

Number	Enzyme or protein	Amino acid	NCBI accession number of FWC3	NCBI accession number <i>Mtc</i> C50C1 ^a	% similarity with <i>Mtc</i> C50C1 ^a	Second hit organism name	NCBI accession number of second hit	% similarity
1	6-phosphogluconolactonase	231 aa	WP_129882445.1	WP_139557518.1	98.26	Betaproteobacteria bacterium CG2_30_59_46	OIP15690.1	57.59
2	Fructokinase (ROK family protein)	299 aa	WP_129882255.1	WP_139556626.1	96.32	Gallionellaceae bacterium	HAF45922.1	67.23
3	GDP-L-fucose synthase	318 aa	WP_129883562.1	WP_139556465.1	98.74	Azohydromonas australica DSM1124	WP_028996357.1	84.11
4	GDP-mannose 4,6-dehydratase	370 aa	WP_129883561.1	WP_139556231.1	98.92	Herbaspirillum sp. YR522	WP_008117390.1	85.33
5	glucose-6-phosphate dehydrogenase	501 aa	WP_129884235.1	WP_139556040.1	99.40	Sulfuricella denitrificans skB26	WP_009206042.1	76.65
6	glycogen/starch/alpha-glucan phosphorylase	842 aa	WP_129884174.1	WP_139558140.1	98.57	Steroidobacter cummioxidans 35Y	WP_116808655.1	73.18
7	glycoside hydrolase family 15 protein	599	WP_129883816.1	WP_139559763.1	99.0	Rhodocyclales bacterium GWA2_65_20]	OHC 71177.1	70.92
8	glycoside hydrolase family 19 protein	533 aa	WP_129882702.1	WP_139558581.1	96.44	Thauera phenylacetica strain B4P	WP_004356967.1	52.50
9	peptidase domain-containing ABC transporter RaxB, CvaB	721 aa	WP_129882739.1	WP_139558511.1	98.61	Ramlibacter tataouinensis 5-10	WP_061500227.1	65.31
10	phosphoenolpyruvate carboxylase	933 aa	WP_129884765.1	WP_139556855.1	97.96	Sulfuritortus calidifontis	WP_126463503.1	66.15
11	sulfate ABC transporter permease subunit CysT	284 aa	WP_129884108.1	WP_139558079.1	98.94	Variovorax paradoxus MEDvA23	WP_042579714.1	76.69
12	sulfate ABC transporter permease subunit CysW	287 aa	WP_129884107.1	WP_139558078.1	99.30	Ralstonia pickettii 52	WP_102067084.1	75.00
13	trehalose-6-phosphate synthase	748 aa	WP_129883814.1	WP_139559761.1	99.73	Betaproteobacteria bacterium RIFCSPLOWO2_12_FULL_6	OGA44806.1	69.07

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14	trehalose-phosphatase	298 aa	WP_129883 815.1	WP_139559 762.1	96.98	Betaproteobacteria bacterium RIFCSPLOWO2_12_FULL_6 3_13	OGA48694.1	53.09
15	ABC transporter ATP-binding protein/permease	581 aa	WP_129883 270.1	WP_139559 302.1	97.76	<i>Candidatus</i> Rokubacteria bacterium	PYM41203.1	56.78
16	ATP-binding cassette domain-containing protein	271 aa	WP_129884 167.1	WP_139558 133.1	93.36	<i>Syntrophobacter fumaroxidans</i> MPOB	WP_0116992 64.1	70.24
17	lipopolysaccharide transport system ATP- binding protein / sugar ABC transporter ATP-binding protein	251 aa	WP_129883 429.1	WP_139559 602.1	99.60	<i>Rhodospirillaceae</i> bacterium	MBC93340.1	58.61
18	acetyl-CoA C-acetyltransferase	455 aa	WP_129883 845.1	WP_139558 891.1	96.46	Beta-ketoadipyl-CoA thiolase Chromatiales bacterium USCg_Taylor	OOO02342.1	96.46
19	acyl-CoA dehydrogenase	749 aa	WP_129883 844.1	WP_139558 892.1	97.60	<i>Ectothiorhodospiraceae</i> bacterium	PCI79469.1	53.95
20	heme exporter protein CcmB	225 aa	WP_129884 534.1	WP_139558 769.1	99.11	<i>Oceanospirillum</i> sp. MED92] gammaproteobacterium	EAR60549.1	64.29
21	molybdenum ABC transporter ATP- binding protein modC	360a a	WP_129883 634.1	WP_139557 358.1	90.17	<i>Pseudomonas oryzae</i> KCTC 32247	WP_0903486 04.1	71.31
22	nitrite reductase small subunit NirD	105 aa	WP_129883 834.1	WP_139558 902.1	98.10	Gammaproteobacteria bacterium RBG_16_57_12	OGT20932.1	64.42
23	phosphate ABC transporter substrate- binding protein	366 aa	WP_129884 923.1	WP_139557 160.1	98.36	<i>Thiobaca trueperi</i> DSM13587, Chromatiales	WP_1329750 72.1	46.36
24	polysialic acid transporter	497 aa	WP_129884 639.1	WP_139558 707.1	99.20	Gammaproteobacteria bacterium HGW	PKM43078.1	63.80
25	6-phosphofructokinase	376 aa	WP_129882 862.1	WP_139559 117.1	98.14	Lentisphaerae bacterium GWF2_44_16	OGV48853.1	66.76
26	Hypothetical protein (pyruvate, water dikinase)	750 aa	WP_129882 846.1	WP_139559 154.1	95.07	<i>Planctomycetaceae</i> bacterium	HBO43257.1	48.61
27	iron ABC transporter permease	550 aa	WP_129883 353.1	WP_139559 362.1	95.45	<i>Verrucomicrobiales</i> bacterium	HCN28513.1	72.63

