SUPPLEMENTARY MATERIAL

Appendix Annotation table of the *M. penetrans* genome

Type	MYPE No.	COG	General name	Definition
CDS	MYPE10	L	*dnaA*	chromosomal replication initiator protein
CDS	MYPE20	L	*dnaN*	DNA polymerase III subunit beta
CDS	MYPE30	L	*gyrB*	DNA gyrase subunit B
CDS	MYPE40	L	*gyrA*	DNA gyrase subunit A
CDS	MYPE50	L		transposase, truncated, C-terminal of MYPE9620
CDS	MYPE60	L		transposase, truncated, N-terminal of MYPE9620
CDS	MYPE70	-		transposase, truncated
CDS	MYPE80	D	*soj*	ParA family of ATPases involved in chromosome partition Soj
CDS	MYPE90	-		hypothetical protein
CDS	MYPE100	J	*cspR*	rRNA methylase
CDS	MYPE110	-		hypothetical protein, MYPE120 paralog
CDS	MYPE120	-		hypothetical protein, paralog family
CDS	MYPE130	J		pseudouridine synthase
CDS	MYPE140	O		peroxiredoxin
CDS	MYPE150	-		hypothetical protein
CDS	MYPE160	M		UTP-glucose-1-phosphate uridylyltransferase
CDS	MYPE170	-		transposase
CDS	MYPE180	-		hypothetical protein
CDS	MYPE190	-		hypothetical protein
CDS	MYPE200	G	*pgm*	phosphoglycerate mutase
CDS	MYPE210	G	*tpiA*	triose phosphate isomerase
CDS	MYPE220	J	*cysS*	cysteinyl-tRNA synthetase
CDS	MYPE230	J	*spoU*	rRNA methylase
CDS	MYPE240	-		conserved hypothetical protein
CDS	MYPE250	J	*rplK*	ribosomal protein L11
CDS	MYPE260	J		ribosomal protein L1
CDS	MYPE270	M		glycosyltransferase
CDS	MYPE280	-		hypothetical protein
CDS	MYPE290	J	*rpsL*	ribosomal protein S12
CDS	MYPE300	J	*rpsG*	ribosomal protein S7
CDS	MYPE310	J	*fusA*	elongation factor G
CDS	MYPE320	J	*tufA*	elongation factor Tu
CDS	MYPE330	-		hypothetical protein
CDS	MYPE340	-		conserved hypothetical protein
CDS	MYPE350	I		Holo-(Acyl Carrier Protein) Synthase
CDS	MYPE360	-		hypothetical protein
CDS	MYPE370	I	*plsC*	1-acyl-sn-glycerol-3-phosphate acyltransferase
CDS	MYPE380	S		conserved hypothetical protein
CDS	MYPE390	K		conserved hypothetical protein
CDS	MYPE400	-		conserved hypothetical protein
CDS	MYPE410	R		predicted GTP-binding protein
CDS	MYPE420	J	*valS*	valyl-tRNA synthetase
CDS	MYPE430	R		predicted competence protein
CDS	MYPE440	-		conserved hypothetical protein
CDS	MYPE450	L		conserved hypothetical protein
CDS	MYPE460	-		putative integral membrane protein
CDS	MYPE470	-		putative integral membrane protein, similar to cytadherence-accessory protein HMW1 homologue of Mycoplasma genitalium MG313, F64234 Expect=2.5e-18, Identities=30%

CDS	MYPE480	J	*rpsT*	ribosomal protein S20
CDS	MYPE490	-		conserved hypothetical protein
CDS	MYPE500	J	*fmt*	methionyl-tRNA formyltransferase
CDS	MYPE510	N	*lepA*	GTP-binding membrane protein
CDS	MYPE520	F	*pyrG*	CTP synthetase
CDS	MYPE530	R		predicted GTPase, containing MMR_HSR1 domain
CDS	MYPE540	-		conserved hypothitical protein
CDS	MYPE550	-		hypothetical protein
CDS	MYPE560	C	*atpB*	ATP synthase subunit A
CDS	MYPE570	C	*atpE*	ATP synthase subunit C
CDS	MYPE580	C	*atpF*	ATP synthase subunit B
CDS	MYPE590	C	*atpH*	ATP synthase subunit delta
CDS	MYPE600	C	*atpA*	ATP synthase subunit alpha
CDS	MYPE610	C	*atpG*	ATP synthase subunit gamma
CDS	MYPE620	C	*atpD*	ATP synthase subunit beta
CDS	MYPE630	C	*atpC*	ATP synthase subunit epsilon
CDS	MYPE640	J	*rpmE*	ribosomal protein L31
CDS	MYPE650	J	*prfA*	peptide chain release factor 1
CDS	MYPE660	J	*hemK*	S-adenosylmethionine-dependent methyltransferase HemK
CDS	MYPE670	J		predicted translation factor Sua5/YciO/YrdC family protein
CDS	MYPE680	G	*rpiB/lacA/lac*	ribose 5-phosphate and galactose-6-phosphate isomerase
CDS	MYPE690	K		putative two-component response regulator
CDS	MYPE700	R		predicted intracellular protease ThiJ family
CDS	MYPE710	K	*hrcA*	heat-inducible transcription repressor
CDS	MYPE720	-		hypothetical protein
CDS	MYPE730	G		deoxyxylulose-5-phosphate synthase
CDS	MYPE740	L		conserved hypothetical protein
CDS	MYPE750	-		hypothetical protein
CDS	MYPE760	O	*nifU*	nitrogen fixation protein NifU
CDS	MYPE770	G	*tkt*	transketolase TKT
CDS	MYPE780	G	*pyk*	pyruvate kinase
CDS	MYPE790	K	*rpoB*	DNA-directed RNA polymerase subunit beta
CDS	MYPE800	K	*rpoC*	DNA-directed RNA polymerase subunit beta’
CDS	MYPE810	J	*rplM*	ribosomal protein L13
CDS	MYPE820	J	*rplI*	ribosomal protein S9
CDS	MYPE830	-		hypothetical protein
CDS	MYPE835	-		hypothetical protein
CDS	MYPE840	R		predicted haloacid dehalogenase-like hydrolase
CDS	MYPE850	F	*nrdE*	ribonucleoside diphosphate reductase subunit alpha
CDS	MYPE860	F	*nrdI*	ribonucleotide reductase NrdI
CDS	MYPE870	F	*nrdF*	ribonucleotide diphosphate reductase subunit beta
CDS	MYPE880	R		predicted permeases, MYPE890 paralog
CDS	MYPE890	-		predicted permeases, paralog family
CDS	MYPE900	Q		conserved hypothetical protein
CDS	MYPE910	-		putative membrane integrated oxidoreductase
CDS	MYPE920	-		hypothetical protein
CDS	MYPE930	-		hypothetical protein
CDS	MYPE940	H	*metK*	S-adenosylmethionine synthetase
CDS	MYPE950	-		hypothetical protein, paralog family
CDS	MYPE960	Q		ABC transporter ATP-binding protein, paralog family
CDS	MYPE970	R		predicted integral membrane protein
CDS	MYPE980	O	*groES*	chaperonin GroES
CDS	MYPE990	O	*groES*	chaperonin GroEL
CDS	MYPE1000	F		deoxyuridine 5’triphosphate nucleotidohydrolase dUTPase
CDS	MYPE1010	J	*rpsP*	ribosomal protein S16
CDS	MYPE1020	J	*trmD*	tRNA (guanine-N1)-methyltransferase

