

Table S2. M. pneumoniae metabolic reactions

Reaction ID	KEGG ID	KEGG?	Enzyme name	Enz abbr.	EC number	Gene	Pathway	Equation	Reversibility
R001	R02628	y	phosphoenolpyruvate-protein phosphotransferase	PTSI	2.7.3.9	MPN627	General	protein histidine + phosphoenolpyruvate = protein N(pi)-phospho-L-histidine + pyruvate	R
R002	R02738	y	PTS system, glucose-specific IIBC component	PTSG	2.7.1.69	MPN207	Glycolysis	D-glucose[e] + protein N(pi)-phospho-L-histidine = D-glucose 6-phosphate + protein histidine	I
R003	R02740	y	glucose-6-phosphate isomerase	PGI	5.3.1.9	MPN250	Glycolysis	D-glucose 6-phosphate = D-fructose 6-phosphate	R
R004	R00756	y	6-phosphofructokinase	PFK	2.7.1.11	MPN302	Glycolysis	ATP + D-fructose 6-phosphate = ADP + D-fructose 1,6-bisphosphate	R
R005	R01068	y	fructose-bisphosphate aldolase	FBA	4.1.2.13	MPN025	Glycolysis	D-fructose 1,6-bisphosphate = glycercione phosphate + D-glyceraldehyde 3-phosphate	R
R006	R01015	y	triose-phosphate isomerase	TIM	5.3.1.1	MPN629	Glycolysis	D-glyceraldehyde 3-phosphate = glycercione phosphate	R
R007	R01061	y	glyceraldehyde-3-phosphate dehydrogenase	GAPDH	1.2.1.12	MPN430	Glycolysis	D-glyceraldehyde 3-phosphate + phosphate + NAD+ = 3-phospho-D-glyceroyl phosphate + NADH + H+	R
R008	R01512	y	phosphoglycerate kinase	PGK	2.7.2.3	MPN429	Glycolysis	3-phospho-D-glyceroyl phosphate + ADP = 3-phospho-D-glycerate + ATP	R
R009	R01518	y	phosphoglycerate mutase	GPM	5.4.2.1	MPN628	Glycolysis	3-phospho-D-glycerate = 2-phospho-D-glycerate	R
R010	R00658	y	enolase	ENO	4.2.1.11	MPN606	Glycolysis	2-phospho-D-glycerate = phosphoenolpyruvate + H2O	R
R011	R00200	y	pyruvate kinase	PYK	2.7.1.40	MPN303	Glycolysis	phosphoenolpyruvate + ADP = pyruvate + ATP	I
R012	R00703	y	L-lactate dehydrogenase	LDH	1.1.1.27	MPN674	Pyruvate metabolism	pyruvate + NADH + H+ = (S)-lactate + NAD+	R
R015	R01699	y	pyruvate dehydrogenase E1 (acetyl-transferring)	PDH-E1	1.2.4.1	MPN392/ MPN393	Pyruvate metabolism	pyruvate + lipoamide = S-acetyldihydroliipoamide + CO2	I
R016	R02569	y	pyruvate dehydrogenase E2 (dihydroliipoamide acetyltransferase)	PDH-E2	2.3.1.12	MPN391	Pyruvate metabolism	S-acetyldihydroliipoamide + CoA = dihydroliipoamide + acetyl-CoA	R
R017	R01698	y	pyruvate dehydrogenase E3 (dihydroliipoamide dehydrogenase)	PDH-E3	1.8.1.4	MPN390	Pyruvate metabolism	dihydroliipoamide + NAD+ = lipoamide + NADH + H+	R
R018	R00230	y	phosphate acetyltransferase	PTA	2.3.1.8	MPN428	Pyruvate metabolism	acetyl-CoA + phosphate = CoA + acetyl phosphate	R
R019	R00315	y	acetate kinase	ACK	2.7.2.1	MPN533	Pyruvate metabolism	acetyl phosphate + ADP = acetate + ATP	R
R020	R00281	y	NADH oxidase	NOX	1.6.99.3	MPN394	Pyruvate metabolism	2 NADH + O2 = 2 NAD+ + H2O2	I
R190	R00086	y	ATP synthase	ATPase	3.6.3.14	MPN597-604	Energy metabolism	ATP + H2O + H+ = ADP + phosphate + H+[e]	R
R021	R03076	y	fructose-permease IIBC component	FRUA	2.7.1.69	MPN078	Fructose and mannose metabolism	D-fructose[e] + protein N(pi)-phospho-L-histidine = D-fructose 1-phosphate + protein histidine	I
R022	R02071	y	1-phosphofructokinase	FRUK	2.7.1.56	MPN079	Fructose and mannose metabolism	D-fructose 1-phosphate + ATP = D-fructose 1,6-bisphosphate + ADP	I
R023	R02568	y	fructose-bisphosphate aldolase	FBA	4.1.2.13	MPN025	Fructose and mannose metabolism	D-fructose 1-phosphate = glycercione phosphate + glyceraldehyde	R
R024	R01041	y	alcohol dehydrogenase	ADH	1.1.1.1	MPN564	Fructose and mannose metabolism	glyceraldehyde + NADH + H+ = glycerol + NAD+	R
R026	?		fructose-permease IIBC component	FRUA	2.7.1.69	MPN078	Fructose and mannose metabolism	D-mannose[e] + protein N(pi)-phospho-L-histidine = D-mannose 6-phosphate + protein histidine	I
R027	R01818	y	phosphomannomutase	PMM	5.4.2.8	MPN066	Fructose and mannose metabolism	D-mannose 1-phosphate = D-mannose 6-phosphate	R
R028	R01819		phosphomannose-6-phosphate isomerase	MPI	5.3.1.8	?	Fructose and mannose metabolism	D-mannose 6-phosphate = D-fructose 6-phosphate	R
R029	R02704	y	PTS system, mannitol-specific component IIA	MTLA	2.7.1.69	MPN651/ MPN653	Fructose and mannose metabolism	D-mannitol[e] + protein N(pi)-phospho-L-histidine = D-mannitol 1-phosphate + protein histidine	I
R030	R00758	y	mannitol-1-phosphate 5-dehydrogenase	MTLD	1.1.1.17	MPN652	Fructose and mannose metabolism	D-mannitol 1-phosphate + NAD+ = D-fructose 6-phosphate + NADH + H+	R
R031	R07671	y	PTS system, 3-keto-L-gulonate/L-ascorbate specific	PTSA	2.7.1.69	MPN494/MP N495/MPN49 6	Ascorbate metabolism	L-ascorbate[e] + protein N(pi)-phospho-L-histidine = L-ascorbate 6-phosphate + protein histidine	I
R032	R07677		L-ascorbate-6-phosphate lactonase	ULAG	3.1.1.-	MPN497?	Ascorbate metabolism	L-ascorbate 6-phosphate + H2O = 3-dehydro-L-gulonate 6-phosphate	R
R033	R07125	y	3-dehydro-L-gulonate-6-phosphate decarboxylase	KGPD	4.1.1.85	MPN493	Ascorbate metabolism	3-dehydro-L-gulonate 6-phosphate + H+ = L-xylulose 5-phosphate + CO2	I
R034	R03244	y	L-ribulose-5-phosphate 3-epimerase	ULAE	5.1.3.22	MPN492	Ascorbate metabolism	L-ribulose 5-phosphate = L-xylulose 5-phosphate	R
R035	R05850	y	L-ribulose-5-phosphate 4-epimerase	ULAF	5.1.3.4	MPN498	Ascorbate metabolism	L-ribulose 5-phosphate = D-xylulose 5-phosphate	R

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R191	R0086	y	D-ribose transporter	RibABC	3.6.3.17	MPN258-260	Pentose phosphate pathway	D-ribose[e] + ATP + H2O = D-ribose + ADP + phosphate	I