28	NADP-dependent phosphogluconate dehydrogenase	500 aa	WP_129884 256.1	WP_139556 061.1	98.00	<i>Bryobacter aggregatus</i> MPL3 (Acidobacteria)	WP_0314999 22.1	78.56
29	triose-phosphate isomerase	249 aa	WP_129884 669.1	WP_139558 948.1	99.20	<i>Alkalitalea saponilacus</i> (Bacteroidetes)	WP_0795578 72.1	68.53
30	Cobalamin B12 containing domain binding protein	144	WP_129883 681	WP_139557 831.1	97	Nitrospirae bacterium	TAJ08022.1	67
31	Enoyl-CoA hydratase/ methylmalonyl-CoA decarboxylase	259 aa	WP_129883 684.1	WP_139557 828.1	97.68	Nitrospirae bacterium	TAJ08019.1	70.66
32	Enoyl-CoA hydratase/ methylmalonyl-CoA decarboxylase	274 aa	WP_129883 790.1	WP_139557 828.1	96.45	Nitrospirae bacterium	TAJ08019.1	76.22
33	UDP-glucose 4-epimerase/SDR family oxidoreductase	318 aa	WP_129884 039.1	WP_139557 409.1	93.08	<i>Geobacter bemidjiensis</i>	WP_0125300 59.1	54.06
34	formate dehydrogenase subunit alpha	714 aa	WP_129883 233.1	WP_139559 514.1	98.04	Proteobacteria bacterium ST_bin11	OQW79218.1	83.33
35	long-chain fatty acid--CoA ligase	626 aa	WP_129883 847.1	WP_139558 889.1	90.73	Bacterium BMS3Bbin13	GBE50223.1	47.45
36	formate-C-acetyl-transferase	743 aa	WP_129885 015.1	WP_139556 721.1	99.06	<i>Hydrogenispora ethanolica</i>	WP_1320132 57.1	77.04
37	Dicarboxylate/amino acid symporter	443 aa	WP_129884 521.1	WP_139558 757.1	99.32 %	Cyanobacteria bacterium UBA11372	HAX77537.1	52.21 %
38	glycoside hydrolase family 16 protein	291	WP_129883 504.1	Absent	absent	<i>Mesorhizobium</i> sp.	TIX81999.1	47.83
39	Alpha-L-Rha alpha-1,2-L-rhamnosyltransferase	1130 aa	WP_129883 427.1	Absent	absent	<i>Lamprocystis purpurea</i>	WP_0839249 96.1	59.96

Supplementary Table 1: Blast hits of genes which have been horizontal transferred. The first hit ^a in all the cases is *Methylothermobacter oryzae* C50C1 (*Mtt* C50C1) (except 35) whereas the second hit is from a different family/ class/ phylum. The yellow highlighted proteins show absence in *Mtc* C50C1 and are only present in FWC3. The blue highlighted proteins show that these could be horizontally transferred from Betaproteobacteria. The green highlighted proteins are ATP binding permeases.

Suppl. Table 2

Enzyme	NCBI Accession	Amino	Closest hit	NCBI Accession	Percent
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	number	acid		number	identity
Particulate methane monooxygenase C-subunit	WP_129883940.1	250 aa	Methylobacterium oryzae C50C1	WP_139556830.1	100
Particulate methane monooxygenase A-subunit	WP_129883941.1	247 aa	Methylobacterium oryzae C50C1	WP_139559040.1	97.98
Particulate methane monooxygenase B-subunit	WP_129884071.1	414 aa	Methylobacterium oryzae C50C1	WP_129884071.1	100
Particulate methane monooxygenase C-subunit	WP_129884881.1	293 aa	Methylobacterium oryzae C50C1	WP_139558021.1	97.95
Particulate methane monooxygenase C-subunit	RYU58954.1	35 aa	Methylobacterium oryzae C50C1	WP_139558060.1	100
Methanol dehydrogenase (mxhF)	WP_129883290.1	186 aa	Methylobacterium oryzae C50C1	WP_139559320.1	97.31
PQQ-dependent dehydrogenase, methanol/ethanol family	WP_129883571.1	620 aa	Methylobacterium oryzae 73a	WP_045226110.1	90.65
formate dehydrogenase subunit delta	WP_129882291.1	81 aa	Methylobacterium oryzae C50C1	WP_139556591.1	98.77
formate dehydrogenase accessory sulfurtransferase FdhD	WP_129882292.1	274 aa	Methylobacterium oryzae C50C1	WP_139556590.1	98.54
formate dehydrogenase subunit alpha (molybdenum)	WP_129882293.1	948 aa	Methylobacterium oryzae C50C1	WP_139556589.1	98.84
formate dehydrogenase subunit gamma	WP_129882295.1	158 aa	Methylobacterium oryzae C50C1	WP_139556587.1	98.10