CDS	MYPE1030	J	*rplS*	ribosomal protein L19
CDS	MYPE1035	-		predicted coding region
CDS	MYPE1040	F	*pnp*	purine nucleoside phosphorylase
CDS	MYPE1050	F	*deoA*	thymidine phosphorylase
CDS	MYPE1060	F	*cdd*	cytidine deaminase
CDS	MYPE1070	G	*manB*	phosphomannomutase
CDS	MYPE1080	-		hypothetical protein
CDS	MYPE1090	K	*nusA*	N-utilization substance protein A
CDS	MYPE1100	-		hypothetical protein
CDS	MYPE1110	J	*infB*	translation initiation factor IF-2
CDS	MYPE1120	J		ribosome binding factor A
CDS	MYPE1130	-		conserved hypothetical protein
CDS	MYPE1140	J	*rpsF*	ribosomal protein S6
CDS	MYPE1150	L	*ssb*	single-strand DNA binding protein
CDS	MYPE1160	J	*rpsR*	ribosomal protein S18
CDS	MYPE1170	F	*deoC*	deoxyribose-phosphate aldolase
CDS	MYPE1180	R		conserved hypothetical protein, similar to hydrolase
CDS	MYPE1190	L	*nfo*	endonuclease IV
CDS	MYPE1200	P	*fur*	ferric uptake regulation protein
CDS	MYPE1210	-		integral membrane protein predicted transporter
CDS	MYPE1220	F	*guaA*	GMP synthase
CDS	MYPE1230	L	*dam*	adenine-specific DNA methyltransferase
CDS	MYPE1240	L		transposase for IS1630-like insertion sequence element
CDS	MYPE1250	-		conserved hypothetical protein
CDS	MYPE1260	L	*uvrC*	excinuclease ABC subunit C
CDS	MYPE1270	L		exonuclease, possibly DNA polymerase III
CDS	MYPE1280	R		predicted phosphoesterase
CDS	MYPE1290	R		ribosomal protein-alanine-acetyltransferase
CDS	MYPE1300	O		conserved hypothetical protein
CDS	MYPE1310	J	*rluB*	pseudouridine synthase
CDS	MYPE1320	N	*lsp*	prolipoprotein signal peptidase
CDS	MYPE1330	I		lytB protein
CDS	MYPE1340	G	*ptsG*	PTS system glucose-specific enzyme II ABC component
CDS	MYPE1350	-		hypothetical protein
CDS	MYPE1370	-		conserved hypotheticalprotein
CDS	MYPE1380	-		conserved hypothetical protein
CDS	MYPE1390	O	*trxB*	thioredoxin reductase
CDS	MYPE1400	R		predicted methyltransferase
CDS	MYPE1410	-		hypothetical protein
CDS	MYPE1420	L		ATP/GTP-binding protein, predicted ATPase
CDS	MYPE1430	-		conserved hypothetical protein
CDS	MYPE1440	-		conserved hypothetical protein
CDS	MYPE1450	J	*pth*	peptidyl-tRNA hydrolase
CDS	MYPE1460	D		predicted cell cycle protein MesJ/ ATPase of the PP-loop superamily
CDS	MYPE1470	I		1-deoxy-D-xylulose 5-phosphate reductoisomerase
CDS	MYPE1480	E	*asnA*	asparagine synthetase A
CDS	MYPE1490	L	*mucB*	DNA-damage repair protein MucB
CDS	MYPE1500	J		hemolysin
CDS	MYPE1510	-		hypothetical protein
CDS	MYPE1520	-		predicted coiled-coil structure containing protein
CDS	MYPE1530	-		predicted cytoskeletal protein, coiled-coil structure containing protein
CDS	MYPE1540	-		predicted coiled-coil structure containing protein
CDS	MYPE1550	D		predicted cytoskeletal protein, ortholog of cytoskeletal protein HMW2 of M. pneumoniae MPN310, NP_109998,

				(SwissProt HMW2_MYCPN), predicted coiled-coil structure containing protein
CDS	MYPE1560	-		predicted cytoskeletal protein, predicted coiled-coil structure containing protein
CDS	MYPE1570	-		predicted cytoskeletal protein, similar to cytoskeletal protein HMW2 homolog MG218 of M. genitalium U39701, Expect = 1.1e-20, Identities = 152/631 (24%), predicted coiled-coil structure containing protein
CDS	MYPE1580	J	*efp*	translation elongation factor P
CDS	MYPE1590	-		low similarity to ATP synthase subunit gamma
CDS	MYPE1600	K	*nusB*	transcription termination factor N-utilization substance protein B
CDS	MYPE1610	S		conserved hypothetical protein
CDS	MYPE1620	-		conserved hypothetical protein
CDS	MYPE1630	J		conserved hypothetical protein
CDS	MYPE1640	P		conserved hypothetical protein
CDS	MYPE1650	-		conserved hypothetical protein
CDS	MYPE1660	-		conserved hypothetical protein
CDS	MYPE1670	D	*gidA*	glucose inhibited division protein
CDS	MYPE1680	-		hypothetical protein
CDS	MYPE1690	R	*nox*	NADH oxidase
CDS	MYPE1700	R	*nodL*	acetyl transferase
CDS	MYPE1710	O	*trxA*	thioredoxin
CDS	MYPE1720	K		transcriptional regulator RpiR family
CDS	MYPE1730	G	*ptsG*	PTS system glucose-specific IIABC component
CDS	MYPE1740	G		N-acetylmannosamine 6-P epimerase
CDS	MYPE1750	G	*nagA*	N-acetylglucosamine 6-P deacetylase
CDS	MYPE1760	G	*nagB*	N-acetylglucosamine 6-phosphate isomerase
CDS	MYPE1770	-		hypothetical protein
CDS	MYPE1780	L	*dam*	adenine-specific DNA methyltransferase
CDS	MYPE1790	L	*dam*	adenine-specific DNA methyltransferase
CDS	MYPE1800	-		conserved hypothetical protein
CDS	MYPE1810	S		conserved hypothetical protein
CDS	MYPE1820	-	*ecsB*	ABC transporter membrane protein
CDS	MYPE1830	-		conserved hypothetical protein
CDS	MYPE1840	L	*ligA*	NAD-dependent DNA ligase
CDS	MYPE1850	L		6-O-methylguanine DNA methyltransferas
CDS	MYPE1860	S		hypothetical protein
CDS	MYPE1870	-		hypothetical protein
CDS	MYPE1880	Q	*ecsA*	ABC transporter ATP-binding protein, MYPE3080 paralog
CDS	MYPE1890	I	*acpD*	acyl carrier protein phosphodiesterase
CDS	MYPE1900	-		hypothetical protein
CDS	MYPE1910	J		hypothetical protein
CDS	MYPE1920	-		conserved hypothetical protein
CDS	MYPE1930	R	*obg*	GTP-binding protein Obg
CDS	MYPE1940	H	*nade*	NH(3)-dependent NAD+ synthetase
CDS	MYPE1950	-		putative integral membrane protein, low similarity to P1-like adhesin precursor of Mycoplasma pirum L19685 Expect=6.3e-03, Identities=19%
CDS	MYPE1960	-		hypothetical protein
CDS	MYPE1970	-		hypothetical protein
CDS	MYPE1980	L	*dnaE*	DNA polymerase III subunit alpha
CDS	MYPE1990	L	*polI*	DNA polymerase I: 5'-3' exonuclease
CDS	MYPE2000	L	*fpg*	formamidopyrimidine-DNA glycosylase
CDS	MYPE2010	H		conserved hypothetical protein
CDS	MYPE2020	L		conserved hypothetical protein
CDS	MYPE2030	L		primosome component