R036	R01051		ribokinase	RBSK	2.7.1.15	?	Pentose phosphate pathway	D-ribose + ATP = D-ribose 5-phosphate + ADP	I
R037	R01067	y	transketolase	TKL	2.2.1.1	MPN082	Pentose phosphate pathway	D-fructose 6-phosphate + D-glyceraldehyde 3-phosphate = D-xylulose 5-phosphate + D-erythrose 4-phosphate	R
R038	R07378		transaldolase	TAL	2.2.1.2	?	Pentose phosphate pathway	D-erythrose 4-phosphate + D-fructose 6-phosphate = sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate	R
R039	R07246	y	transketolase	TKL	2.2.1.1	MPN082	Pentose phosphate pathway	sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate = D-ribose 5-phosphate + D-xylulose 5-phosphate	R
R040	R01529	y	ribulose-phosphate 3-epimerase	RPE	5.1.3.1	MPN251	Pentose phosphate pathway	D-ribulose 5-phosphate = D-xylulose 5-phosphate	R
R041	R01056	y	ribose-5-phosphate isomerase	RPIA	5.3.1.6	MPN595	Pentose phosphate pathway	D-ribose 5-phosphate = D-ribulose 5-phosphate	R
R042	R01049	y	ribose-phosphate diphosphokinase	PRPS	2.7.6.1	MPN073	Pentose phosphate pathway /Nucleotide metabolism	D-ribose 5-phosphate + ATP = 5-phospho-D-ribose 1-diphosphate + AMP	R
R043	R01057		phosphopentomutase	DEOB	5.4.2.7	MPN066	Pentose phosphate pathway /Nucleotide metabolism	D-ribose 1-phosphate = D-ribose 5-phosphate	R
R044	R02749		phosphopentomutase	DEOB	5.4.2.7	MPN066	Pentose phosphate pathway /Nucleotide metabolism	2-deoxy-D-ribose 1-phosphate = 2-deoxy-D-ribose 5-phosphate	R
R046	R1066	y	deoxyribose-phosphate aldolase	DERA	4.1.2.4	MPN063	Pentose phosphate pathway /Nucleotide metabolism	2-deoxy-D-ribose 5-phosphate = D-glyceraldehyde 3-phosphate + acetaldehyde	R
R047	R00228		acetaldehyde dehydrogenase	ADH	1.2.1.10	MPN564	Pyruvate metabolism	acetyl-CoA + NADH + H+ = acetaldehyde + CoA + NAD+	R
R048	R00754	y	alcohol dehydrogenase	ADH	1.1.1.1	MPN564	Pyruvate metabolism	acetaldehyde + NADH + H+ = ethanol + NAD+	R
R192	-	y	glycerol uptake facilitator	GlpF	-	MPN043	Glycerophospholipid metabolism	glycerol [e] = glycerol	R
R049	R00847	y	glycerol kinase	GK	2.7.1.30	MPN050	Glycerophospholipid metabolism	glycerol + ATP = ADP + glycerol 3-phosphate	I
R193	-	y	sn-glycerol-3-phosphate transporter	GiyABC	-	MPN133-136	Glycerophospholipid metabolism	glycerol 3-phosphate[e] + ATP + H2O = glycerol 3-phosphate + ADP + phosphate	I
R050	R00842	y	glycerol-3-phosphate dehydrogenase	GPDH	1.1.99.5	MPN051	Glycerophospholipid metabolism	glycerol 3-phosphate + NAD+ = glycerone phosphate + NADH + H+	R
R186	R00846		glycerol-3-phosphate oxidase	GPO	1.1.3.21	MPN051	Glycerophospholipid metabolism	glycerol 3-phosphate + O2 = glycerone phosphate + H2O2	R
R051	R01010		spontaneous	-	-	-	Glycerophospholipid metabolism	glycerone phosphate + H2O = glycerone + phosphate	I
R052	R01011	nec	glycerone kinase	DHAK	2.7.1.29	MPN547	Glycerophospholipid metabolism	glycerone + ATP = glycerone phosphate + ADP	I
R053	R00851	nec	glycerol-3-phosphate O-acyltransferase	GPAM	2.3.1.15	MPN350/ MPN546	Glycerophospholipid metabolism	acyl-[acyl-carrier protein] + sn-glycerol 3-phosphate = [acyl-carrier protein] + 1-acyl-sn-glycerol 3-phosphate	I
R054	R02241	y	1-acyl-sn-glycerol-3-phosphate acyltransferase	AGPAT	2.3.1.51	MPN299	Glycerophospholipid metabolism	acyl-[acyl-carrier protein] + 1-acyl-sn-glycerol 3-phosphate = [acyl-carrier protein] + 1,2-diacyl-sn-glycerol 3-phosphate	R
R055	R01799	y	phosphatidate cytidyltransferase	CDP-DG	2.7.7.41	MPN637	Glycerophospholipid metabolism	phosphatidate + CTP = CDP-diacylglycerol + diphosphate	R
R056	R01801	y	phosphatidylglycerophosphate synthase	PGP	2.7.8.5	MPN253	Glycerophospholipid metabolism	CDP-diacylglycerol + glycerol 3-phosphate = 3(3-sn-phosphatidyl)-sn-glycerol 1-phosphate + CMP	R
R057	R02029		phosphatidylglycerophosphatase	PGPB	3.1.3.27	?	Glycerophospholipid metabolism	phosphatidylglycerophosphate + H2O = phosphatidylglycerol + phosphate	R
R058	R02030		cardiolipin synthase	CLS	2.7.8.-	?	Glycerophospholipid metabolism	phosphatidylglycerol + CDP-diacylglycerol = cardiolipin + CMP	I
R059	R02239		phosphatidate phosphatase	PPT	3.1.3.4	MPN455	Glycolipid metabolism	phosphatidate + H2O = 1,2-diacyl-sn-glycerol + phosphate	I
R060	R00959	nec	phosphoglucomutase	PGM	5.4.2.2	MPN066	Glycolipid metabolism	D-glucose 1-phosphate = D-glucose 6-phosphate	R
R061	R00289	y	UDP glucose pyrophosphorylase	UGP	2.7.7.9	MPN667	Glycolipid metabolism	D-glucose 1-phosphate + UTP = UDP-glucose + diphosphate	R
R062	R00291	y	UDP-glucose 4-epimerase	UGE	5.1.3.2	MPN257	Glycolipid metabolism	UDP-glucose = UDP-galactose	R
R063	R02689		glycosyl transferase	?	2.4.1.157	MPN483	Glycolipid metabolism	diacylglycerol + UDP-glucose = D-glucosyl-1,2-diacylglycerol + UDP	I

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R064	R02691		glycosyl transferase	?	2.4.1.46	MPN483	Glycolipid metabolism	diacyl-sn-glycerol + UDP-galactose = D-galactosyl-1,2-diacylglycerol + UDP	I
R178	R01021	nec	choline kinase	CHK	2.7.1.32	MPN532	Lipid metabolism	choline + ATP = choline phosphate + ADP	R
R179	R01030	y	glycerophosphoryl diester phosphodiesterase	GlpQ	3.1.4.46	MPN566	Lipid metabolism	sn-glycero-3-phosphocholine + H2O = choline + sn-glycerol 3-phosphate	R
