.83 E-1	23.177	23.302	24.241	-0.095	Y	🟡
	MltA [Methylobacillus flagellatus KT]637939559 YP_546739															
MFLA2636	1.59 E-8	5.282	3.627	5.680	1.397	R	🔴	🟡	Y	2.43 E-1	23.702	23.623	24.663	-0.031	Y	🟡
	ApaG [Methylobacillus flagellatus KT]637939560 YP_546740															
MFLA2637		4.675	5.509	6.151	-1.303	Y	🟡	🟡	Y	5.2 E-2	24.179	25.520	26.000	-1.237	Y	🟡
	thiazole biosynthesis [Methylobacillus flagellatus KT]637939561 YP_546741															
MFLA2638		3.318	2.585	3.997	-0.333	Y	🟡	🟡	Y	4.63 E-2	23.362	23.017	24.200	-0.660	Y	🟡
	thiamine biosynthesis protein ThiS [Methylobacillus flagellatus KT]637939562 YP_546742															
MFLA2639		3.952	4.609	5.317	-0.633	Y	🟡	🟡	Y	2.29 E-1	23.056	23.126	24.092	-0.033	Y	🟡
	Tetratricopeptide TPR_2 [Methylobacillus flagellatus KT]637939563 YP_546743															
MFLA2640		3.159	3.213	4.186	0.155	Y	🟡	🟡	Y	2.31 E-1	20.985	20.665	21.834	0.206	Y	🟡
	DegT/DnrJ/EryC1/StrS aminotransferase [Methylobacillus flagellatus KT]637939564 YP_546744															
MFLA2641		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	acyl carrier protein [Methylobacillus flagellatus KT]637939565 YP_546745															
MFLA2642	1.09 E-1	5.515	5.733	6.628	-0.235	Y	🟡	🟡	Y	1.39 E-2	24.830	25.677	26.315	-0.863	Y	🟡
	3-oxoacyl-(acyl-carrier protein) synthase [Methylobacillus flagellatus KT]637939566 YP_546746															
MFLA2643		3.996	4.162	5.081	-0.173	Y	🟡	🟡	Y	1.23 E-1	21.615	22.201	22.938	-0.900	Y	🟡
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637939567 YP_546747															
MFLA2644	1.22 E-4	5.327	4.398	5.936	0.847	R	🔴	🟡	Y	2.72 E-1	22.687	22.702	23.695	-0.105	Y	🟡
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637939568 YP_546748															
MFLA2645		2.746	3.008	3.883	-0.443	Y	🟡	🟡	Y	1.11 E-1	20.548	21.866	22.352	-0.962	Y	🟡
	acetyltransferase [Methylobacillus flagellatus KT]637939569 YP_546749															
MFLA2646		2.521	2.226	3.381	1.394	Y	🟡	🟡	Y	1.52 E-1	21.393	22.179	22.839	0.236	Y	🟡
	Rieske (2Fe-2S) region [Methylobacillus flagellatus KT]637939570 YP_546750															
MFLA2647		0.813		0.813		Y	🟡	🟡	Y		18.842		18.842		Y	🟡
	hypothetical protein [Methylobacillus flagellatus KT]637939571 YP_546751															
MFLA2648	1.84 E-2	5.838	6.319	7.098	-0.484	Y	🟡	🟡	Y	2.22 E-1	24.858	24.797	25.828	0.076	Y	🟡
	Methyltransferase FkbM [Methylobacillus flagellatus KT]637939572 YP_546752															
MFLA2649		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	hypothetical protein [Methylobacillus flagellatus KT]637939573 YP_546753															
MFLA2650		3.270	4.669	5.133	-1.765	Y	🟡	🟡	Y	2.39 E-2	21.868	23.262	23.727	-1.706	Y	🟡
	" glycosyl transferase, family 2 [Methylobacillus flagellatus KT]637939574 YP_546754 """															
MFLA2651		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	CsbD-like protein [Methylobacillus flagellatus KT]637939575 YP_546755															
MFLA2652		0.000	0.000				⬛	⬛			0.000	0.000				⬛
	1-aminocyclopropane-1-carboxylate deaminase-like protein [Methylobacillus flagellatus KT]637939576 YP_546756															
MFLA2653	0	6.773	0.000	6.786	5.692	R	🔴	🟡	Y	1.16 E-1	25.075	18.267	25.088	5.419	R	🔴
	TonB-dependent receptor [Methylobacillus flagellatus KT]637939577 YP_546757															

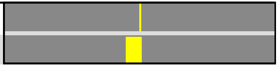