CDS	MYPE2040	O		conserved hypothetical protein
CDS	MYPE2050	L	*dnaB*	replicative DNA helicase
CDS	MYPE2060	-		hypothetical protein
CDS	MYPE2070	L	*udg*	uracil-DNA glycosylase
CDS	MYPE2080	-		glutamyl-tRNA amidotransferase subunit C-related protein
CDS	MYPE2090	J	*gatC*	glutamyl-tRNA amidotransferase subunit C
CDS	MYPE2100	J	*gatA*	glutamyl-tRNA amidotransferase subunit A
CDS	MYPE2110	J	*gatB*	glutamyl-tRNA amidotransferase subunit B
CDS	MYPE2120	S		conserved hypothetical protein
CDS	MYPE2130	P	*pacL*	cation-transporting P-type ATPase
CDS	MYPE2140	-		hypothetical protein, paralog family
CDS	MYPE2150	-		hypothetical protein, MYPE2140 paralog
CDS	MYPE2160	-		hypothetical protein, MYPE2140 paralog
CDS	MYPE2170	L		Insertion sequence IS232 putative ATP-binding protein
CDS	MYPE2180	-		transposase for IS232-like insertion sequence element
CDS	MYPE2190	P		hypothetical protein
CDS	MYPE2200	Q		ABC transporter ATP-binding protein
CDS	MYPE2210	Q		ABC transporter ATP-binding protein
CDS	MYPE2220	-		conserved hypothetical protein
CDS	MYPE2230	-		hypothetical protein
CDS	MYPE2240	-		conserved hypothetical protein
CDS	MYPE2250	R		conserved hypothetical protein, MYPE4220 paralog
CDS	MYPE2260	-		hypothetical protein
CDS	MYPE2270	-		hypothetical protein
CDS	MYPE2280	F	*cmk*	cytidylate kinase
CDS	MYPE2290	R		predicted ATP/GTP-binding protein
CDS	MYPE2300	C	*gpsA*	NAD-dependent glycerol-3-phosphate dehydrogenase
CDS	MYPE2310	-		transposase for IS1202-like insertion sequence element
CDS	MYPE2330	S		conserved hypothetical protein
CDS	MYPE2340	-		transposase
CDS	MYPE2350	-		predicted integral membrane protein, MYPE2360 paralog
CDS	MYPE2360	-		predicted integral membrane protein, low similarity to histidine kinase, paralog family
CDS	MYPE2370	-		predicted integral membrane protein, MYPE2360 paralog
CDS	MYPE2380	-		predicted integral membrane protein, MYPE2360 paralog
CDS	MYPE2390	-		hypothetical protein
CDS	MYPE2400	-		predicted integral membrane protein, MYPE2360 paralog
CDS	MYPE2410	-		predicted integral membrane protein, MYPE2360 paralog
CDS	MYPE2420	-		predicted integral membrane protein
CDS	MYPE2430	-		predicted integral membrane protein
CDS	MYPE2440	-		conserved hypothetical protein
CDS	MYPE2450	-		predicted integral membrane protein
CDS	MYPE2460	R		recombination protein U
CDS	MYPE2470	Q		ABC transporter ATP-binding protein, paralog family
CDS	MYPE2480	Q		ABC transporter ATP-binding protein
CDS	MYPE2490	L	*hupA*	DNA-binding histone-like protein HU-alpha
CDS	MYPE2500	-		predicted integral membrane protein
CDS	MYPE2510	-		conserved hypothetical protein
CDS	MYPE2520	-		conserved hypothetical protein
CDS	MYPE2530	N	*ffh*	signal recognition particle GTPase Ffh
CDS	MYPE2540	M		predicted Zn-dependent protease
CDS	MYPE2545	R		conserved hypothetical protein, MYPE2560 paralog, partial
CDS	MYPE2550	-		conserved hypothetical protein, MYPE2560 paralog, partial
CDS	MYPE2560	-		conserved hypothetical protein, paralog family
CDS	MYPE2570	K		conserved hypothetical protein

CDS	MYPE2580	-		conserved hypothetical protein, MYPE2560 paralog
CDS	MYPE2590	J		acetyltransferase GNAT family
CDS	MYPE2600	J		acetyltransferase GNAT family
CDS	MYPE2610	-		hypothetical protein, MYPE2560 paralog
CDS	MYPE2620	-		P35 lipoprotein homologue
CDS	MYPE2630	-		P35 lipoprotein homologue
CDS	MYPE2640	R		permease
CDS	MYPE2650	E		D-lactate dehydrogenase, D-LDH
CDS	MYPE2660	-		conserved hypothetical protein, MYPE2560 paralog
CDS	MYPE2670	-		conserved hypothetical protein, MYPE2560 paralog
CDS	MYPE2680	-		conserved hypothetical protein, MYPE2560 paralog
CDS	MYPE2690	-		P35 lipoprotein homologue
CDS	MYPE2700	-		P35 lipoprotein homologue
CDS	MYPE2710	-		conserved hypothetical protein, MYPE2560 paralog
CDS	MYPE2715	-		hypothetical protein
CDS	MYPE2720	-		conserved hypothetical protein
CDS	MYPE2730	E		serine hydroxymethyl transferase
CDS	MYPE2740	J	*thrS*	threonyl-tRNA synthetase
CDS	MYPE2750	S		conserved hypothetical protein
CDS	MYPE2760	-		conserved hypothetical protein
CDS	MYPE2770	I		cytidine diphosphocholine pyrophosphorylase
CDS	MYPE2780	L	*ruvB*	holliday junction DNA helicase RuvB
CDS	MYPE2790	L	*ruvA*	holliday junction DNA helicase RuvA
CDS	MYPE2800	G	*ptsH*	histidine-containing phosphocarrier protein of the PTS
CDS	MYPE2810	I	*cls*	cardiolipin synthase
CDS	MYPE2820	E	*pepF*	oligoendopeptidase F
CDS	MYPE2830	-		hypothetical protein
CDS	MYPE2840	-		hypothetical protein
CDS	MYPE2850	-		hypothetical protein
CDS	MYPE2860	J	*hisS*	histidyl-tRNA synthetase
CDS	MYPE2870	J	*aspS*	aspartyl-tRNA synthetase
CDS	MYPE2880	R		predicted S-adenosylmethionine-dependent methyltransferase
CDS	MYPE2890	-		conserved hypothetical protein
CDS	MYPE2900	L		integrase-recombinase protein
CDS	MYPE2910	-		conserved hypothetical protein
CDS	MYPE2920	-		conserved hypothetical protein
CDS	MYPE2930	P		ferritin-like protein Rsg
CDS	MYPE2940	-		hypothetical prottein, similar to beta-glycosidase lacS of Sulfolobus solfataricus AE006893 Expect=7.5e-01, Identities=35%
CDS	MYPE2950	R		predicted NADPH-dependent reductase
CDS	MYPE2960	K		transcriptional regulator MarR family
CDS	MYPE2970	-		predicted MutT/ NUDIX hydrolases
CDS	MYPE2980	-		hypothetical protein
CDS	MYPE2990	T	*hprK*	HPr serine/threonine protein kinase
CDS	MYPE3000	M	*lgt*	prolipoprotein diacylglyceryl transferase
CDS	MYPE3010	P	*trkA*	potassium uptake protein KtrA
CDS	MYPE3020	R		putative integral membrane protein
CDS	MYPE3030	Q		ABC transporter ATP-binding protein
CDS	MYPE3040	-		conserved hypothetical protein
CDS	MYPE3050	G	*rpe*	d-ribulose-5-phosphate 3 epimerase
CDS	MYPE3060	R		conserved hypothetical protein
CDS	MYPE3070	-		putative integral membrane protein
CDS	MYPE3080	Q		ABC transporter ATP-binding protein, paralog family
CDS	MYPE3090	-		conserved hypothetical protein
CDS	MYPE3100	-		hypothetical protein