R180	R01890		choline-phosphate cytidylyltransferase	PCT	2.7.7.15	MPN336	Lipid metabolism	choline phosphate + CTP = CDP-choline + pyrophosphate	R
R182	R01030	y	glycerophosphoryl diester phosphodiesterase	GlpQ	3.1.4.46	MPN420	Lipid metabolism	sn-glycero-3-phosphocholine + H2O = choline + sn-glycerol 3-phosphate	R
R187	R01309		phosphatidylcholine acylhydrolase	PldB	3.1.1.5	MPN445?	Lipid metabolism	phosphatidylcholine + 2 H2O = sn-glycero-3-phosphocholine + 2 fatty acid	R
R183	R02250	nec	triacylglycerol lipase	Lip	3.1.1.3	MPN519	Lipid metabolism	triacylglycerol + H2O = 1,2-diacyl-sn-glycerol + fatty acid	I
R184	R02687	nec	triacylglycerol lipase	Lip	3.1.1.3	MPN519	Lipid metabolism	1,2-diacyl-sn-glycerol + H2O = 1-acyl-sn-glycerol 3-phosphate + fatty acid	I
R065	R00190	y	adenine phosphoribosyltransferase	APRT	2.4.2.7	MPN395	Purine metabolism	adenine + 5-phospho-D-ribose 1-diphosphate = AMP + diphosphate	R
R066	R01561	y	purine-nucleoside phosphorylase	PNP	2.4.2.1	MPN062	Purine metabolism	adenosine + phosphate = adenine + D-ribose 1-phosphate	R
R067	R00183		5'-nucleotidase	NT5	3.1.3.5	?	Purine metabolism	AMP + H2O = adenosine + phosphate	I
R068	R00127	y	adenylate kinase	AK	2.7.4.3	MPN185	Purine metabolism	AMP + ATP = 2 ADP	R
R069	R02017	y	ribonucleoside-diphosphate reductase	RDR	1.17.4.1	MPN322/MPN323/MPN324	Purine metabolism	ADP + thioredoxin = dADP + thioredoxin disulfide + H2O	I
R070	R02016	y	thioredoxin-disulfide reductase	TXNRD	1.8.1.9	MPN240	Nucleotide metabolism	thioredoxin disulfide + NADPH + H+ = thioredoxin + NADP+	I
R071	R00435	y	DNA-directed RNA polymerase	RNAP	2.7.7.6	MPN516	Purine metabolism	RNAn + ATP = RNAn+1 + diphosphate	I
R072	R00004	y	Inorganic diphosphatase	PPA	3.6.1.1	MPN528	Nucleotide metabolism	Diphosphate + H2O = 2 phosphate	I
R073	R02557	y	purine-nucleoside phosphorylase	PNP	2.4.2.1	MPN062	Purine metabolism	deoxyadenosine + phosphate = adenine + 2-deoxy-D-ribose 1-phosphate	R
R074	R02089	nec	deoxyadenosine kinase	DAK	2.7.1.76	MPN386	Purine metabolism	deoxyadenosine + ATP = dAMP + ADP	I
R075	R01547	y	adenylate kinase	AK	2.7.4.3	MPN185	Purine metabolism	dAMP + ATP = dADP + ADP	R
R076	R01138	y	pyruvate kinase	PYK	2.7.1.40	MPN303	Purine metabolism	phosphoenolpyruvate + dADP = pyruvate + dATP	I
R175	?		phosphoglycerate kinase	PGK	2.7.2.3	MPN429	Purine metabolism	3-phospho-D-glyceroyl phosphate + dADP = 3-phospho-D-glycerate + dATP	R
R077	R00375	y	DNA-directed DNA polymerase	DNAP	2.7.7.7	MPN034/MPN378/MPN672	Purine metabolism	DNAn + dATP = DNAn+1 + diphosphate	I
R078	R01229	y	hypoxanthine-guanine phosphoribosyltransferase	HPRT	2.4.2.8	MPN672	Purine metabolism	guanine + 5-phospho-D-ribose 1-diphosphate = GMP + diphosphate	R
R079	R02147	y	purine-nucleoside phosphorylase	PNP	2.4.2.1	MPN062	Purine metabolism	guanosine + phosphate = guanine + D-ribose 1-phosphate	R
R080	R01227		5'-nucleotidase	NT5	3.1.3.5	?	Purine metabolism	GMP + H2O = guanosine + phosphate	I
R081	R00332	y	guanylate kinase	GUK	2.7.4.8	MPN246	Purine metabolism	GMP + ATP = GDP + ADP	R
R082	R02019	y	ribonucleoside-diphosphate reductase	RDR	1.17.4.1	MPN322/MPN323/MPN324	Purine metabolism	GDP + thioredoxin = dGDP + thioredoxin disulfide + H2O	I
R083	R00430	y	pyruvate kinase	PYK	2.7.1.40	MPN303	Purine metabolism	phosphoenolpyruvate + GDP = pyruvate + GTP	I
R176	R01517		phosphoglycerate kinase	PGK	2.7.2.3	MPN429	Purine metabolism	3-phospho-D-glyceroyl phosphate + GDP = 3-phospho-D-glycerate +GTP	R
R084	R00441	y	DNA-directed RNA polymerase	RNAP	2.7.7.6	MPN516	Purine metabolism	RNAn + GTP = RNAn+1 + diphosphate	I
R085	R01969	y	purine-nucleoside phosphorylase	PNP	2.4.2.1	MPN062	Purine metabolism	deoxyguanosine + phosphate = guanine + 2-deoxy-D-ribose 1-phosphate	R
R086	R01967	nec	deoxyguanosine kinase	DGK	2.7.1.113	MPN386	Purine metabolism	deoxyguanosine + ATP = dGMP + ADP	I
R087	R02090	y	guanylate kinase	GUK	2.7.4.8	MPN246	Purine metabolism	dGMP + ATP = dGDP + ADP	R
R088	R01858	y	pyruvate kinase	PYK	2.7.1.40	MPN303	Purine metabolism	phosphoenolpyruvate + dGDP = pyruvate + dGTP	I
R177	?		phosphoglycerate kinase	PGK	2.7.2.3	MPN429	Purine metabolism	3-phospho-D-glyceroyl phosphate + dGDP= 3-phospho-D-glycerate + dGTP	R
R089	R00376	y	DNA-directed DNA polymerase	DNAP	2.7.7.7	MPN034/MPN378/MPN033	Purine metabolism	DNAn + dGTP = DNAn+1 + diphosphate	I
R090	R00966	y	uracil phosphoribosyltransferase	UPRT	2.4.2.9	MPN033	Pyrimidine metabolism	uracil + 5-phospho-D-ribose 1-diphosphate = UMP + diphosphate	R
R091	R01876		uridine phosphorylase	UPP	2.4.2.3	MPN064?	Pyrimidine metabolism	uridine + phosphate = uracil + D-ribose 1-phosphate	R
R092	R00963		5'-nucleotidase	NT5	3.1.3.5	?	Pyrimidine metabolism	UMP + H2O = uridine + phosphate	I
R093	R00964	y	uridine kinase	UCK	2.7.1.48	MPN561	Pyrimidine metabolism	Uridine + ATP = UMP + ADP	I
R094	R00158	y	uridylate kinase	UMPK	2.7.4.22	MPN632	Pyrimidine metabolism	UMP + ATP = UDP + ADP	R

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R095	R00659	y	pyruvate kinase	PYK	2.7.1.40	MPN303	Pyrimidine metabolism	phosphoenolpyruvate + UDP = pyruvate + UTP	I
R096	R02018	y	ribonucleoside-diphosphate reductase	RDR	1.17.4.1	MPN322/MPN323/MPN324	Pyrimidine metabolism	UDP + thioredoxin = dUDP + thioredoxin disulfide + H2O	I
R097	R01878	nec	cytidine deaminase	CDA	3.5.4.5	MPN065	Pyrimidine metabolism	cytidine + H2O = uridine + NH3	R