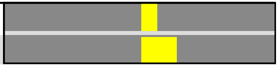
	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Sc Sum	log$_2$Ratio	Regulation				*q*-value	log$_2$ Methylamine	log$_2$ Methanol	log$_2$ Pi Sum	log$_2$Ratio	Consensus	
MFLA2654		0.000	0.000				■	■			0.000	0.000				■
	major facilitator superfamily MFS_1 [Methylobacillus flagellatus KTJ637939579 YP_546758															
MFLA2655		5.719	5.098	6.442	0.503	Y	🟡	🟡	Y	2.02 E-1	24.656	24.518	25.589	0.093	Y	🟡
	response regulator receiver (CheY-like) modulated metal dependent phosphohydrolase [Methylobacillus flagellatus KTJ637939580 YP_546759															
MFLA2656		4.481	3.924	5.229	0.523	Y	🟡	🟡	Y	2.18 E-1	23.088	22.820	23.960	0.158	Y	🟡
	multi-sensor hybrid histidine kinase [Methylobacillus flagellatus KTJ637939581 YP_546760															
MFLA2657		0.000	0.000				■	■			0.000	0.000				■
	Enoyl-CoA hydratase/isomerase [Methylobacillus flagellatus KTJ637939582 YP_546761															
MFLA2658		4.080		4.080		Y	🟡	🟡	Y		23.375		23.375		Y	🟡
	membrane protein involved in aromatic hydrocarbon degradation [Methylobacillus flagellatus KTJ637939583 YP_546762															
MFLA2659		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KTJ637939584 YP_546763															
MFLA2660		4.435	5.093	5.801	-0.657	Y	🟡	🟡	Y	2.7 E-2	24.365	25.223	25.857	-0.841	Y	🟡
	UspA [Methylobacillus flagellatus KTJ637939585 YP_546764															
MFLA2661	5.74 E-2	5.631	5.541	6.587	0.043	Y	🟡	🟡	Y	2.23 E-1	23.979	23.906	24.943	0.070	Y	🟡
	" ATPase, E1-E2 type [Methylobacillus flagellatus KTJ637939586 YP_546765 """															
MFLA2662		4.696	4.281	5.504	0.436	Y	🟡	🟡	Y	2.66 E-1	24.496	24.548	25.522	-0.362	Y	🟡
	Phosphomethylpyrimidine kinase [Methylobacillus flagellatus KTJ637939587 YP_546766															
MFLA2663			1.184	1.184		Y	🟡	🟡	Y			20.634	20.634		Y	🟡
	thiamine-phosphate pyrophosphorylase [Methylobacillus flagellatus KTJ637939588 YP_546767															
MFLA2664	3.6 E-4	4.787	5.689	6.308	-0.949	G	🟢	🟡	Y	1.17 E-2	24.467	25.622	26.157	-1.149	G	🟢
	" glutamate-1-semialdehyde-2,1-aminomutase [Methylobacillus flagellatus KTJ637939589 YP_546768 """															
MFLA2665		1.843	2.739	3.360	0.105	Y	🟡	🟡	Y	2.71 E-1	18.846	19.883	20.456	0.184	Y	🟡
	hypothetical protein [Methylobacillus flagellatus KTJ637939590 YP_546769															
MFLA2666		4.875	4.654	5.769	0.212	Y	🟡	🟡	Y	2.08 E-1	24.028	23.811	24.923	0.232	Y	🟡
	uroporphyrinogen decarboxylase [Methylobacillus flagellatus KTJ637939591 YP_546770															
MFLA2667		7.967	8.439	9.222	-0.427	Y	🟡	🟡	Y	8.94 E-3	27.545	28.017	28.800	-0.475	Y	🟡
	Peptidoglycan-binding LysM [Methylobacillus flagellatus KTJ637939592 YP_546771															
MFLA2668		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KTJ637939593 YP_546772															
MFLA2669		5.638	6.115	6.896	-0.640	Y	🟡	🟡	Y	1.15 E-1	25.272	25.631	26.463	-0.355	Y	🟡
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KTJ637939594 YP_546773															
MFLA2670		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KTJ637939595 YP_546774															
MFLA2671		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KTJ637939596 YP_546775															
MFLA2672		0.521	2.000	2.442	-1.479	Y	🟡	🟡	Y		19.312	20.316	20.899	-1.004	Y	🟡
	primosomal protein N' [Methylobacillus flagellatus KTJ637939597 YP_546776															