formate dehydrogenase subunit alpha	WP_129883233.1	714 aa	Methylothermobacter oryzae C50C1	WP_139559514.1	98.04
Hypothetical protein (formate dehydrogenase subunit delta)	WP_129883234.1	99 aa	Methylococcus sp.	RQW79128.1	75.56
formate dehydrogenase accessory protein FdhE	WP_129883430.1	316 aa	Methylothermobacter oryzae C50C1	WP_139559603.1	92.31
formate dehydrogenase-N subunit alpha (nitrate inducible)	WP_129883870.1	1065 aa	Methylothermobacter oryzae C50C1	WP_139558858.1	98.12
formate dehydrogenase subunit beta	WP_129883871.1	290 aa	Methylothermobacter oryzae C50C1	WP_139558857.1	97.93
formate dehydrogenase subunit gamma	WP_129883872.1	214 aa	Methylothermobacter oryzae C50C1	WP_139558856.1	95.79
serine hydroxymethyltransferase	WP_129883539.1	418 aa	aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme [Methylothermobacter oryzae C50C1]	WP_139556254.1	99.04
Enolase (phosphopyruvate hydratase)	WP_129884748.1	427 aa	Methylocaldum sp. 0917	WP_133717242.1	81.41
phosphoenolpyruvate carboxylase	WP_129884765.1	933 aa	Methylothermobacter oryzae C50C1	WP_139556855.1	97.96
malate dehydrogenase	WP_129884035.1	325 aa	Methylothermobacter oryzae C50C1	WP_139557413.1	96.92
CoA ester lyase (malyl-CoA/(S)-citramalyl-CoA lyase)	WP_129882552.1	323 aa	Methylothermobacter oryzae C50C1	WP_139555806.1	99.38

class II fructose-bisphosphate aldolase	WP_129884379.1	359 aa	Methyloctetracoccus oryzae C50C1	WP_139556105.1	99.72
class 1 fructose-bisphosphatase	WP_129884928.1	332 aa	Methyloctetracoccus oryzae C50C1	WP_139557154.1	98.49
6-phosphofructokinase	WP_129882862.1	376 aa	ATP-dependent phosphofructokinase (Methyloctetracoccus oryzae C50C1)	WP_139559117.1	98.14
6-phospho-3-hexuloisomerase	WP_129884377.1	177 aa	Methylocaldum marinum S8	WP_119628761.1	85.88
3-hexulose-6-phosphate synthase	WP_129884177.1	389 aa	Methyloctetracoccus oryzae C50C1	WP_139558143.1	99.74
3-hexulose-6-phosphate synthase	WP_129884376.1	213 aa	Methylocaldum sp. SAD2	WP_086133943.1	91.04
formylmethanofuran dehydrogenase subunit B	WP_129883488.1	426 aa	Methyloctetracoccus oryzae C50C1	WP_139559045.1	95.77
formylmethanofuran dehydrogenase subunit A	WP_129883489.1	555 aa	Methyloctetracoccus oryzae C50C1	WP_139559044.1	98.74
formylmethanofuran--tetrahydromethanopterin formyltransferase	WP_129883490.1	298 aa	Methyloctetracoccus oryzae C50C1	WP_139559043.1	99.66
formylmethanofuran dehydrogenase subunit C	WP_129883491.1	269 aa	Methyloctetracoccus oryzae C50C1	WP_139559042.1	94.80
methenyltetrahydromethanopterin cyclohydrolase	WP_129883486.1	331 aa	Methyloctetracoccus oryzae C50C1	WP_139559047.1	99.40