CDS	MYPE3110	R		ortholog of YwnB of Bacillus subtilis
CDS	MYPE3120	K		ortholog of YwnA of Bacillus subtilis
CDS	MYPE3130	M		predicted choline kinase
CDS	MYPE3140	-		conserved hypothetical protein, MYPE2560 paralog
CDS	MYPE3150	F	*guaB*	inosine-5’-monophosphate dehydrogenase
CDS	MYPE3155	-		hypothetical protein
CDS	MYPE3160	I		3-hydroxyisobutyrate dehydrogenase
CDS	MYPE3170	R		HAD superfamily hydrolase
CDS	MYPE3180	G	*nagB*	glucosamine-6-phosphate isomerase
CDS	MYPE3190	-		predicted integral membrane protein
CDS	MYPE3200	L		DNA-3-methyladenine glycosidase I
CDS	MYPE3210	-		predicted integral membrane protein
CDS	MYPE3220	M		methyltransferase
CDS	MYPE3230	-		conserved hypothetical protein
CDS	MYPE3240	P	*pacL*	cation-transporting p-type ATPase
CDS	MYPE3250	P		cation-transporting p-type ATPase
CDS	MYPE3260	O	*trxA*	thioredoxin
CDS	MYPE3270	M		large-conductance mechanosensitive channel
CDS	MYPE3280	-		hypothetical protein
CDS	MYPE3290	-		hypothetical protein
CDS	MYPE3300	N	*secG*	predicted protein-export protein SecG
CDS	MYPE3310	K		3’-5’ exoribonuclease RNase R
CDS	MYPE3320	G		dihydroxyacetone kinase
CDS	MYPE3330	G		dihydroxyacetone kinase
CDS	MYPE3340	S	*ptsI*	PTS system enzyme I
CDS	MYPE3350	R		conserved hypothetical protein
CDS	MYPE3360	M	*dgkA*	diacylglycerol kinase
CDS	MYPE3370	R	*era*	GTP-binding protein Era homolog
CDS	MYPE3380	L		conserved hypothetical protein
CDS	MYPE3390	J	*glyS*	glycyl-tRNA synthetase
CDS	MYPE3400	L	*dnaG*	DNA primase
CDS	MYPE3410	-		hypothetical protein, MYPE8480 paralog
CDS	MYPE3420	-		hypothetical protein, MYPE8480 paralog
CDS	MYPE3430	-		hypothetical protein, MYPE8480 paralog
CDS	MYPE3440	-		putative integral membrane protein
CDS	MYPE3450	E		amino acid permease
CDS	MYPE3460	-		hypothetical protein
CDS	MYPE3490	R		ABC transporter ATP-binding protein, MYPE3080 paralog
CDS	MYPE3500	F	*hit*	histidine triad protein HIT
CDS	MYPE3510	-		hypothetical protein
CDS	MYPE3520	-		conserved hypothetical protein
CDS	MYPE3530	O	*smpB*	tmRNA-binding small protein B
CDS	MYPE3540	R		hippurate hydrolase
CDS	MYPE3550	R		conserved hypothetical protein
CDS	MYPE3560	Q		ABC transporter ATP-binding protein, MYPE960 paralog
CDS	MYPE3570	R		ABC transporter ATP-binding protein
CDS	MYPE3580	-		predicted integral membrane protein, paralog family
CDS	MYPE3590	-		hypothetical protein, MYPE3580 paralog
CDS	MYPE3600	-		hypothetical protein, MYPE3580 paralog
CDS	MYPE3610	-		hypothetical protein, MYPE3580 paralog
CDS	MYPE3620	-		conserved hypothetical protein
CDS	MYPE3630	R		ABC transporter ATP-binding protein, MYPE3080 paralog
CDS	MYPE3640	I	*plsX*	fatty acid/phospholipid synthesis protein
CDS	MYPE3650	K	*rnc*	ribonuclease III
CDS	MYPE3660	-		hypothetical protein
CDS	MYPE3670	K	*greA*	transcription elongation factor

CDS	MYPE3700	-		conserved hypothetical protein
CDS	MYPE3710	-	*ndhF*	NADH dehydrogenase
CDS	MYPE3720	-		hypothetical protein
CDS	MYPE3730	G	*tpiA*	triose phosphate isomerase
CDS	MYPE3740	G	*pgm*	phosphoglycerate mutase
CDS	MYPE3750	G	*eno*	enolase
CDS	MYPE3760	-		hypothetical protein
CDS	MYPE3770	-		conserved hypothetical protein
CDS	MYPE3780	S		conserved hypothetical protein
CDS	MYPE3790	O	*clpB*	ATP-dependent protease binding subunit
CDS	MYPE3800	-		hypothetical protein
CDS	MYPE3810	-		hypothetical protein
CDS	MYPE3820	-		hypothetical protein
CDS	MYPE3830	-		hypothetical protein
CDS	MYPE3840	-		hypothetical protein
CDS	MYPE3850	-		hypothetical protein
CDS	MYPE3860	-		hypothetical protein
CDS	MYPE3870	F	*pyrC*	dihydroorotase
CDS	MYPE3880	J	*rpsO*	ribosomal protein S15
CDS	MYPE3890	J	*leuS*	leucyl-tRNA synthetase
CDS	MYPE3900	J	*rpmG*	ribosomal protein L33
CDS	MYPE3910	E	*pepP*	aminopeptidase P
CDS	MYPE3920	C	*dhaS*	aldehyde dehydrogenase
CDS	MYPE3930	R		esterase/lipase 1
CDS	MYPE3940	-		hypothetical protein
CDS	MYPE3950	-		hypothetical protein
CDS	MYPE3960	R		putative two-component regulator
CDS	MYPE3970	S		conserved hypothetical protein
CDS	MYPE3980	O	*tpx*	thiol peroxidase
CDS	MYPE3985	-		hypothetical protein
CDS	MYPE3990	-		hypothetical protein
CDS	MYPE4000	-		hypothetical protein
CDS	MYPE4010	-		hypothetical protein
CDS	MYPE4020	S		putative integral membrane protein
CDS	MYPE4030	J	*rpL28*	ribosomal protein L28
CDS	MYPE4040	J	*asnS*	asparaginyl-tRNA synthetase
CDS	MYPE4050	I	*pgsA*	phosphatidylglycerophosphate synthase
CDS	MYPE4060	J	*serS*	seryl-tRNA synthetase
CDS	MYPE4070	-		conserved hypothetical protein, MYPE6060 paralog
CDS	MYPE4080	-		hypothetical protein
CDS	MYPE4090	Q		ABC transporter ATP-binding protein, MYPE2470 paralog
CDS	MYPE4100	Q		ABC transporter ATP-binding protein, MYPE2470 paralog
CDS	MYPE4110	C		aldehyde dehydrogenase
CDS	MYPE4120	-		conserved hypothetical protein
CDS	MYPE4130	R		predicted dihydroacetone kinase
CDS	MYPE4140	L	*topA*	DNA topoisomerase I
CDS	MYPE4150	-		hypothetical protein
CDS	MYPE4160	I	*acp*	acyl carrier protein
CDS	MYPE4170	L		predicted endo/excinuclease
CDS	MYPE4180	-		transposase for IS232-like insertion sequence element
CDS	MYPE4190	L		Insertion sequence IS232 putative ATP-binding protein
CDS	MYPE4200	-		hypothetical protein
CDS	MYPE4210	-		hypothetical protein
CDS	MYPE4220	R		conserved hypothetical protein, paralog family
CDS	MYPE4230	R		conserved hypothetical protein, paralog family
CDS	MYPE4240	-		hypothetical protein