MFLA2673	1.74 E-4	7.864	8.224	9.055	-0.351	Y	🟡	🟡	Y	2.72 E-1	26.581	26.560	27.571	-0.148	Y	🟡
	arginyl-tRNA synthetase [Methylobacillus flagellatus KTJ637939598 YP_546777															
MFLA2674	2.78 E-3	4.701	5.450	6.123	-0.772	G	🟢	🟡	Y	3.86 E-2	24.827	25.622	26.279	-0.824	G	🟢
	Sporulation related [Methylobacillus flagellatus KTJ637939599 YP_546778															
MFLA2675		7.347	7.664	8.514	-0.275	Y	🟡	🟡	Y	1.13 E-1	27.977	28.388	29.197	-0.387	Y	🟡
	DSBA oxidoreductase [Methylobacillus flagellatus KTJ637939600 YP_546779															



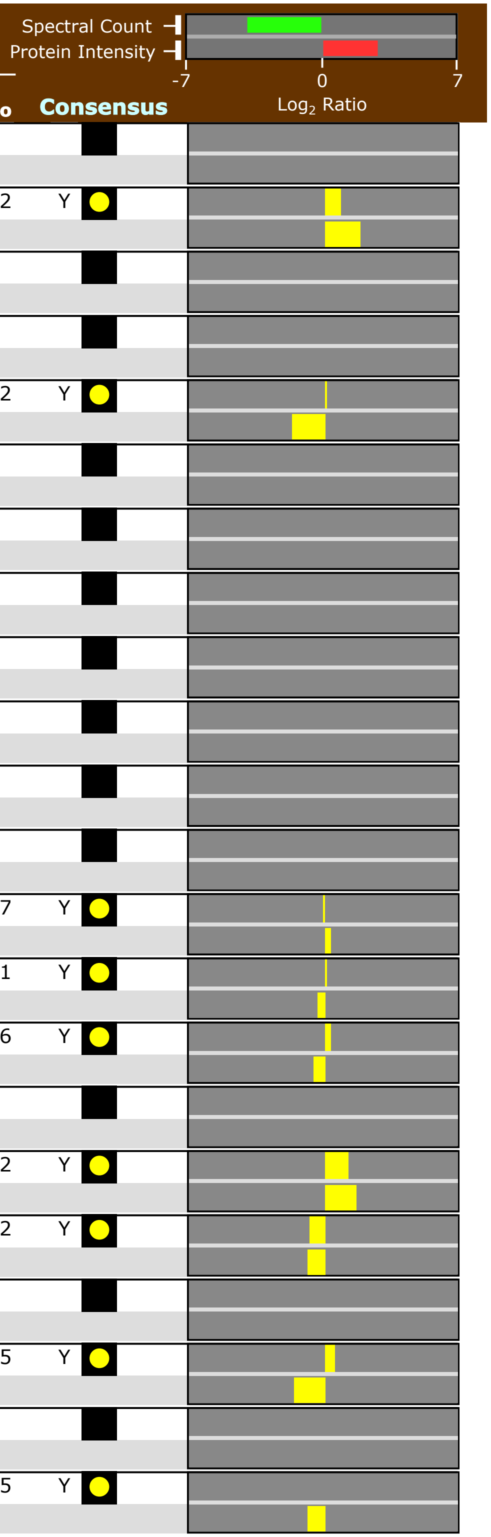
Spectral Count 🟩
Protein Intensity 🟥
-7 0 7
$\log_2$ Ratio

ORF	AM/OH *M Flagellatus* Spectral Count *q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	AM/OH *M Flagellatus* Protein Intensity *q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus
MFLA2676		0.000	0.000			■ ■		0.000	0.000			■
	short-chain dehydrogenase/reductase SDR [Methylobacillus flagellatus KT]637939601 YP_546780											
MFLA2677		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939602 YP_546781											
MFLA2678		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939603 YP_546782											
MFLA2679		0.000	0.000			■ ■		0.000	0.000			■
	TonB-dependent receptor [Methylobacillus flagellatus KT]637939604 YP_546783											
MFLA2680		0.000	0.000			■ ■		0.000	0.000			■
	putative FecR [Methylobacillus flagellatus KT]637939605 YP_546784											
MFLA2681		0.000	0.000			■ ■		0.000	0.000			■
	sigma-24 (FecI-like) [Methylobacillus flagellatus KT]637939606 YP_546785											
MFLA2682		1.521		1.521	Y	● ●	Y	18.823		18.823	Y	●
	DNA adenine methylase [Methylobacillus flagellatus KT]637939607 YP_546786											
MFLA2683		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939608 YP_546787											
MFLA2684		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939609 YP_546788											
MFLA2685		0.000	0.000			■ ■		0.000	0.000			■
	Phage-related protein tail component-like protein [Methylobacillus flagellatus KT]637939610 YP_546789											
MFLA2686		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939611 YP_546790											
MFLA2687		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939612 YP_546791											
MFLA2688		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939613 YP_546792											
MFLA2689		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939614 YP_546793											
MFLA2690		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939615 YP_546794											
MFLA2691		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939616 YP_546795											
MFLA2692		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939617 YP_546796											
MFLA2693		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939618 YP_546797											
MFLA2694		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939619 YP_546798											
MFLA2695		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939620 YP_546799											
MFLA2696			2.562	2.562	Y	● ●	Y		21.401	21.401	Y	●
	hypothetical protein [Methylobacillus flagellatus KT]637939621 YP_546800											
MFLA2697		0.000	0.000			■ ■		0.000	0.000			■
	hypothetical protein [Methylobacillus flagellatus KT]637939622 YP_546801											