methylenetetrahydromethanopterin dehydrogenase	WP_129883184.1	301 aa	Methyloctetracoccus oryzae C50C1	WP_139559456.1	97.67
methylenetetrahydromethanopterin dehydrogenase	WP_129883185.1	301 aa	Methyloctetracoccus oryzae C50C1	WP_139559455.1	98.67
5,6,7,8-tetrahydromethanopterin hydro-lyase (formaldehyde-activating enzyme)	WP_129883485.1	170 aa	Methylocaldum sp. 14B	WP_077732049.1	91.18
acetate kinase	WP_129884575.1	412 aa	Methyloctetracoccus oryzae C50C1	WP_139558676.1	93.69
Hypothetical protein (pyruvate, water dikinase)	WP_129882846.1	750 aa	Methyloctetracoccus oryzae C50C1	WP_139559154.1	95.07
2,3-bisphosphoglycerate-independent phosphoglycerate mutase	WP_129883001.1	547 aa	Methyloctetracoccus oryzae C50C1	WP_139555950.1	98.35
MFS transporter	WP_129885011.1	427 aa	Methyloctetracoccus oryzae C50C1	WP_139556699.1	97.42
nitrate reductase	WP_129883833.1	896 aa	molybdopterin-dependent oxidoreductase [Methyloctetracoccus sp. C50C1]	WP_139558903.1	93.75
nitrite reductase small subunit NirD	WP_129883834.1	105 aa	Methyloctetracoccus oryzae C50C1	WP_139558902.1	98.10
nitric-oxide reductase subunit B norB	WP_129884912.1	493 aa	Methyloctetracoccus oryzae C50C1	WP_139559705.1	98.38
nitrogenase iron protein nifH	WP_129883077.1	293 aa	Methyloctetracoccus oryzae C50C1	WP_139557892.1	99.66

nitrogenase molybdenum-iron protein alpha chain nifD	WP_129883078. 1	485 aa	Methyloendococcus oryzae C50C1	WP_139557893 .1	99.76
nitrogenase molybdenum-iron protein subunit beta nifK	WP_129883079. 1	519 aa	Methyloendococcus oryzae C50C1	WP_139557894 .1	99.61
nitrogenase iron-molybdenum cofactor biosynthesis protein NifE	WP_129883087. 1	562 aa	Methyloendococcus oryzae C50C1	WP_139557896 .1	99.82
nitrogenase iron-molybdenum cofactor biosynthesis protein NifN	WP_129883088. 1	457 aa	Methyloendococcus oryzae C50C1	WP_139557897 .1	99.12
nitrogenase cofactor biosynthesis protein NifB	WP_129883122. 1	522 aa	Methyloendococcus oryzae C50C1	WP_139557927 .1	99.81
glutamate--ammonia ligase glnA	WP_129882617. 1	469 aa	Methyloendococcus oryzae C50C1	WP_139555860 .1	96.80
glutamate synthase large subunit	WP_129882495. 1	1542 aa	Methyloendococcus oryzae C50C1	WP_139555759 .1	97.92
glutamate synthase subunit beta	WP_129882496. 1	479 aa	Methyloendococcus oryzae C50C1	WP_139555760 .1	97.70
carbonic anhydrase	WP_129884654. 1	216 aa	Methylocaldum sp. 14B	WP_077729851 .1	72.51
carbonic anhydrase	WP_129884655. 1	215 aa	Methyloendococcus oryzae C50C1	WP_139558936 .1	99.53
glucose-6-phosphate isomerase	WP_129883590. 1	548 aa	Methyloendococcus oryzae C50C1	WP_139557317 .1	98.72

triose-phosphate isomerase	WP_129884669.1	249 aa	Methylothermobacter oryzae C50C1	WP_139558948.1	99.20
type I glyceraldehyde-3-phosphate dehydrogenase (gap)	WP_129884929.1	337 aa	Methylothermobacter oryzae C50C1	WP_139557153.1	99.41
phosphoglycerate kinase	WP_129883304.1	393 aa	Methylothermobacter oryzae C50C1	WP_139559331.1	99.24
pyruvate kinase	WP_129884234.1	494 aa	Methylothermobacter oryzae C50C1	WP_139556039.1	98.18
pyruvate kinase	WP_129884960.1	489 aa	Methylothermobacter oryzae C50C1	WP_139557294.1	98.77
pyruvate dehydrogenase (acetyl-transferring), homodimeric type	WP_129883765.1	894 aa	Methylothermobacter oryzae C50C1	WP_139557721.1	98.99
dihydrolipoyllysine-residue acetyltransferase	WP_129883766.1	444 aa	Methylothermobacter oryzae C50C1	WP_139557719.1	97.75
pyruvate:ferredoxin (flavodoxin) oxidoreductase	WP_129884633.1	1195 aa	Methylothermobacter oryzae C50C1	WP_139558620.1	99.33
zinc-dependent alcohol dehydrogenase family protein	WP_129882421.1	342 aa	Methylothermobacter oryzae C50C1	WP_139557540.1	97.95
iron-containing alcohol dehydrogenase	WP_129883182.1	396 aa	Methylothermobacter oryzae C50C1	WP_139559458.1	95.19
alpha-D-glucose phosphate-specific phosphoglucomutase	WP_129883715.1	544 aa	Methylothermobacter oryzae C50C1	WP_139557798.1	98.35
hypothetical protein (sugar dehydrogenase)	WP_129885010.1	715 aa	Nostoc sphaeroides strain Kutzing En	WP_118163853.1	57.31