R098	R00571		CTP synthase	CTPS	6.3.4.2	MPN256?	Pyrimidine metabolism	UTP + ATP + NH3 = CTP + ADP + phosphate	I
R099	R00443	y	DNA-directed RNA polymerase	RNAP	2.7.7.6	MPN516	Pyrimidine metabolism	RNAn + UTP = RNAn+1 + diphosphate	I
R100	R00513	y	cytidine kinase	UCK	2.7.1.48	MPN561	Pyrimidine metabolism	cytidine + ATP = CMP + ADP	I
R101	R00511		5'-nucleotidase	NT5	3.1.3.5	?	Pyrimidine metabolism	CMP + H2O = cytidine + phosphate	I
R102	R00512	nec	cytidylate kinase	CMPK	2.7.4.14	MPN476	Pyrimidine metabolism	CMP + ATP = CDP + H2O	R
R103	R00572	y	pyruvate kinase	PYK	2.7.1.40	MPN303	Pyrimidine metabolism	phosphoenolpyruvate + CDP = pyruvate + CTP	I
R104	R00442	y	DNA-directed RNA polymerase	RNAP	2.7.7.6	MPN516	Pyrimidine metabolism	RNAn + CTP = RNAn+1 + diphosphate	I
R105	R02024	y	ribonucleoside-diphosphate reductase	RDR	1.17.4.1	MPN322/MPN323/MPN324	Pyrimidine metabolism	CDP + thioredoxin = dCDP + thioredoxin disulfide + H2O	I
R106	R01666		deoxycytidine kinase	DCK	2.7.1.74	?	Pyrimidine metabolism	deoxycytidine + ATP = dCMP + ADP	I
R107	R01664		5'-nucleotidase	NT5	3.1.3.5	?	Pyrimidine metabolism	dCMP + H2O = deoxycytidine + phosphate	I
R108	R01665	nec	deoxycytidylate kinase	CMPK	2.7.4.14	MPN476	Pyrimidine metabolism	dCMP + ATP = dCDP + ADP	R
R109	R02320	nec	pyruvate kinase	PYK	2.7.1.40	MPN303	Pyrimidine metabolism	phosphoenolpyruvate + dCDP = pyruvate + dCTP	I
R110	R00377	y	DNA-directed DNA polymerase	DNAP	2.7.7.7	MPN034/MPN378	Pyrimidine metabolism	DNAn + dCTP = DNAn+1 + diphosphate	I
R174	R01878	nec	deoxycytidine deaminase	CDA	3.5.4.5	MPN065	Pyrimidine metabolism	deoxycytidine + H2O = deoxyuridine + NH3	R
R111	R02484		uridine phosphorylase	UPP	2.4.2.3	MPN064?	Pyrimidine metabolism	deoxyuridine + phosphate = uracil + 2-deoxyD-ribose 1-phosphate	R
R112	R02099	y	thymidine kinase	TK	2.7.1.21	MPN044	Pyrimidine metabolism	deoxyuridine + ATP = dUMP + ADP	I
R113	R07297		5'-nucleotidase	NT5	3.1.3.5	?	Pyrimidine metabolism	dUMP + H2O = deoxyuridine + phosphate	I
R189	R02098	nec	thymidylate kinase	TMPK	2.7.4.9	MPN006	Pyrimidine metabolism	dUMP + ATP = dUDP + ADP	R
R114	R02101	y	thymidylate synthase	THY	2.1.1.45	MPN320	Pyrimidine metabolism /One carbon pool by folate	dUMP + 5,10-methylenetetrahydrofolate = dTMP + dihydrofolate	I
R115	R01570	y	thymidine phosphorylase	UPP	2.4.2.4	MPN064	Pyrimidine metabolism	thymidine + phosphate = thymine + 2-deoxyD-ribose 1-phosphate	R
R116	R01567	y	thymidine kinase	TK	2.7.1.21	MPN044	Pyrimidine metabolism	thymidine + ATP = dTMP + ADP	I
R117	R01569		5'-nucleotidase	NT5	3.1.3.5	?	Pyrimidine metabolism	dTMP + H2O = thymidine + phosphate	I
R118	R02094	y	thymidylate kinase	TMPK	2.7.4.9	MPN006	Pyrimidine metabolism	dTMP + ATP = dTDP + ADP	R
R119	R02320	nec	pyruvate kinase	PYK	2.7.1.40	MPN303	Pyrimidine metabolism	phosphoenolpyruvate + dTDP = pyruvate + dTTP	I
R120	R00378	y	DNA-directed DNA polymerase	DNAP	2.7.7.7	MPN034/MPN378	Pyrimidine metabolism	DNAn + dTTP = DNAn+1 + diphosphate	I
R121	R00552	y	arginine deiminase	ArcA	3.5.3.6	MPN304/MPN305	Arginine metabolism	L-arginine + H2O = L-citrulline + NH3	I
R122	R00552	y	arginine deiminase	ArcA	3.5.3.6	MPN560	Arginine metabolism	L-arginine + H2O = L-citrulline + NH3	I
R123	R01398	y	ornithine carbamoyltransferase	OTC	2.1.3.3	MPN306	Arginine metabolism	L-citrulline + phosphate = L-ornithine + carbamoyl phosphate	R
R124	R00150	y	carbamate kinase	Ckase	2.7.2.2	MPN307	Arginine metabolism	carbamoyl phosphate + ADP = NH3 + CO2 + ATP	R
R125	R02235	y	dihydrofolate reductase	DHFR	1.5.1.3	MPN321/MPN300?	One carbon pool by folate	folate + NADH + H+ = dihydrofolate + NAD+	R
R126	R00936	y	dihydrofolate reductase	DHFR	1.5.1.3	MPN321/MPN300?	One carbon pool by folate	dihydrofolate + NADH + H+ = tetrahydrofolate + NAD+	R
R127	R00943		formate tetrahydrofolate ligase	FHS	6.3.4.3	MPN017?	One carbon pool by folate	tetrahydrofolate + formate + ATP = 10-formyltetrahydrofolate + ADP + phosphate	R
R128	R01655	y	methylenetetrahydrofolate cyclohydrolase	MTHFC	3.5.4.9	MPN017	One carbon pool by folate	10-formyltetrahydrofolate + H+ = 5,10-methylenetetrahydrofolate + H2O	R

Reaction ID	KEGG ID	KEGG?	Enzyme name	Enz abbr.	EC number	Gene	Pathway	Equation	Reversibility
R129	R03940	y	methionyl-tRNA formyltransferase	MTFMT	2.1.2.9	MPN543	One carbon pool by folate /Aminoacyl-tRNA biosynthesis	L-methionyl-tRNA <sup>Met</sup> + 10-formyltetrahydrofolate + H <sub>2</sub> O = N-formylmethionyl-tRNA <sup>Met</sup> + tetrahydrofolate	I
R130	R00945	y	glycine hydroxymethyltransferase	SHMT	2.1.2.1	MPN576	One carbon pool by folate /Amino acid metabolism	5,10-methylenetetrahydrofolate + glycine + H <sub>2</sub> O = tetrahydrofolate + L-serine	R
R131	R01220	y	methylenetetrahydrofolate dehydrogenase	MTHFD	1.5.1.5	MPN017	One carbon pool by folate	5,10-methylenetetrahydrofolate + NADP <sup>+</sup> = 5,10-methenyltetrahydrofolate + NADPH + H <sup>+</sup>	R
R132	R02301	nec	5-formyltetrahydrofolate cyclo-ligase	MTHFS	6.3.3.2	MPN348	One carbon pool by folate	5-formyltetrahydrofolate + ATP + H <sup>+</sup> = 5,10-methenyltetrahydrofolate + ADP + phosphate	I
R185	R02300?		methenyltetrahydrofolate hydrolase?	MTHFH	?	MPN576	One carbon pool by folate	5,10-methenyltetrahydrofolate + H <sub>2</sub> O = 5-formyltetrahydrofolate + H <sup>+</sup>	I