	AM/OH *M Flagellatus* Spectral Count						AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	Log$_2$ Ratio
MFLA2698		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939623 YP_546802												
MFLA2699		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939624 YP_546803												
MFLA2700		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939625 YP_546804												
MFLA2701		0.000	0.000			■ ■		0.000	0.000			■	
	Mu-like prophage FluMu protein gp28-like [Methylobacillus flagellatus KT]637939626 YP_546805												
MFLA2702		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939627 YP_546806												
MFLA2703		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939628 YP_546807												
MFLA2704		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939629 YP_546808												
MFLA2705		0.000	0.000			■ ■		0.000	0.000			■	
	" transcriptional regulators, TraR/DksA family [Methylobacillus flagellatus KT]637939630 YP_546809 """												
MFLA2706		0.000	0.000			■ ■		0.000	0.000			■	
	bacteriophage lysis protein [Methylobacillus flagellatus KT]637939631 YP_546810												
MFLA2707		0.000	0.000			■ ■		0.000	0.000			■	
	" N-acetylmuramoyl-L-alanine amidase, family 2 [Methylobacillus flagellatus KT]637939632 YP_546811 """												
MFLA2708		1.813	2.871	3.437	-0.056	Y ● ● Y	1.01 E-1	18.745	20.596	20.949	-0.814	Y ●	
	hypothetical protein [Methylobacillus flagellatus KT]637939633 YP_546812												
MFLA2709		4.687	2.907	5.056	0.771	Y ● ● Y	1.4 E-1	25.025	21.689	25.161	1.765	Y ●	
	hypothetical protein [Methylobacillus flagellatus KT]637939634 YP_546813												
MFLA2710			2.000	2.000		Y ● ● Y			21.637	21.637		Y ●	
	" transcriptional regulator, XRE family [Methylobacillus flagellatus KT]637939635 YP_546814 """												
MFLA2711		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939636 YP_546815												
MFLA2712		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939637 YP_546816												
MFLA2713		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939638 YP_546817												
MFLA2714		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939639 YP_546818												
MFLA2715		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939640 YP_546819												
MFLA2716			0.000	0.000		Y ● ● Y			18.280	18.280		Y ●	
	hypothetical protein [Methylobacillus flagellatus KT]637939641 YP_546820												
MFLA2717		0.000	0.000			■ ■		0.000	0.000			■	
	conserved hypothetical phage-related protein [Methylobacillus flagellatus KT]637939642 YP_546821												
MFLA2718		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939643 YP_546822												
MFLA2719		0.000	0.000			■ ■		0.000	0.000			■	
	hypothetical protein [Methylobacillus flagellatus KT]637939644 YP_546823												

	AM/OH *M Flagellatus* Spectral Count									AM/OH *M Flagellatus* Protein Intensity						
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation				*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	Consensus	
MFLA2720		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939645 YP_546824															
MFLA2721		0.813	0.000	1.463	0.813	Y	●	●	Y		20.506	18.754	20.881	1.752	Y	●
	hypothetical protein [Methylobacillus flagellatus KT]637939646 YP_546825															
MFLA2722		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939647 YP_546826															