Citrate synthase	WP_129883180.1	432 aa	Methylobacterium oryzae C50C1	WP_139559460.1	99.31
Aconitate hydratase	WP_129883996.1	646 aa	Methylobacterium oryzae C50C1	WP_139557453.1	99.38
isocitrate/isopropylmalate dehydrogenase family protein	WP_129884925.1	338 aa	Methylobacterium oryzae C50C1	WP_139557157.1	99.11
2-oxoglutarate dehydrogenase E1 component	WP_129882268.1	950 aa	Methylobacterium oryzae C50C1	WP_139556614.1	99.37
2-oxoglutarate dehydrogenase E2 component	WP_129882269.1	424 aa	Methylobacterium oryzae C50C1	WP_139556613.1	95.28
dihydrolipoamide dehydrogenase	WP_129883767.1	479 aa	Methylobacterium oryzae C50C1	WP_139557718.1	97.91
ADP-forming succinate--CoA ligase subunit alpha	WP_129884549.1	290 aa	Methylobacterium oryzae C50C1	WP_139558782.1	99.31
ADP-forming succinate--CoA ligase subunit beta	WP_129884548.1	387 aa	Methylobacterium oryzae C50C1	WP_139558781.1	98.97
malate dehydrogenase	WP_129884035.1	325 aa	Methylobacterium oryzae C50C1	WP_139557413.1	96.92
glucose-6-phosphate dehydrogenase	WP_129884235.1	501 aa	Methylobacterium oryzae C50C1	WP_139556040.1	99.40
6-phosphogluconolactonase	WP_129882445.1	231 aa	Methylobacterium oryzae C50C1	WP_139557518.1	98.26

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NADP-dependent phosphogluconate dehydrogenase	WP_129884256. 1	500 aa	Methyloctetracoccus oryzae C50C1	WP_139556061 .1	98.00
Transketolase	WP_129884378. 1	670 aa	Methyloctetracoccus oryzae C50C1	WP_139556106 .1	99.85
Transaldolase	WP_129884380. 1	334 aa	Calothrix sp. NIES-2098	WP_096587692 .1	82.93
ribose-5-phosphate isomerase RpiA	WP_129884497. 1	218 aa	Methylococcus capsulatus str. Bath	WP_010959716 .1	70.97
ribose-5-phosphate isomerase RpiA	WP_129884931. 1	225 aa	Methyloctetracoccus oryzae C50C1	WP_139557151 .1	92.89
3-hexulose-6-phosphate synthase	WP_129884376. 1	213 aa	Methylocaldum sp. SAD2	WP_086133943 .1	91.04
6-phospho-3-hexuloisomerase	WP_129884377. 1	177 aa	Methylocaldum marinum S8	WP_119628761 .1	85.88
3-hexulose-6-phosphate synthase	WP_129884177. 1	389 aa	Methyloctetracoccus oryzae C50C1	WP_139558143 .1	99.74
ribose-phosphate diphosphokinase	WP_129884068. 1	317 aa	Methyloctetracoccus oryzae C50C1	WP_139557385 .1	99.68
NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	WP_129884230. 1	543 aa	Sporomusa sphaeroides DSM 2875	WP_075757966 .1	69.57
Pyrophosphate-dependent fructose 6-phosphate-1-kinase	WP_129884977. 1	409 aa	Methyloctetracoccus oryzae C50C1	WP_139556814 .1	99.27

UDP-glucose/GDP-mannose dehydrogenase family protein	WP_129884030.1	444 aa	Methylobacterium oryzae C50C1	WP_139557419.1	96.61
UDP-glucose/GDP-mannose dehydrogenase family protein	WP_129884706.1	444 aa	Methylobacterium oryzae C50C1	WP_139557419.1	95.02
Fructokinase (ROK family protein)	WP_129882255.1	299 aa	Methylobacterium oryzae C50C1	WP_139556626.1	96.32
mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase	WP_129882468.1	490 aa	Methylobacterium oryzae C50C1	WP_139557496.1	99.59
Phosphomannomutase	WP_129884239.1	579 aa	Methylobacterium oryzae C50C1	WP_139556044.1	91.88
GDP-mannose 4,6-dehydratase	WP_129883561.1	370 aa	Methylobacterium oryzae C50C1	WP_139556231.1	98.92
GDP-L-fucose synthase	WP_129883562.1	318 aa	NAD-dependent epimerase/dehydratase family protein [Methylobacterium sp. C50C1]	WP_139556465.1	98.74
NAD-dependent epimerase/dehydratase family protein	WP_129883495.1	303 aa	Desulfobulbus sp. Tol-SR]	KGO33396.1	67.00
UDP-glucose 4-epimerase/SDR family oxidoreductase	WP_129884039.1	318 aa	Methylobacterium oryzae C50C1	WP_139557409.1	93.08