R181	R11519		formate dehydrogenase	FDH	1.2.1.2	?	One carbon pool by folate	CO <sub>2</sub> + NADH + H <sup>+</sup> = formate + NAD <sup>+</sup>	R
R133	R00177	y	methionine adenosyltransferase	MAT	2.5.1.6	MPN060	Methionine metabolism	L-methionine + ATP + H <sub>2</sub> O = S-adenosyl-L-methionine + diphosphate + phosphate	I
R134	R04858	y	DNA (cytosine-5-)-methyltransferase	DCM	2.1.1.37	MPN108	Methionine metabolism	S-adenosyl-L-methionine + DNA = S-adenosyl-L-homocysteine + 5-methylcytosine DNA	I
R135	R00192		adenosylhomocysteinase	AHC	3.3.1.1	?	Methionine metabolism	S-adenosyl-L-homocysteine + H <sub>2</sub> O = L-homocysteine + adenosine	R
R136	R01724	nec	nicotinate phosphoribosyltransferase	PNCB	2.4.2.12	MPN047	Nicotinate and nicotinamide metabolism	nicotinate + 5-phospho-D-ribose 1-diphosphate = nicotinate D-ribonucleotide + diphosphate	I
R137	R03005	y	nicotinamide-nucleotide adenyltransferase	NADD	2.7.7.18	MPN336	Nicotinate and nicotinamide metabolism	nicotinate D-ribonucleotide + ATP = deamido-NAD <sup>+</sup> + diphosphate	R
R138	R00189	y	NAD <sup>+</sup> synthase	NADE	6.3.1.5	MPN562	Nicotinate and nicotinamide metabolism	deamido-NAD <sup>+</sup> + ATP + NH <sub>3</sub> = NAD <sup>+</sup> + AMP + diphosphate	I
R139	R00104	y	NAD <sup>+</sup> kinase	NADK	2.7.1.23	MPN267	Nicotinate and nicotinamide metabolism	NAD <sup>+</sup> + ATP = NADP <sup>+</sup> + ADP	I
R173	R00105		NAD <sup>+</sup> kinase	NADK	2.7.1.23	MPN267	Nicotinate and nicotinamide metabolism	NADH + ATP = NADPH + ADP	I
R140	R00549	y	riboflavin kinase	RFK	2.7.1.26	MPN158	Riboflavin metabolism	riboflavin + ATP = FMN + ADP	I
R141	R00161	y	FAD synthetase	FAD	2.7.7.2	MPN158	Riboflavin metabolism	FMN + ATP = FAD + diphosphate	R
R142	R00174		pyridoxal kinase	PDXK	2.7.1.35	?	Vitamin B6 metabolism	pyridoxal + ATP = pyridoxal 5'-phosphate + ADP	I
R143	R02134		thiamine kinase	THIK	2.7.1.89	?	Thiamine metabolism	thiamine + ATP = thiamine phosphate + ADP	I
R144	R00617	nec	thiamine-phosphate kinase	THIL	2.7.4.16	MPN550	Thiamine metabolism	thiamine phosphate + ATP = thiamine diphosphate + ADP	I
R145	R02971		pantothenate kinase	PANK	2.7.1.33	?	Pantothenate and CoA biosynthesis	pantetheine + ATP = pantetheine 4'-phosphate + ADP	I
R146	R03035		pantetheine-phosphate adenyltransferase	COASY	2.7.7.3	MPN336	Pantothenate and CoA biosynthesis	pantetheine 4'-phosphate + ATP = dephospho-CoA + diphosphate	R
R147	R00130	y	dephospho-CoA kinase	COAE	2.7.1.24	MPN382	Pantothenate and CoA biosynthesis	dephospho-CoA + ATP = CoA + ADP	I
R148	R01625	y	holo-[acyl-carrier-protein] synthase	ACPS	2.7.8.7	MPN298	Pantothenate and CoA biosynthesis	apo-[acyl-carrier protein] + CoA = holo-[acyl-carrier protein] + adenosine 3',5'-bisphosphate	R
R149	R01623	y	[acyl-carrier-protein] phosphodiesterase	ACPH	3.1.4.14	MPN479	Pantothenate and CoA biosynthesis	holo-[acyl-carrier protein] + H <sub>2</sub> O = pantetheine 4'-phosphate + apo-[acyl-carrier protein]	I
R188	R00188		3'(2'),5'-bisphosphate nucleotidase	BPNT	3.1.3.7	?	Pantothenate and CoA biosynthesis	adenosine 3',5'-bisphosphate + H <sub>2</sub> O = AMP + phosphate	R
R150	R07325		long-chain-fatty-acid [acyl-carrier-protein] ligase	AAS	6.2.1.20	?	Pantothenate and CoA biosynthesis /Glycerophospholipid metabolism	fatty acid + [acyl-carrier protein] + ATP = acyl-[acyl-carrier protein] + AMP + diphosphate	I
R151	R03905	y	glutaminyl-tRNA synthase	GAT	6.3.5.7	MPN236/ MPN237/ MPN238	Aminoacyl-tRNA biosynthesis	glutamyl-tRNA <sup>Gln</sup> + L-asparagine + ATP = glutaminyl-tRNA <sup>Gln</sup> + L-aspartate + ADP + phosphate	I

Reaction ID	KEGG ID	KEGG?	Enzyme name	Enz abbr.	EC number	Gene	Pathway	Equation	Reversibility
R152	R03905	y	glutamyl-tRNA synthase	GAT	6.3.5.7	MPN236/ MPN237/ MPN238	Aminoacyl-tRNA biosynthesis	glutamyl-tRNA <sup>Gln</sup> + L-glutamine + ATP = glutamyl-tRNA <sup>Gln</sup> + L-glutamate + ADP + phosphate	I
R153	R03659	y	methionyl-tRNA synthetase	METS	6.1.1.10	MPN023	Aminoacyl-tRNA biosynthesis	L-methionine + tRNA <sup>Met</sup> + ATP = L-methionyl-tRNA <sup>Met</sup> + AMP + diphosphate	R
R154	R03656	y	isoleucyl-tRNA synthetase	ILES	6.1.1.5	MPN520	Aminoacyl-tRNA biosynthesis	L-isoleucine + tRNA <sup>Ile</sup> + ATP = L-isoleucyl-tRNA <sup>Ile</sup> + AMP + diphosphate	R
R155	R03665	y	valyl-tRNA synthetase	VALS	6.1.1.9	MPN480	Aminoacyl-tRNA biosynthesis	L-valine + tRNA <sup>Val</sup> + ATP = L-valyl-tRNA <sup>Val</sup> + AMP + diphosphate	R
R156	R03657	y	leucyl-tRNA synthetase	LEUS	6.1.1.4	MPN384	Aminoacyl-tRNA biosynthesis	L-leucine + tRNA <sup>Leu</sup> + ATP = L-leucyl-tRNA <sup>Leu</sup> + AMP + diphosphate	R
R157	R03650	y	cysteinyl-tRNA synthetase	CYSS	6.1.1.16	MPN356	Aminoacyl-tRNA biosynthesis	L-cysteine + tRNA <sup>Cys</sup> + ATP = L-cysteinyl-tRNA <sup>Cys</sup> + AMP + diphosphate	R
R158	R05578	y	glutamyl-tRNA synthetase	GLTX	6.1.1.17	MPN678	Aminoacyl-tRNA biosynthesis	L-glutamate + tRNA <sup>Glu</sup> + ATP = L-glutamyl-tRNA <sup>Glu</sup> + AMP + diphosphate	R
R159	R03651	y	glutamyl-tRNA synthetase	GLTX	6.1.1.17	MPN678	Aminoacyl-tRNA biosynthesis	L-glutamate + tRNA <sup>Gln</sup> + ATP = L-glutamyl-tRNA <sup>Gln</sup> + AMP + diphosphate	R
R160	R03646	y	arginyl-tRNA synthetase	ARGS	6.1.1.19	MPN556	Aminoacyl-tRNA biosynthesis	L-arginine + tRNA <sup>Arg</sup> + ATP = L-arginyl-tRNA <sup>Arg</sup> + AMP + diphosphate	R