MFLA2723		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939648 YP_546827															
MFLA2724	1.49 E-2	5.064	5.014	6.039	0.059	Y	●	●	Y	3.96 E-2	21.691	22.969	23.467	-1.712	Y	●
	histone-like DNA-binding protein [Methylobacillus flagellatus KT]637939649 YP_546828															
MFLA2725		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939650 YP_546829															
MFLA2726		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939651 YP_546830															
MFLA2727		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939652 YP_546831															
MFLA2728		0.000	0.000				■	■			0.000	0.000				■
	protein of unknown function DUF1018 [Methylobacillus flagellatus KT]637939653 YP_546832															
MFLA2729		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939654 YP_546833															
MFLA2730		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939655 YP_546834															
MFLA2731		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939656 YP_546835															
MFLA2732		2.761	2.627	3.696	-0.056	Y	●	●	Y	1.59 E-1	21.986	21.423	22.732	0.257	Y	●
	Sel1 [Methylobacillus flagellatus KT]637939657 YP_546836															
MFLA2733	1.48 E-1	5.985	5.864	6.926	0.121	Y	●	●	Y	4.07 E-2	24.616	24.993	25.817	-0.391	Y	●
	flavodoxin/nitric oxide synthase [Methylobacillus flagellatus KT]637939658 YP_546837															
MFLA2734		7.200	6.892	8.055	0.288	Y	●	●	Y	1.66 E-2	25.104	25.650	26.402	-0.556	Y	●
	Glutamate synthase (NADPH) [Methylobacillus flagellatus KT]637939659 YP_546838															
MFLA2735		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939660 YP_546839															
MFLA2736		3.844	2.788	4.411	1.210	Y	●	●	Y	4.29 E-2	21.440	19.994	21.891	1.572	Y	●
	putative FecR [Methylobacillus flagellatus KT]637939661 YP_546840															
MFLA2737		5.020	5.689	6.393	-0.831	Y	●	●	Y	1.06 E-1	24.025	24.641	25.366	-0.942	Y	●
	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains) with PAS/PAC sensor(s) [Methylobacillus flagellatus KT]637939662 YP_546841															
MFLA2738		0.000	0.000				■	■			0.000	0.000				■
	periplasmic sensor signal transduction histidine kinase [Methylobacillus flagellatus KT]637939663 YP_546842															
MFLA2739	4.16 E-2	5.341	4.839	6.112	0.489	Y	●	●	Y	4.25 E-2	22.865	24.151	24.647	-1.565	Y	●
	" two component transcriptional regulator, winged helix family [Methylobacillus flagellatus KT]637939664 YP_546843 """															
MFLA2740		0.000	0.000				■	■			0.000	0.000				■
	hypothetical protein [Methylobacillus flagellatus KT]637939665 YP_546844															
MFLA2741	8.68 E-2	6.511	6.506	7.509	0.004	Y	●	●	Y	1.89 E-2	25.287	26.171	26.795	-0.905	Y	●
	" glucosamine--fructose-6-phosphate aminotransferase, isomerizing [Methylobacillus flagellatus KT]637939666 YP_546845 """															



	AM/OH *M Flagellatus* Spectral Count							AM/OH *M Flagellatus* Protein Intensity					
ORF	*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Sc Sum	$\log_2$Ratio	Regulation		*q*-value	$\log_2$ Methylamine	$\log_2$ Methanol	$\log_2$ Pi Sum	$\log_2$Ratio	**Consensus**
MFLA2742	2.56 E-2	5.969	5.734	6.857	0.178	Y 🟡	🟡 Y	4.38 E-2	23.481	24.459	25.051	-1.214	Y 🟡
	UDP-N-acetylglucosamine pyrophosphorylase [Methylobacillus flagellatus KT]637939667 YP_546846												