glucose-1-phosphate adenylyltransferase	WP_129882518.1	424 aa	Methylobacterium oryzae C50C1	WP_139555782.1	99.76
glycogen synthase GlgA	WP_129882519.1	528 aa	Methylobacterium oryzae C50C1	WP_139555783.1	98.28
1,4-alpha-glucan branching protein GlgB	WP_129882666.1	728 aa	Methylobacterium oryzae C50C1	WP_139556178.1	98.07
glycogen/starch/alpha-glucan phosphorylase	WP_129882614.1	836 aa	Methylobacterium oryzae C50C1	WP_139555858.1	98.92
glycogen/starch/alpha-glucan phosphorylase	WP_129884174.1	842 aa	Methylobacterium oryzae C50C1	WP_139558140.1	98.57
glycogen/starch/alpha-glucan phosphorylase	WP_129884574.1	783 aa	Methylobacterium oryzae C50C1	WP_139558677.1	94.13
4-alpha-glucanotransferase malQ	WP_129882665.1	519 aa	Methylobacterium oryzae C50C1	WP_139556177.1	97.50
malto-oligosyltrehalose synthase	WP_129883982.1	1730 aa	Methylobacterium oryzae C50C1	WP_139559770.1	94.75
malto-oligosyltrehalose trehalohydrolase	WP_129884076.1	610 aa	Methylobacterium oryzae C50C1	WP_139559776.1	95.90
trehalose-6-phosphate synthase	WP_129883814.1	748 aa	Methylobacterium oryzae C50C1	WP_139559761.1	99.73
trehalose-phosphatase	WP_129883815.1	298 aa	Methylobacterium oryzae C50C1	WP_139559762.1	96.98
acetyl-CoA C-acetyltransferase	WP_129883845.1	455 aa	Methylobacterium oryzae C50C1	WP_139558891.1	96.46

Enoyl-CoA hydratase/ decarboxylase	methylmalonyl-CoA	WP_129883684. 1	259 aa	Methylotherotetracoccus oryzae C50C1	WP_139557828 .1	97.68
Enoyl-CoA hydratase/ decarboxylase	methylmalonyl-CoA	WP_129883790. 1	274 aa	Methylotherotetracoccus oryzae C50C1	WP_139557828 .1	96.45
acyl-CoA dehydrogenase		WP_129883844. 1	749 aa	Methylotherotetracoccus oryzae C50C1	WP_139558892 .1	97.60
long-chain fatty acid--CoA ligase		WP_129882493. 1	515 aa	Methylotherotetracoccus oryzae C50C1	WP_139555757 .1	95.92
AMP-binding protein		WP_129883033. 1	806 aa	Methylotherotetracoccus oryzae C50C1	WP_139555978 .1	97.02
long-chain fatty acid--CoA ligase		WP_129883847. 1	626 aa	Methylotherotetracoccus oryzae C50C1	WP_139558889 .1	90.73
sulfate ABC transporter permease subunit CysT		WP_129884108. 1	284 aa	Methylotherotetracoccus oryzae C50C1	WP_139558079 .1	98.94
sulfate ABC transporter permease subunit CysW		WP_129884107. 1	287 aa	Methylotherotetracoccus oryzae C50C1	WP_139558078 .1	99.30
sulfate ABC transporter ATP-binding protein CysA		WP_129884106. 1	367 aa	Methylotheroterricola oryzae 73a	WP_045227284 .1	67.85
molybdate ABC transporter substrate-binding protein modA		WP_129883630. 1	248 aa	Methylotherotetracoccus oryzae C50C1	WP_139557471 .1	92.51
molybdate ABC transporter substrate-binding protein modA		WP_129883631. 1	256 aa	Jeongeupia sp. USM3	WP_070527221 .1	78.52