R161	R02918	y	tyrosyl-tRNA synthetase	TYRS	6.1.1.1	MPN669	Aminoacyl-tRNA biosynthesis	L-tyrosine + tRNA <sup>Tyr</sup> + ATP = L-tyrosyl-tRNA <sup>Tyr</sup> + AMP + diphosphate	R
R162	R03664	y	tryptophanyl-tRNA synthetase	TRPS	6.1.1.2	MPN265	Aminoacyl-tRNA biosynthesis	L-tryptophan + tRNA <sup>Trp</sup> + ATP = L-tryptophyl-tRNA <sup>Trp</sup> + AMP + diphosphate	R
R163	R03662	y	seryl-tRNA synthetase	SERS	6.1.1.11	MPN005	Aminoacyl-tRNA biosynthesis	L-serine + tRNA <sup>Ser</sup> + ATP = L-seryl-tRNA <sup>Ser</sup> + AMP + diphosphate	R
R164	R03663	y	threonyl-tRNA synthetase	THRS	6.1.1.3	MPN553	Aminoacyl-tRNA biosynthesis	L-threonine + tRNA <sup>Thr</sup> + ATP = L-threonyl-tRNA <sup>Thr</sup> + AMP + diphosphate	R
R165	R03661	y	prolyl-tRNA synthetase	PROS	6.1.1.15	MPN402	Aminoacyl-tRNA biosynthesis	L-proline + tRNA <sup>Pro</sup> + ATP = L-prolyl-tRNA <sup>Pro</sup> + AMP + diphosphate	R
R166	R05577	y	aspartyl-tRNA synthetase	ASPS	6.1.1.12	MPN046	Aminoacyl-tRNA biosynthesis	L-aspartate + tRNA <sup>Asp</sup> + ATP = L-aspartyl-tRNA <sup>Asp</sup> + AMP + diphosphate	R
R167	R03648	y	asparaginyl-tRNA synthetase	ASNS	6.1.1.22	MPN252	Aminoacyl-tRNA biosynthesis	L-asparagine + tRNA <sup>Asn</sup> + ATP = L-asparagine + tRNA <sup>Asn</sup> + AMP + diphosphate	R
R168	R03658	y	lysyl-tRNA synthetase	LYSS	6.1.1.6	MPN277	Aminoacyl-tRNA biosynthesis	L-lysine + tRNA <sup>Lys</sup> + ATP = L-lysyl-tRNA <sup>Lys</sup> + AMP + diphosphate	R
R169	R03655	y	histidyl-tRNA synthetase	HISS	6.1.1.21	MPN045	Aminoacyl-tRNA biosynthesis	L-histidine + tRNA <sup>His</sup> + ATP = L-lysyl-tRNA <sup>Lys</sup> + AMP + diphosphate	R
R170	R03660	y	phenylalanyl-tRNA synthetase	PHES	6.1.1.20	MPN105/ MPN106	Aminoacyl-tRNA biosynthesis	L-phenylalanine + tRNA <sup>Phe</sup> + ATP = L-phenylalanyl-tRNA <sup>Phe</sup> + AMP + diphosphate	R
R171	R03038	y	alanyl-tRNA synthetase	ALAS	6.1.1.7	MPN418	Aminoacyl-tRNA biosynthesis	L-alanine + tRNA <sup>Ala</sup> + ATP = L-alanyl-tRNA <sup>Ala</sup> + AMP + diphosphate	R
R172	R03654	y	glycyl-tRNA synthetase	GLYS	6.1.1.14	MPN354	Aminoacyl-tRNA biosynthesis	glycine + tRNA <sup>Gly</sup> + ATP = glycyl-tRNA <sup>Gly</sup> + AMP + diphosphate	R

**Table S3. Enzymes catalyzing multiple reactions**

Gene number	Enzyme	# Reactions	Reactions ID
MPN006	TMPK	2	R118, R189
MPN017	MTHFD	3	R127, R128, R131
MPN025	FBA	2	R005, R023
MPN044	TK	2	R112, R116
MPN051	GPO	2	R050, R186
MPN062	PNP	4	R066, R073, R079, R085
MPN064	UPP	3	R091, R111, R115
MPN065	CDA	2	R097, R174
MPN066	PGM	4	R027, R043, R044, R060
MPN078	FRUA	2	R021, R026
MPN082	TKL	2	R037, R039
MPN158	FAD	2	R140, R141
MPN185	AK	2	R068, R075
MPN236-8	GAT	2	R151, R152
MPN246	GUK	2	R081, R087
MPN267	NADK	2	R139, R173
MPN300	DHFR	2	R125, R126
MPN303	PYK	8	R011, R076, R083, R088, R095, R103, R109, R119
MPN321	THY	2	R125, R126
MPN322-4	RDR	4	R069, R082, R096, R105
MPN336	COASY	3	R137, R146, R180
MPN386	DAK	2	R074, R086
MPN429	PGK	4	R008, R175, R176, R177
MPN476	CMPK	2	R102, R108
MPN483	?	>2	R063, R064
MPN519	Lip	2	R183, R184
MPN561	UCK	2	R093, R100
MPN564	ADH	3	R024, R047, R048
MPN576	MTHFH	2	R130, R185
MPN678	GLTX	2	R158, R159
-	NT5	7	R067, R080, R092, R101, R107, R113, R117
32 enzymes		91 reactions	
(25%)		(48%)	

Table S4. New reactions

Reaction ID	Enzyme name	Enz abbr.	EC number	Gene number	Pathway	Equation	Evidence
R026	fructose-permease IIBC component	FRUA	2.7.1.69	MPN078	Fructose and mannose metabolism	D-mannose + protein N(pi)-phospho-L-histidine = D-mannose 6-phosphate + protein histidine	1) Competition studies with other suggars; 2) ortholog of <i>E. coli</i> FruA, that up takes mannose (Kornberg & Lambourne,1992)
R028	phosphomannose-6-phosphate isomerase	MPI	5.3.1.8	?	Fructose and mannose metabolism	D-mannose 6-phosphate = D-fructose 6-phosphate	1) Mannose is being metabolized, so there is a need for this enzyme to enter glycolysis
R032	L-ascorbate-6-phosphate lactonase	ULAG	3.1.1.-	MPN497	Ascorbate metabolism	L-ascorbate 6-phosphate + H2O = 3-dehydro-L-gulonate 6-phosphate	1) Genomic context; 2) gap filling
R036	ribokinase	RBSK	2.7.1.15	?	Pentose phosphate pathway	D-ribose + ATP = D-ribose 5-phosphate + ADP	Free ribose is metabolized (minimal medium)
R038	transaldolase	TAL	2.2.1.2	?	Pentose Phosphate pathway	D-erythrose 4-phosphate + D-fructose 6-phosphate = sedoheptulose 7-phosphate + D-glyceraldehyde 3-phosphate	1) Functional pentose phosphate pathway; 2) enzymatic activity (deSantis et al., 1989)
R043	phosphopentomutase	DEOB	5.4.2.7	MPN066	Nucleotide metabolism	D-ribose 1-phosphate = D-ribose 5-phosphate	1) sequence homology with <i>Mycoplasma hyopneumoniae</i> DeoB; 2) gene co-occurrence
R044	phosphopentomutase	DEOB	5.4.2.7	MPN066	Nucleotide metabolism	2-deoxy-D-ribose 1-phosphate = 2-deoxy-D-ribose 5-phosphate	Gap filling (2-deoxy-D-ribose-5-phosphate is used in reaction R046)
R047	acetaldehyde dehydrogenase	ADH	1.2.1.10	MPN564	Pyruvate metabolism	acetyl-CoA + NADH + H+ = acetaldehyde + CoA + NAD+	Alternative activity for this enzyme in <i>Thermoanaerobacter ethanolicus</i> (Burdette and Zeikus, 1994)
R051	spontaneous	-	-	-	Glycerolipid metabolism	glycerone phosphate + H2O = glycerone + phosphate	Spontaneous reaction (see Molin, Norbeck et al., 2003)