CDS	MYPE4250	-		hypothetical protein
CDS	MYPE4260	G		6-phosphogluconate dehydrogenase
CDS	MYPE4270	-		conserved hypothetical protein
CDS	MYPE4280	S		proline dipeptidase
CDS	MYPE4290	F	*purB*	adenylosuccinate synthetase
CDS	MYPE4300	-		hypothetical protein
CDS	MYPE4310	J		putative integral membrane protein, immuno-dominant variable surface antigen of Entamoeba histolytica CAA38847.1, Expect=3.0e-16, Identities=29%
CDS	MYPE4320	-		putative integral membrane protein
CDS	MYPE4330	-		hypothetical protein, paralog family
CDS	MYPE4340	-		hypothetical protein, MYPE4340 paralog
CDS	MYPE4350	-		hypothetical protein, MYPE4340 paralog
CDS	MYPE4360	-		hypothetical protein, MYPE4340 paralog
CDS	MYPE4370	-		hypothetical protein
CDS	MYPE4380	-	*mnuA*	membrane nuclease
CDS	MYPE4390	-		hypothetical protein
CDS	MYPE4400	C	*ppa*	inorganic pyrophosphatase
CDS	MYPE4410	-		putative integral membrane protein
CDS	MYPE4420	J	*rpL21*	ribosomal protein L21
CDS	MYPE4430	J		conserved hypothetical protein
CDS	MYPE4440	J	*rpmA*	ribosomal protein L27
CDS	MYPE4450	-		hypothetical protein
CDS	MYPE4460	G	*ppe*	d-ribulose-5-phosphate 3 epimerase
CDS	MYPE4470	L		transcriptional antiterminator BglG family
CDS	MYPE4480	G		PTS system enzyme IIA component
CDS	MYPE4490	G		conserved hypothetical protein
CDS	MYPE4500	S		PTS system enzyme IIC component
CDS	MYPE4510	G	*tktA*	transketolase I
CDS	MYPE4520	-		HAD superfamily hydrolase
CDS	MYPE4530	-		hypothetical protein
CDS	MYPE4540	G		PTS system enzyme IIBC components
CDS	MYPE4550	G	*bglH*	beta glucosidase
CDS	MYPE4560	G	*bglH*	beta glucosidase
CDS	MYPE4570	R		conserved hypothetical protein
CDS	MYPE4580	J	*trpS*	tryptophanyl-tRNA synthetase
CDS	MYPE4590	P		conserved hypothetical protein
CDS	MYPE4600	R		conserved hypothetical protein
CDS	MYPE4610	G		conserved hypothetical protein
CDS	MYPE4620	E	*gbsB*	alcohol dehydrogenase
CDS	MYPE4630	-		hypothetical protein, paralog family
CDS	MYPE4640	-		hypothetical protein
CDS	MYPE4650	-		hypothetical protein, MYPE4630 paralog
CDS	MYPE4660	-		hypothetical protein, MYPE4630 paralog
CDS	MYPE4680	-		hypothetical protein, MYPE4630 paralog
CDS	MYPE4690	G	*pgi*	glucose-6-phosphate isomerase
CDS	MYPE4700	-		conserved hypothetical protein
CDS	MYPE4710	C	*gap*	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
CDS	MYPE4720	R		oxidoreductase-aldo/keto reductase family, paralog family
CDS	MYPE4730	-		hypothetical protein, similar to CagA protein of Helicobacter pylori AJ269854, Expect=2.4e-01, Identities=40%
CDS	MYPE4740	-		hypothetical protein, MYPE 5680paralog
CDS	MYPE4750	-		hypothetical protein, MYPE 5680paralog
CDS	MYPE4760	-		hypothetical protein, MYPE 5680paralog
CDS	MYPE4765	-		hypothetical protein
CDS	MYPE4770	L		conserved hypothetical protein

CDS	MYPE4780	L		N-4 cytosine-specific and N-6 adenine-specific DNA methylases
CDS	MYPE4790	L		hypothetical ATP/GTP-binding protein
CDS	MYPE4800	-		hypothetical ATP/GTP-binding protein
CDS	MYPE4810	R		oxidoreductase, MYPE4720 paralog
CDS	MYPE4820	-		hypothetical protein
CDS	MYPE4830	D		structural maintenance of chromosomes SMC superfamily proteins
CDS	MYPE4840	N	*ftsY*	signal recognition particle SRP- homologue of FtsY
CDS	MYPE4850	S		conserved hypothetical protein
CDS	MYPE4860	-		hypothetical protein
CDS	MYPE4870	-		hypothetical protein
CDS	MYPE4880	L		transposase for IS1630-like insertion sequence element
CDS	MYPE4890	-		hypothetical protein
CDS	MYPE4900	D		hypothetical protein
CDS	MYPE4910	-		hypothetical protein
CDS	MYPE4920	S		conserved hypothetical protein
CDS	MYPE4930	-		conserved hypothetical protein
CDS	MYPE4940	L		cytosine-specific DNA methyltransferase
CDS	MYPE4950	R		haloacid dehalogenase-like hydrolase
CDS	MYPE4960	F	*nrdD*	anaerobic ribonucleoside-triphosphate reductase
CDS	MYPE4970	O	*nrdG*	anaerobic ribonucleoside-triphosphate reductase activating protein
CDS	MYPE4980	-		conserved hypothetical protein, similar to HMW1 of Mycoplasma pneumoniae, Pfam ELK domain Accession number: PF03789
CDS	MYPE4990	-		hypothetical protein, paralog family
CDS	MYPE5000	-		hypothetical protein, MYPE 4990 paralog
CDS	MYPE5010	H	*hemN*	oxygen-independent coproporphyrinogen III oxidase
CDS	MYPE5020	J	*miaA*	tRNA-isopentenyl pyrophosphate transferase
CDS	MYPE5030	C	*pta*	phosphotransacetylase
CDS	MYPE5040	-		hypothetical protein
CDS	MYPE5050	-		putative transcription antiterminator BglG family
CDS	MYPE5060	-		hypothetical protein
CDS	MYPE5070	D		conserved hypothetical protein
CDS	MYPE5080	C	*pdhA*	pyruvate dehydrogenase E1 component subunit alpha
CDS	MYPE5090	C	*pdhB*	pyruvate dehydrogenase E1 component subunit beta
CDS	MYPE5100	C	*pdhC*	dihydrolipoamide acetyltransferase of pyruvate dehydrogenase E2 component
CDS	MYPE5110	C	*pdhD*	dihydrolipoamide dehydrogenase of pyruvate dehydrogenase E3 component
CDS	MYPE5120	O		gluthatione peroxidase
CDS	MYPE5130	C		putative oxidoreductase
CDS	MYPE5140	K		transcriptional regulator AcrR family
CDS	MYPE5150	-		conserved hypothetical protein
CDS	MYPE5160	-		conserved hypothetical protein
CDS	MYPE5170	E	*aapA*	amino acid permease
CDS	MYPE5180	S		conserved hypothetical protein
CDS	MYPE5190	R		putative haloacid dehalogenase-like hydrolase
CDS	MYPE5200	H		putative nucleotidyl transferase
CDS	MYPE5210	F	*pfs*	5'-Methylthioadenosine/S-adenosylhomocysteine nucleosidase
CDS	MYPE5220	R		conserved hypothetical protein
CDS	MYPE5230	R	*adhA*	NADP-dependent alcohol dehydrogenase
CDS	MYPE5240	F		putative xanthosine triphosphate pyrophosphatase HAM1 family