MFLA2743	3.42 E-5	6.349	6.993	7.707	-0.629	G 🟢	🟡 Y	2.27 E-1	26.754	26.562	27.661	-0.018	Y 🟡
	" ATP synthase F1, epsilon subunit [Methylobacillus flagellatus KT]637939668 YP_546847 """												
MFLA2744	0	11.115	11.685	12.428	-0.567	G 🟢	🟡 Y	3.85 E-2	31.688	31.928	32.813	-0.235	G 🟢
	" ATP synthase F1, beta subunit [Methylobacillus flagellatus KT]637939669 YP_546848 """												
MFLA2745	1.09 E-13	8.496	7.809	9.193	0.684	R 🔴	🟡 Y	2.07 E-1	27.846	27.951	28.900	-0.153	Y 🟡
	" ATP synthase F1, gamma subunit [Methylobacillus flagellatus KT]637939670 YP_546849 """												
MFLA2746	0	10.562	10.895	11.738	-0.346	Y 🟡	🟡 Y	1.66 E-2	31.242	31.464	32.357	-0.222	Y 🟡
	" ATP synthase F1, alpha subunit [Methylobacillus flagellatus KT]637939671 YP_546850 """												
MFLA2747	0	8.919	9.755	10.397	-0.859	G 🟢	🟡 Y	7.03 E-2	27.577	28.078	28.849	-0.575	G 🟢
	" ATP synthase F1, delta subunit [Methylobacillus flagellatus KT]637939672 YP_546851 """												
MFLA2748	0	6.468	7.612	8.151	-1.132	G 🟢	🟡 Y	1.32 E-2	26.542	28.077	28.505	-1.693	G 🟢
	" ATP synthase F0, B subunit [Methylobacillus flagellatus KT]637939673 YP_546852 """												
MFLA2749		0.000	0.000			■	■		0.000	0.000			■
	" ATP synthase F0, C subunit [Methylobacillus flagellatus KT]637939674 YP_546853 """												
MFLA2750		0.000	0.000			■	■		0.000	0.000			■
	" ATP synthase F0, A subunit [Methylobacillus flagellatus KT]637939675 YP_546854 """												
MFLA2751		0.000	0.000			■	■		0.000	0.000			■
	ATP synthase protein I [Methylobacillus flagellatus KT]637939676 YP_546855												
MFLA2752		6.485	6.913	7.714	-0.488	Y 🟡	🟡 Y	1.59 E-1	26.132	26.242	27.188	-0.128	Y 🟡
	parB-like partition proteins [Methylobacillus flagellatus KT]637939677 YP_546856												
MFLA2753	4.48 E-11	6.054	4.341	6.438	1.731	R 🔴	🟡 Y	5.93 E-2	24.120	22.585	24.548	1.481	R 🔴
	" Cobyrinic acid a,c-diamide synthase [Methylobacillus flagellatus KT]637939678 YP_546857 """												
MFLA2754		1.843	3.334	3.773	-0.492	Y 🟡	🟡 Y	2.04 E-1	21.892	22.999	23.549	-0.090	Y 🟡
	methyltransferase GidB [Methylobacillus flagellatus KT]637939679 YP_546858												
MFLA2755	1.38 E-1	5.723	5.646	6.685	0.066	Y 🟡	🟡 Y	9.14 E-2	23.929	24.329	25.143	-0.356	Y 🟡
	glucose inhibited division protein A [Methylobacillus flagellatus KT]637939680 YP_546859												
MFLA2756		0.000	0.000			■	■		0.000	0.000			■
	protein of unknown function DUF1555 [Methylobacillus flagellatus KT]637939681 YP_546860												
MFLA2757		4.700	5.218	5.982	-0.521	Y 🟡	🟡 Y	1.49 E-1	22.658	22.998	23.838	-0.516	Y 🟡
	tRNA modification GTPase TrmE [Methylobacillus flagellatus KT]637939682 YP_546861												
MFLA2758	4.46 E-2	6.542	6.430	7.487	0.110	Y 🟡	🟡 Y	5.07 E-2	26.121	26.757	27.474	-0.692	Y 🟡
	60 kDa inner membrane insertion protein [Methylobacillus flagellatus KT]637939683 YP_546862												
MFLA2759		0.000	0.000			■	■		0.000	0.000			■
	protein of unknown function DUF37 [Methylobacillus flagellatus KT]637939684 YP_546863												
MFLA2760		1.106		1.106		Y 🟡	🟡 Y		20.977		20.977		Y 🟡
	ribonuclease P protein component [Methylobacillus flagellatus KT]637939685 YP_546864												
MFLA2761		0.000	0.000			■	■		0.000	0.000			■
	ribosomal protein L34 [Methylobacillus flagellatus KT]637939686 YP_546865