molybdate ABC transporter permease subunit modB	WP_129883633.1	224 aa	Methylococcaceae bacterium	TAN46543.1	84.38
iron ABC transporter permease	WP_129883353.1	550 aa	Methyloctetracoccus oryzae C50C1	WP_139559362.1	95.45
molybdenum ABC transporter ATP-binding protein modC	WP_129883634.1	360 aa	Methyloctetracoccus oryzae C50C1	WP_139557358.1	90.17
ATP-binding cassette domain-containing protein modC	WP_129883100.1	405 aa	Methyloctetracoccus oryzae C50C1	WP_139557905.1	96.06
ABC transporter ATP-binding protein / spermidine/putrescine transport potA	WP_129883272.1	360 aa	Methyloctetracoccus oryzae C50C1	WP_139559303.1	83.06
ABC transporter ATP-binding protein/ multiple sugar transport	WP_129883952.1	392 aa	Methyloctetracoccus oryzae C50C1	WP_139559029.1	98.98
ABC transporter ATP-binding protein/ multiple sugar transport	WP_129884438.1	377 aa	Methyloctetracoccus oryzae C50C1	WP_139558249.1	96.02
ABC transporter / phospholipid transport system substrate-binding protein	WP_129883193.1	228 aa	Methyloctetracoccus oryzae C50C1	WP_139559446.1	96.05
outer membrane lipid asymmetry maintenance protein MlaD	WP_129882381.1	167 aa	Candidatus Methyloctetradiphilus alinensis	PZN72443.1	65.66
lipid asymmetry maintenance ABC transporter permease subunit MlaE	WP_129882649.1	257 aa	Methyloctetracoccus oryzae C50C1	WP_139557578.1	99.61
ATP-binding cassette domain-containing protein	WP_129882382.1	312 aa	Methylocaldum sp. SAD2	WP_086135254.1	78.73
ABC transporter permease	WP_129882953.1	379 aa	Methyloctetracoccus oryzae C50C1	WP_139555902.1	99.21

MCE family protein	WP_129882955.1	307 aa	Methylotherotetracoccus oryzae C50C1	WP_139555904.1	99.02
MlaE family lipid ABC transporter permease subunit	WP_129883897.1	381 aa	Methylotherotetracoccus oryzae C50C1	WP_139558833.1	95.01
outer membrane lipid asymmetry maintenance protein MlaD	WP_129882381.1	167 aa	Candidatus Methylothermidiphilus alinensis	PZN72443.1	65.66
lipid asymmetry maintenance ABC transporter permease subunit MlaE	WP_129882649.1	260 aa	Methylotherotetracoccus oryzae C50C1	WP_139557578.1	99.62
STAS domain-containing protein mlaB	WP_129882380.1	125 aa	Methylotherotetracoccus oryzae C50C1	WP_139557579.1	98.40
ATP-binding cassette domain-containing protein	WP_129882382.1	282 aa	Methylotheraldum sp. SAD2	WP_086135254.1	78.73
ATP-binding cassette domain-containing protein	WP_129882954.1	256 aa	Methylotherotetracoccus oryzae C50C1	WP_139555903.1	99.61
ATP-binding cassette domain-containing protein	WP_129883898.1	267 aa	Methylotherotetracoccus oryzae C50C1	WP_139558832.1	97.38
ATP-binding cassette domain-containing protein	WP_129884167.1	271 aa	Methylotherotetracoccus oryzae C50C1	WP_139558133.1	93.36
phosphate ABC transporter substrate-binding protein PstS	WP_129884397.1	355 aa	Methylotherotetracoccus oryzae C50C1	WP_139556111.1	88.41
hypothetical protein (OmpA family protein)	WP_129884370.1	526 aa	Pseudomonas sp. 2FG	WP_137819794.1	40.93
PstS family phosphate ABC transporter substrate-binding protein	WP_129884365.1	349 aa	Methylotherotetracoccus oryzae C50C1	WP_139556117.1	95.42

phosphate ABC transporter substrate-binding protein	WP_129884923.1	366 aa	Methylobacterium oryzae C50C1	WP_139557160.1	98.36
urea ABC transporter substrate-binding protein UrtA	WP_129882407.1	433 aa	Methylobacterium oryzae C50C1	WP_139557555.1	98.61
urea ABC transporter permease subunit UrtB	WP_129882655.1	563 aa	Methylobacterium oryzae C50C1	WP_139557554.1	98.31
urea ABC transporter permease subunit UrtC	WP_129882408.1	363 aa	Methylobacterium oryzae C50C1	WP_139557553.1	96.97
urea ABC transporter ATP-binding protein UrtD	WP_129882409.1	274 aa	Methylobacterium oryzae C50C1	WP_139557552.1	97.81
urea ABC transporter ATP-binding subunit UrtE	WP_129882410.1	231 aa	Methylobacterium oryzae C50C1	WP_139557551.1	97.40
zinc ABC transporter substrate-binding protein ZnuA	WP_129883363.1	290 aa	Methylobacterium oryzae C50C1	WP_139557665.1	97.30
lipopolysaccharide transport system ATP-binding protein / sugar ABC transporter ATP-binding protein	WP_129883429.1	251 aa	Methylobacterium oryzae C50C1	WP_139559602.1	99.60
carbohydrate efflux ABC transporter, ATP-binding protein, NodI family	WP_129882911.1	296 aa	Methylobacterium oryzae C50C1	WP_139559089.1	99.32
nodulation protein NodJ	WP_129882886.1	254 aa	Methylobacterium oryzae C50C1	WP_139559088.1	98.03
lipoprotein-releasing ABC transporter permease subunit LolC_E	WP_129884414.1	415 aa	Methylobacterium oryzae C50C1	WP_139558296.1	99.52
lipoprotein-releasing ABC transporter ATP-binding protein LolD	WP_129884413.1	224 aa	Methylobacterium szegediense O-12	WP_026608675.1	76.34