CDS	MYPE5250	-		hypothetical protein
CDS	MYPE5260	R		conserved hypothetical protein, MYPE4230 paralog
CDS	MYPE5270	-		conserved hypothetical protein
CDS	MYPE5280	S	*spot*	ppGpp 3'-pyrophosphohydrolase
CDS	MYPE5290	R		conserved hypothetical protein
CDS	MYPE5300	-		hypothetical protein, paralog family
CDS	MYPE5310	-		hypothetical protein
CDS	MYPE5330	-		hypothetical protein
CDS	MYPE5340	-		hypothetical protein
CDS	MYPE5350	L		transposase for IS1630-like insertion sequence element
CDS	MYPE5360	-		hypothetical protein
CDS	MYPE5370	-		hypothetical protein
CDS	MYPE5380	-		hypothetical protein
CDS	MYPE5390	-		hypothetical protein, MYPE5300 paralog
CDS	MYPE5400	L		transposase for IS1630-like insertion sequence element
CDS	MYPE5410	-		transposase for IS1202-like insertion sequence element
CDS	MYPE5420	-		hypothetical protein
CDS	MYPE5430	-		hypothetical protein, MYPE5300 paralog
CDS	MYPE5440	R		predicted HD superfamily hydrolase
CDS	MYPE5445	-		hypothetical protein
CDS	MYPE5450	G	*ptsI*	PTS system enzyme I
CDS	MYPE5460	R		lipase-esterase related protein
CDS	MYPE5470	N	*secA*	preprotein translocase SecA
CDS	MYPE5480	-		hypothetical protein
CDS	MYPE5490	-		transposase for IS232-like insertion sequence element
CDS	MYPE5500	L		IS232 putative ATP-binding protein IstB
CDS	MYPE5505	-		hypothetical protein
CDS	MYPE5510	-		hypothetical protein
CDS	MYPE5520	R	*oppF*	oligopeptide transport ATP-binding protein OppF
CDS	MYPE5530	R	*oppD*	oligopeptide transport ATP-binding protein OppD
CDS	MYPE5540	E	*oppC*	oligopeptide transport system permease protein OppC
CDS	MYPE5550	E	*oppB*	oligopeptide transport system permease protein OppB
CDS	MYPE5560	-		conserved hypothetical protein
CDS	MYPE5570	R		glutamine transport ATP-binding protein, MYPE3080 paralog
CDS	MYPE5580	-		conserved hypothetical protein
CDS	MYPE5590	-		conserved hypothetical protein
CDS	MYPE5600	-		predicted methylase
CDS	MYPE5610	O	*pmsR*	peptide methionine sulfoxide reductase
CDS	MYPE5620	T		protein phosphatase
CDS	MYPE5630	R		ortholog of YloN of Bacillus subtilis
CDS	MYPE5640	F	*gmk*	guanylate kinase
CDS	MYPE5650	J	*def*	polypeptide deformylase
CDS	MYPE5660	L		transposase for IS1630-like insertion sequence element
CDS	MYPE5670	-		hypothetical protein, MYPE5680 paralog
CDS	MYPE5680	-		hypothetical protein, paralog family
CDS	MYPE5690	-		hypothetical protein
CDS	MYPE5700	C	*ackA*	acetate kinase
CDS	MYPE5710	-		transposase for IS1202-like insertion sequence element
CDS	MYPE5720	L		transposase for IS1202-like insertion sequence element
CDS	MYPE5730	J	*rplL*	ribosomal protein L7/L12
CDS	MYPE5740	J	*rplJ*	ribosomal protein L10
CDS	MYPE5750	C	*glpQ*	glycerophosphoryl diester phosphodiesterase
CDS	MYPE5760	G		permease
CDS	MYPE5770	-		hypothetical protein

CDS	MYPE5780	-		hypothetical protein
CDS	MYPE5790	-		hypothetical protein
CDS	MYPE5800	R		predicted AAA family ATPase
CDS	MYPE5810	F	*htp*	hypoxanthine-guanine phosphoribosyltransferase
CDS	MYPE5820	F		adenylosuccinate lyase
CDS	MYPE5830	F		adenylosuccinate synthetase
CDS	MYPE5840	-		hypothetical protein
CDS	MYPE5850	R		predicted phosphoesterase
CDS	MYPE5860	H	*thiI*	thiamin biosynthesis protein
CDS	MYPE5870	R		sugar ABC transporter permease
CDS	MYPE5880	R		sugar ABC transporter permease
CDS	MYPE5890	G		sugar ABC transporter ATP-binding protein
CDS	MYPE5900	N		putative lipoprotein
CDS	MYPE5910	G		PTS system enzyme IIABC component
CDS	MYPE5920	G	*pfk*	6-phosphofructokinase
CDS	MYPE5930	-		hypothetical protein
CDS	MYPE5940	K		MerR subfamily transcriptional regulator
CDS	MYPE5950	-		conserved hypothetical protein, MYPE5960 paralog
CDS	MYPE5960	R		conserved hypothetical protein, paralog family
CDS	MYPE5970	R		hypothetical protein
CDS	MYPE5980	-		conserved hypothetical protein, MYPE5960 paralog
CDS	MYPE5990	-		predicted lipase
CDS	MYPE6000	-		hypothetical protein
CDS	MYPE6010	-		predicted lipase
CDS	MYPE6020	-		hypothetical protein
CDS	MYPE6030	-		predicted lipase
CDS	MYPE6040	-		hypothetical protein
CDS	MYPE6050	-		predicted integral membrane protein
CDS	MYPE6060	-		predicted integral membrane protein, paralog family, low similarity to 116 kDa surface antigen of Mycoplasma genitalium Expect=1.4e-09, Identities=22%
CDS	MYPE6070	-		hypothetical protein, MYPE6060 paralog
CDS	MYPE6080	E	*arcA*	arginine deiminase
CDS	MYPE6090	E	*arcB*	ornithine carbamoyltransferase
CDS	MYPE6100	E	*arcC*	carbamate kinase
CDS	MYPE6110	E		amino acid permeases
CDS	MYPE6120	J	*argS*	arginyl tRNA synthetase
CDS	MYPE6130	R		predicted permiase, MYPE890 paralog
CDS	MYPE6140	-		hypothetical protein
CDS	MYPE6155	-		hypothetical protein
CDS	MYPE6160	-		hypothetical protein
CDS	MYPE6175	-		hypothetical protein
CDS	MYPE6180	-		conserved hypothetical protein
CDS	MYPE6190	-		conserved hypothetical protein
CDS	MYPE6200	-		hypothetical protein, MYPE6410 paralog
CDS	MYPE6210	C		NADH-dependent butanol dehydrogenase
CDS	MYPE6220	-		hypothetical protein
CDS	MYPE6230	-		hypothetical protein
CDS	MYPE6240	Q	*aldB*	alpha-acetolactate decarboxylase
CDS	MYPE6250	Q		probable 3-ketoacyl-acyl carrier protein reductase
CDS	MYPE6260	P		formate/ nitrite transporter
CDS	MYPE6270	S		conserved hypothetical protein
CDS	MYPE6275	-		conserved hypothetical protein
CDS	MYPE6280	-		conserved hypothetical protein
CDS	MYPE6290	-		transposase for IS232-like insertion sequence element
CDS	MYPE6300	L		IS232 putative ATP-binding protein IstB