R057	phosphatidylglycerophosphatase	PGPB	3.1.3.27	?	Glycerophospholipid metabolism	phosphatidylglycerophosphate + H2O = phosphatidylglycerol + phosphate	Needed for the synthesis of cardiolipin, a bacterial lipid found in Mpn that cannot be uptaken from the host (Placket, Marmion et al., 1969)
R058	cardiolipin synthase	CLS	2.7.8.-	?	Glycerophospholipid metabolism	phosphatidylglycerol + CDP-diacylglycerol = cardiolipin + CMP	Needed for the synthesis of cardiolipin, a bacterial lipid found in Mpn that cannot be uptaken from the host (Placket, Marmion et al., 1969)
R059	phosphatidate phosphatase	PPT	3.1.3.4	?	Glycolipid metabolism	phosphatidate + H2O = 1,2-diacyl-sn-glycerol + phosphate	1) Needed for the synthesis of glycolipids (see Klement, Ojemyr et al., 2007); 2) gap filling
R063	glycosyl transferase	?	2.4.1.157	MPN483	Glycolipid metabolism	diacylglycerol + UDP-glucose = 3-D-glucosyl-1,2-diacylglycerol + UDP	Enzymatic activity (see Klement, Ojemyr et al., 2007)
R064	glycosyl transferase	?	2.4.1.46	MPN483	Glycolipid metabolism	diacyl-sn-glycerol + UDP-galactose = 3-beta-D-galactosyl-1,2-diacyl-sn-glycerol + UDP	Enzymatic activity (see Klement, Ojemyr et al., 2007)
R067	5'-nucleotidase	NT5	3.1.3.5	?	Purine metabolism	AMP + H2O = adenosine + phosphate	Enzymatic activity (McElwain et al., 1988; Pollack and Hoffmann, 1982)
R080	5'-nucleotidase	NT5	3.1.3.5	?	Purine metabolism	GMP + H2O = guanosine + phosphate	Enzymatic activity (McElwain et al., 1988)
R091	uridine phosphorylase	UPP	2.4.2.3	MPN064	Pyrimidine metabolism	uridine + phosphate = uracil + D-ribose 1-phosphate	Enzymatic activity (McElwain and Pollack, 1987; McGarrityJ, Gamonet al., 1985)
R092	5'-nucleotidase	NT5	3.1.3.5	?	Pyrimidine metabolism	UMP + H2O = uridine + phosphate	Enzymatic activity (Hamet et al., 1980)
R098	CTP synthase	CTPS	6.3.4.2	MPN256	Pyrimidine metabolism	UTP + ATP + NH3 = CTP + ADP + phosphate	1) Sequence homology; 2) effect of uridine in minimal medium
R101	5'-nucleotidase	NT5	3.1.3.5	?	Pyrimidine metabolism	CMP + H2O = cytidine + phosphate	Predicted from the existence of a non-specific 5'-nucleotidase
R106	deoxycytidine kinase	DCK	2.7.1.74	?	Pyrimidine metabolism	deoxycytidine + ATP = dCMP + ADP	1) Gap filling; 2) Enzymatic activity (Williams and Pollack, 1990; Cowen and Smith, 1972; Wang et al., 2001)



Reaction ID	Enzyme name	Enz abbr.	EC number	Gene number	Pathway	Equation	Evidence
R111	uridine phosphorylase	UPP	2.4.2.3	MPN064	Pyrimidine metabolism	deoxyuridine + phosphate = uracil + 2-deoxyD-ribose 1-phosphate	Enzymatic activity (McElwain and Pollack , 1987; McGarrityJ, Gamonet al., 1985)
R117	5'-nucleotidase	NT5	3.1.3.5	?	Pyrimidine metabolism	dTMP + H2O = thymidine + phosphate	Predicted from the existence of a non-specific 5'-nucleotidase
R127	formate tetrahydrofolate ligase	FHS	6.3.4.3	MPN017	One carbon pool by folate	tetrahydrofolate + formate + ATP = 10-formyltetrahydrofolate + ADP + phosphate	1) Gap filling; 2) predicted from eukaryotes
R135	adenosylhomocysteinease	AHC	3.3.1.1	?	Methionine metabolism	S-adenosyl-L-homocysteine + H2O = L-homocysteine + adenosine	Gap filling, S-adenosyl-L-homocysteine clearance
R142	pyridoxal kinase	PDXK	2.7.1.35	?	Vitamin B6 metabolism	pyridoxal + ATP = pyridoxal 5'-phosphate + ADP	Needed for functional pyridoxal 5'-phosphate cofactor synthesis
R145	pantothenate kinase	PANK	2.7.1.33	?	Pantothenate and CoA biosynthesis	pantetheine + ATP = pantetheine 4'-phosphate + ADP	Pantothenate assimilation (minimal medium)
R146	pantetheine-phosphate adenylyltransferase	COASY	2.7.7.3	MPN336	Pantothenate and CoA biosynthesis	pantetheine 4'-phosphate + ATP = 3'-dephospho-CoA + diphosphate	Sequence homology, Smart, Swissprot
R150	long-chain-fatty-acid [acyl-carrier-protein] ligase	AAS	6.2.1.20	?	Glycerophospholipid metabolism	fatty acid + [acyl-carrier protein] + ATP = acyl-[acyl-carrier protein] + AMP + diphosphate	Needed for lipid synthesis
R173	NAD+ kinase	NADK	2.7.1.23	MPN267	Nicotinate and nicotinamide metabolism	NADH + ATP = NADPH + ADP	Needed for NADPH synthesis (see Mori, Kawai et al., 2006)
R175	phosphoglycerate kinase	PGK	2.7.2.3	MPN429	Purine metabolism	3-phospho-D-glyceroyl phosphate + dADP = 3-phospho-D-glycerate + dATP	Enzymatic activity (Pollack, Myers et al., 2002)
R176	phosphoglycerate kinase	PGK	2.7.2.3	MPN429	Purine metabolism	3-phospho-D-glyceroyl phosphate + GDP = 3-phospho-D-glycerate +GTP	Enzymatic activity (Pollack, Myers et al., 2002)
R177	phosphoglycerate kinase	PGK	2.7.2.3	MPN429	Purine metabolism	3-phospho-D-glyceroyl phosphate + dGDP= 3-phospho-D-glycerate + dGTP	Enzymatic activity (Pollack, Myers et al., 2002)
R180	choline-phosphate cytidylyltransferase	PCT	2.7.7.15	MPN336	Lipid metabolism	choline phosphate + CTP = CDP-choline + pyrophosphate	Sequence homology, Smart, Swissprot
R181	formate dehydrogenase	FDH	1.2.1.2	?	One carbon pool by folate	formate + NAD+ = CO2 + NADH	Formate needed for formylation of methionine for protein synthesis (see R127)
R185	methenyltetrahydrofolate hydrolase?	MTHFH	?	MPN576	One carbon pool by folate	5,10-methenyltetrahydrofolate + H2O = 5-formyltetrahydrofolate + H+	Needed to explain 5-formylTHF generation (used in R132), and Stover and Schirch, 1990.