heme ABC transporter permease CcmC	WP_129884533.1	243 aa	Methylobacterium oryzae C50C1	WP_139558768.1	99.59
heme exporter protein CcmB	WP_129884534.1	225 aa	Methylobacterium oryzae C50C1	WP_139558769.1	99.11
cytochrome c biogenesis heme-transporting ATPase CcmA	WP_129884535.1	212 aa	Methylobacterium oryzae C50C1	WP_139558770.1	99.53
LPS export ABC transporter permease LptF	WP_129882457.1	401 aa	Methylobacterium oryzae C50C1	WP_139557646.1	98.32
LPS export ABC transporter permease LptG	WP_129882458.1	356 aa	Methylobacterium oryzae C50C1	WP_139557506.1	99.44
LPS export ABC transporter ATP-binding protein LptB	WP_129882598.1	241 aa	Methylobacterium oryzae C50C1	WP_045224292.1	81.33
lipid A export permease/ATP-binding protein MsbA	WP_129884544.1	608 aa	Methylobacterium szegediense O-12	WP_051331528.1	72.04
type I secretion system permease/ATPase EexD	WP_129884985.1	585 aa	Methylobacterium oryzae C50C1	WP_139556798.1	98.98
peptidase domain-containing ABC transporter RaxB, CvaB	WP_129882739.1	721 aa	Methylobacterium oryzae C50C1	WP_139558511.1	98.61
ABC transporter ATP-binding protein/permease BacA	WP_129884676.1	578 aa	Methylobacterium oryzae C50C1	WP_139558955.1	99.31
ABC transporter ATP-binding protein/permease BacA	WP_129882306.1	581 aa	Methylobacterium oryzae C50C1	WP_139556709.1	97.00
ABC transporter ATP-binding protein/permease BacA	WP_129883270.1	581 aa	Methylobacterium oryzae C50C1	WP_139559302.1	97.76

polysialic acid transporter	WP_129884639.1	497 aa	Methylobacterium oryzae C50C1	WP_139558707.1	99.20
sugar ABC transporter permease	WP_129883950.1	289 aa	Methylobacterium methanica MC09	WP_139559031.1	97.23
carbohydrate ABC transporter permease	WP_129883951.1	282 aa	Methylobacterium oryzae C50C1	WP_139559030.1	98.94
Porin	WP_129885012.1	458 aa	Methylobacterium oryzae C50C1	WP_139556700.1	97.82
glycoside hydrolase family 57	WP_129882505.1	392 aa	Methylobacterium oryzae C50C1	WP_139555770.1	99.49
glycoside hydrolase family 15 protein	WP_129883816.1	599 aa	Methylobacterium oryzae C50C1	WP_139559763.1	99.00
glycoside hydrolase family 19 protein	WP_129882702.1	533 aa	Methylobacterium oryzae C50C1	WP_139558581.1	96.44
TolC family outer membrane protein	WP_129884160.1	485 aa	Methylobacterium oryzae C50C1	WP_139558126.1	99.18
protein translocase subunit SecD	WP_129883551.1	616 aa	Methylobacterium oryzae C50C1	WP_139556240.1	99.19
protein translocase subunit SecF	WP_129883550.1	332 aa	Methylobacterium oryzae C50C1	WP_139556241.1	95.78
preprotein translocase subunit SecG	WP_129883554.1	124 aa	Methylobacterium oryzae C50C1	WP_139556238.1	98.39

preprotein translocase subunit SecA	WP_129882620.1	905 aa	Methylothermobacter oryzae C50C1	WP_139555863.1	98.67
protein-export chaperone SecB	WP_129882611.1	157 aa	Methylothermobacter oryzae C50C1	WP_139555855.1	97.45
preprotein translocase subunit YajC	WP_129883552.1	122 aa	Methylobacterium capsulatus str. Bath	WP_010960021.1	71.43
membrane protein insertase YidC	WP_129883378.1	552 aa	Methylothermobacter oryzae C50C1	WP_139557250.1	97.46
twin-arginine translocase TatA/TatE family subunit	WP_129884980.1	49 aa	Marinobacter fuscus NH169-3	WP_106762178.1	67.35
twin-arginine translocase TatA/TatE family subunit	WP_129882572.1	70 aa	Methylocaldum sp. 14B	WP_077730047.1	63.08
twin-arginine translocase subunit TatB	WP_129882571.1	112 aa	Methylothermobacter oryzae C50C1	WP_139555824.1	92.86
twin-arginine translocase subunit TatC	WP_129882570.1	256 aa	Methylothermobacter oryzae C50C1	WP_139555823.1	97.66

Supplementary Table 2: Protein blast analysis of FWC3 with their closest relatives with accession numbers and percentage similarities.