CDS	MYPE6310	-		conserved hypothetical protein
CDS	MYPE6320	-		conserved hypothetical protein
CDS	MYPE6330	-		conserved hypothetical protein
CDS	MYPE6340	M		putative glycosyl transferase
CDS	MYPE6360	C	*glpK*	glycerol kinase
CDS	MYPE6370	R	*glpA*	glycerol-3-phosphate dehydrogenase
CDS	MYPE6380	G	*glpF*	glycerol uptake facilitator protein
CDS	MYPE6390	L	*recA*	recombination protein RecA
CDS	MYPE6400	R	*cinA*	putative competence-damage inducible protein CinA
CDS	MYPE6410	-		hypothetical protein
CDS	MYPE6420	R		NADPH oxidoreductase
CDS	MYPE6430	C		NADPH flavin oxidoreductase
CDS	MYPE6440	R		conserved hypothetical ATP/GTP-binding protein
CDS	MYPE6450	R		conserved hypothetical protein
CDS	MYPE6460	J		conserved hypothetical proteins
CDS	MYPE6470	L	*parC*	DNA topoisomerase IV subunit A
CDS	MYPE6480	L	*parE*	DNA topoisomerase IV subunit B
CDS	MYPE6490	-		P35 lipoprotein homologue
CDS	MYPE6495	-		P35 lipoprotein homologue fragment, MYPE6495 and MYPE6500 are predicted as the same gene with a frameshift
CDS	MYPE6500	-		P35 lipoprotein homologue fragment, MYPE6495 and MYPE6500 are predicted as the same gene with a frameshift
CDS	MYPE6510	-		P35 lipoprotein homologue
CDS	MYPE6520	-		P33 lipoprotein homologue fragment, MYPE6520 and MYPE6525 are predicted as the same gene with a frameshift
CDS	MYPE6525	-		P33 lipoprotein homologue fragment, MYPE6520 and MYPE6525 are predicted as the same gene with a frameshift
CDS	MYPE6530	-		P35 lipoprotein homologue
CDS	MYPE6540	-		P35 lipoprotein homologue
CDS	MYPE6550	-		P35 lipoprotein homologue
CDS	MYPE6560	-		P35 lipoprotein homologue
CDS	MYPE6570	-		P35 lipoprotein homologue
CDS	MYPE6580	-		P35 lipoprotein homologue
CDS	MYPE6590	-		P35 lipoprotein homologue
CDS	MYPE6600	P		transport system permease, similar to P69 of Mycoplasma hyorhinis Expect=3.3e-80, Identities=33%
CDS	MYPE6610	P		ABC transporter ATP-binding protein, MYPE3080 paralog
CDS	MYPE6620	-		high affinity transport system protein, similar to P37 of Mycoplasma hyorhinis Expect=4.3e-54, Identities=35%
CDS	MYPE6630	-		P35 lipoprotein homologue reported as putative lipoprotein IMP13
CDS	MYPE6640	-		P35 lipoprotein homologue
CDS	MYPE6650	-		P35 lipoprotein homologue
CDS	MYPE6660	-		P35 lipoprotein homologue
CDS	MYPE6670	-		P35 lipoprotein homologue
CDS	MYPE6680	-		P35 lipoprotein homologue
CDS	MYPE6690	-		P35 lipoprotein homologue
CDS	MYPE6700	-		hypothetical protein
CDS	MYPE6710	-		P35 lipoprotein homologue
CDS	MYPE6720	-		P35 lipoprotein homologue
CDS	MYPE6730	-		P35 lipoprotein homologue
CDS	MYPE6740	-		P35 lipoprotein homologue
CDS	MYPE6750	-		P35 lipoprotein homologue
CDS	MYPE6760	-		conserved hypothetical protein
CDS	MYPE6770	-		conserved hypothetical protein, similar to exported protein of Yersinia pestis AJ414151, Expect=1.3e-20, Identities =38%

CDS	MYPE6780	-		P35 lipoprotein homologue reported as gene for P38 lipoprotein
CDS	MYPE6790	-		P35 lipoprotein homologue
CDS	MYPE6800	-		P35 lipoprotein homologue reported as gene for P33 lipoprotein
CDS	MYPE6810	-		P35 lipoprotein
CDS	MYPE6820	-		P35 lipoprotein homologue reported as IMP14
CDS	MYPE6830	-		P35 lipoprotein homologue
CDS	MYPE6840	-		P35 lipoprotein homologue
CDS	MYPE6850	-		pupative lipoprotein, paralog family
CDS	MYPE6860	H	*dhfR*	dihyrofolate reductase
CDS	MYPE6870	F	*thyA*	thymidylate synthase
CDS	MYPE6880	H	*folD*	methylenetetrahydrofolate dehydrogenase(NADP+)/methenyltetrahydrofolate cyclohydrolase
CDS	MYPE6890	E		pyruvate decarboxylase
CDS	MYPE6900	C	*bdhA*	butanol dehydrogenas
CDS	MYPE6910	O	*lon*	ATP-dependent protease La
CDS	MYPE6920	O	*tig*	trigger factor, FKBP-type peptidyl-prolyl cis-transisomerase
CDS	MYPE6930	E	*aapA*	amino acid permease
CDS	MYPE6940	-		conserved hypothetical protein, predicted integrated membrane protein
CDS	MYPE6950	-		conserved hypothetical protein, MYPE6970 paralog, similar to putative liporotein of Mycoplasma genitalium U39711
CDS	MYPE6960	-		conserved hypothetical protein, MYPE6970 paralog, similar to putative liporotein of Mycoplasma genitalium U39711
CDS	MYPE6970	-		conserved hypothetical protein, paralog family, similar to putative liporotein of Mycoplasma genitalium U39711
CDS	MYPE6980	-		conserved hypothetical protein, MYPE6970 paralog, similar to putative liporotein of Mycoplasma genitalium U39711
CDS	MYPE6990	-		conserved hypothetical protein, MYPE6970 paralog, similar to putative liporotein of Mycoplasma genitalium U39711
CDS	MYPE7000	-		conserved hypothetical protein, MYPE6970 paralog truncated
CDS	MYPE7010	-		conserved hypothetical protein, MYPE6970 paralog, similar to putative liporotein of Mycoplasma genitalium U39711
CDS	MYPE7020	-		signal-peptide-less P35 lipoprotein homologue
CDS	MYPE7030	-		signal-peptide-less P35 lipoprotein homologue, MYPE7030 and MYPE7035 are predicted as the same gene with a frameshift
CDS	MYPE7035	-		signal-peptide-less P35 lipoprotein homologue, MYPE7030 and MYPE7035 are predicted as the same gene with a frameshift
CDS	MYPE7040	-		signal-peptide-less P35 lipoprotein homologue
CDS	MYPE7050	-		signal-peptide-less P35 lipoprotein homologue
CDS	MYPE7060	-		signal-peptide-less P35 lipoprotein homologue
CDS	MYPE7070	-		signal-peptide-less P35 lipoprotein homologue
CDS	MYPE7080	-		hypothetical protein
CDS	MYPE7090	-		hypothetical protein
CDS	MYPE7100	L		transposase for IS150-like insertion sequence element
CDS	MYPE7110	-		hypothetical protein, MYPE6850 paralog
CDS	MYPE7115	-		hypothetical protein
CDS	MYPE7120	-		transposase for IS232-like insertion sequence element
CDS	MYPE7130	L		Insertion sequence IS232 putative ATP-binding protein
CDS	MYPE7140	-		hypothetical protein, MYPE6850 paralog
CDS	MYPE7150	-		conserved hypothetical protein
CDS	MYPE7160	G	*sgaE*	L-ribulose-5-phosphate 4-epimerase family protein