R186	glycerol-3-phosphate oxidase	GPO	1.1.3.21	MPN051	Glycerophospholipid metabolism	glycerol 3-phosphate + O2 = glycerone phosphate + H2O2	From Hames et al., (2009).
R187	phosphatidylcholine acylhydrolase	PldB	3.1.1.5	MPN445?	Lipid metabolism	phosphatidylcholine + 2 H2O = sn-glycero-3-phosphocholine + 2 fatty acid	Sequence homology to <i>M. mobile</i> enzyme (MMOB3850)
R188	3'(2'),5'-bisphosphate nucleotidase	BPNT	3.1.3.7	?	Pantothenate and CoA biosynthesis	adenosine 3',5'-bisphosphate + H2O = AMP + phosphate	Needed to close the panthenonate cycle (adenosin-3',5'-bisphosphate was not used in any other reaction)

**Table S5. Uncharacterized metabolic genes**

Gene number	Gene name	Protein Description	EC number	Function	COG	Functional category?
MPN009	yabD	Uncharacterized deoxyribonuclease MG009 homolog (EC 3.1.21.-)	3.1.21.-	Endodeoxyribonuclease activity, producing 5'-phosphomonoesters	F	Nucleotide metabolism
MPN028	trsB	Uncharacterized glycosyl transferase	2.4.1.-	Glycosyl transferase	G	Carbohydrate and energy metabolism
MPN071	yabC	Predicted methyltransferase	3.1.26.8	Methyltransferase	F	Nucleotide metabolism
MPN075	ywdF	Uncharacterized glycosyltransferase family 2 (EC 2.4.-.-)	2.4.-.-	Glycosyltransferase	G	Carbohydrate and energy metabolism
MPN076	uhpT	Hexose phosphate transport protein	?		G	Carbohydrate and energy metabolism
MPN077	uhpT	Hexosephosphate transport protein	?		G	Carbohydrate and energy metabolism
MPN081	glnQ	Glutamine transport ATP-binding protein glnQ	?	ATP-dependent glutamine permease	E	Amino acid metabolism
MPN095	mpn095	Uncharacterized amino acid permease	-		E	Amino acid metabolism
MPN096	mpn096	Uncharacterized amino acid permease	-		E	Amino acid metabolism
MPN107	mpn107	Predicted methylase	?		F	Nucleotide metabolism
MPN114	cpt2	Putative acetyltransferase MPN_114 (EC 2.3.1.-)	2.3.1.-; 2.3.1.7	Acyltransferase	I	Lipid metabolism
MPN126	ysnB	Putative metallophosphoesterase ysnB (EC 3.1.4.-)	3.1.4.-	Hydrolase	R	General function prediction
MPN140	ytqI	Oligoribonuclease (DHH family phosphoesterases)	?	Hydrolase	F	Nucleotide metabolism
MPN193	cbiO	Cobalt import ATP-binding protein CbiO 1 (EC 3.6.3.-)	3.6.3.-	ATP dependent cobalt transporter (ATPase)	P	Ion transport
MPN194	hisP	Cobalt import ATP-binding protein CbiO 2 (EC 3.6.3.-)	3.6.3.-	ATP dependent cobalt transporter (ATPase)	P	Ion transport
MPN195	cbiQ	Similar to cobalt ABC transporter CbiQ	3.6.3.-	ATP dependent cobalt transporter (permease)	P	Ion transport
MPN209	mgtA	Probable cation-transporting P-type ATPase (EC 3.6.3.-)	3.6.3.-	ATP dependent cation (Mg <sup>2+</sup> , Ca <sup>2+</sup> ) permease	P	Ion transport
MPN255	ygbP	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase-like	2.7.7.60	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase?	R	General function prediction
MPN264	mpn264	Uncharacterized hydrolase, haloacid dehalogenase-like family protein (EC 3.1.-.-)	3.1.-.-	Hydrolase	R	General function prediction
MPN268	ptsG	Putative phosphotransferase enzyme IIB component MPN_268 (EC 2.7.1.69)	2.7.1.69	Protein-N(Pi)-phosphohistidine-sugar phosphotransferase	G	Carbohydrate and energy metabolism
MPN269	ymdA	HD superfamily hydrolase (EC 3.1.4.16) 2',3'-cyclic-nucleotide 2'-phosphodiesterase	3.1.4.16; 3.1.-.-	Exoribonuclease?	F	Nucleotide metabolism
MPN278	yefE	UDP-galactopyranose mutase (EC 5.4.99.9)	5.4.99.9	UDP-galactopyranose mutase, oxidoreductase	G	Carbohydrate and energy metabolism
MPN308	mpn308	Uncharacterized amino acid permease	-		E	Amino acid metabolism
MPN318	mpn318	Putative amino acid permease	-		E	Amino acid metabolism
MPN319	gap1	Putative amino acid permease	-		E	Amino acid metabolism
MPN381	yidA	HAD superfamily hydrolase/phosphatase	3.1.-.-; 3.1.3.-	Hydrolase or phosphatase (sugar phosphatase?)	GR	Carbohydrate and energy metabolism
MPN383	yidA	Cof-like hydrolase	3.1.3.-	Hydrolase or phosphatase	R	General function prediction
MPN407	mpn407	Predicted lipase	3.1.-.-		I	Lipid metabolism
MPN431	cbiQ	Similar to CbiQ, cobalt ABC transporter ATP-binding protein	3.6.3.-	ATP dependent cobalt transporter (permease)	P	Ion transport
MPN432	artP	Putative cobalt ABC transporter ATP-binding protein	3.6.3.-	ATP dependent cobalt transporter (ATPase)	P	Ion transport
MPN433	cbiO	Putative cobalt ABC transporter ATP-binding protein CbiO	3.6.3.-	ATP dependent cobalt transporter (ATPase)	P	Ion transport
MPN460	ktrB	Ktr system potassium uptake protein B	-	Potassium importer (integral membrane) subunit	P	Ion transport
MPN461	ktrA	Ktr system potassium uptake protein A	-	Potassium importer (cytoplasmic catalytic subunit)	P	Ion transport
MPN473	lip2	Putative esterase/lipase 2 (EC 3.1.-.-)	3.1.-.-	Carboxylesterase	I	Lipid metabolism
MPN491	mnuA	Membrane nuclease A	3.1.-.-	Nuclease	F	Nucleotide metabolism
MPN609	pstB	Phosphate import ATP-binding protein pstB (EC 3.6.3.27) (Phosphate-transporting ATPase) (ABC phosphate transporter)	3.6.3.27	Phosphate transport system (ATPase)	P	Ion transport
MPN610	pstA	Phosphate transport system permease protein pstA homolog	3.6.3.27	Phosphate transport system (permease)	P	Ion transport
MPN611	pstS	Phosphate-binding protein pstS (PBP)	3.6.3.27	Phosphate transport system (substrate binding)	P	Ion transport
MPN673	ygbB	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase-like	4.6.1.12	Nucleotidyl transferase??	R	General function prediction