CDS	MYPE7170	G	*sgaU*	hexulose-6-phosphate isomerase
CDS	MYPE7180	G	*sgaH*	hexulose-6-phosphate synthase
CDS	MYPE7190	-		PTS system enzyme IIA component
CDS	MYPE7200	G	*sgaB*	PTS system enzyme IIB component
CDS	MYPE7210	-		similar to transport protein SgaT
CDS	MYPE7220	S	*sgaT*	transport protein SgaT
CDS	MYPE7230	-		hypothetical protein
CDS	MYPE7240	R		phosphotriesterase family protein
CDS	MYPE7250	-		conserved hypothetical protein
CDS	MYPE7260	-		hypothetical protein
CDS	MYPE7270	R		conserved hypothetical protein, predicted integral membrane protein
CDS	MYPE7280	Q		ABC transporter ATP-binding protein, MYPE960 paralog
CDS	MYPE7290	-		hypothetical protein
CDS	MYPE7300	-		conserved hypothetical protein, MYPE2560 paralog
CDS	MYPE7310	R		conserved hypothetical, similar to OrfE1 of Mycoplasma fermentans AF179376 Expect=4.6e-52, Identities=33%
CDS	MYPE7320	-		conserved hypothetical protein, MYPE2560 paralog
CDS	MYPE7330	-		P35 lipoprotein homologue
CDS	MYPE7340	-		conserved hypothetical protein
CDS	MYPE7350	-		conserved hypothetical protein, MYPE8480 paralog
CDS	MYPE7360	-		conserved hypothetical protein, MYPE8480 paralog
CDS	MYPE7370	-		P35 lipoprotein homologue
CDS	MYPE7375	-		P35 lipoprotein homologue fragment, MYPE7375 and MYPE7380 are predicted as the same gene with a frameshift
CDS	MYPE7380	-		P35 lipoprotein homologue fragment, MYPE7375 and MYPE7380 are predicted as the same gene with a frameshift
CDS	MYPE7400	-		P35 lipoprotein homologue
CDS	MYPE7410	R		conserved hypothetical protein
CDS	MYPE7420	C	*nifU*	nitrogen fixation protein NifU
CDS	MYPE7430	E	*nifS*	nitrogen fixation protein NifS, aminotransferase class-V
CDS	MYPE7440	R		conserved hypothetical protein
CDS	MYPE7450	R		ABC transporter ATP-binding protein
CDS	MYPE7460	-		predicted acetyltransferase (GNAT) family protein
CDS	MYPE7470	Q		ABC transporter ATP-binding protein
CDS	MYPE7480	-		conserved hypothetical protein, MYPE7490 paralog
CDS	MYPE7490	-		conserved hypothetical protein, paralog family
CDS	MYPE7500	-		conserved hypothetical protein, MYPE7490 paralog
CDS	MYPE7510	-		conserved hypothetical protein, MYPE7490 paralog
CDS	MYPE7520	-		conserved hypothetical protein, MYPE7490 paralog
CDS	MYPE7530	Q		ABC transporter ATP-binding protein, MYPE2470 paralog
CDS	MYPE7540	Q		ABC transporter ATP-binding protein, MYPE2470 paralog
CDS	MYPE7550	J	*rpsD*	ribosomal protein S4
CDS	MYPE7560	-		conserved hypothetical protein
CDS	MYPE7570	-		putataive lipoprotein, partial sequence of MYPE7590 paralog, similar to lipoprotein of Mycoplasma genitalium U39713 Expect = 7.5e-91, Identities = 32%
CDS	MYPE7580	-		putative lipoprotein
CDS	MYPE7590	-		putative lipoprotein, paralog family, similar to lipoprotein of Mycoplasma genitalium U39713
CDS	MYPE7600	-		putative lipoprotein, MYPE7590 paralog, similar to lipoprotein of Mycoplasma genitalium U39713
CDS	MYPE7610	-		putative lipoprotein, MYPE7590 paralog, similar to lipoprotein of Mycoplasma genitalium U39713
CDS	MYPE7620	-		putative lipoprotein, MYPE7590 paralog, similar to

				lipoprotein of Mycoplasma genitalium U39713
CDS	MYPE7630	-		hypothetical protein
CDS	MYPE7640	-		hypothetical protein
CDS	MYPE7650	R		conserved hypothetical protein, MYPE5960 paralog, Pfam domain DUF234 archaebacterial proteins
CDS	MYPE7660	-		conserved hypothetical protein, MYPE7720 paralog
CDS	MYPE7670	G	*fruA*	PTS system fructose-specific enzyme IIABC component
CDS	MYPE7680	-		hypothetical protein
CDS	MYPE7690	-		conserved hypothetical protein, putative regulatory protein
CDS	MYPE7700	G	*pmi*	mannose-6-phosphate isomerase
CDS	MYPE7710	-		conserved hypothetical protein, MYPE7720 paralog
CDS	MYPE7720	-		conserved hypothetical protein, paralog family, predicted integral membrane protein
CDS	MYPE7730	-		conserved hypothetical protein, MYPE7720 paralog
CDS	MYPE7750	G	*fruK*	1-phosphofructokinase
CDS	MYPE7760	G	*fruA*	PTS system fructose-specific IIABC component
CDS	MYPE7770	-		transcriptional regulator DeoR family protein
CDS	MYPE7780	-		transposase for IS1202-like insert secuence element
CDS	MYPE7790	-		conserved hypothetical protein, MYPE7800 paralog
CDS	MYPE7800	-		conserved hypothetical protein, predicted integral membrane protein, paralog family
CDS	MYPE7810	-		conserved hypothetical protein, MYPE7800 paralog
CDS	MYPE7820	-		hypothetical protein
CDS	MYPE7830	R		conserved hypothetical protein, predicted ATPase, MYPE4220 paralog
CDS	MYPE7840	F	*pyrE*	orotate phosphoribosyltransferase
CDS	MYPE7850	F	*pyrF*	orotidine-5-phosphate decarboxylase
CDS	MYPE7860	F	*pyrD*	dihydroorotate dehydrogenase
CDS	MYPE7870	C	*pyrDII*	dihydroorotate dehydrogenase electron transfer subunit
CDS	MYPE7880	F	*pyrC*	dihydroorotase
CDS	MYPE7890	F	*pyrB*	aspartate carbamoyltransferase
CDS	MYPE7900	F	*pyrR*	pyrimidine operon repressor
CDS	MYPE7910	-		hypothetical protein, paralog family, predicted integral membrane protein
CDS	MYPE7920	-		hypothetical protein, MYPE7910 paralog
CDS	MYPE7930	-		hypothetical protein, MYPE7910 paralog
CDS	MYPE7940	J		conserved hypotehtical protein
CDS	MYPE7950	-		conserved hypothetical protein
CDS	MYPE7960	J	*tyrS*	tyrosyl-tRNA synthetase
CDS	MYPE7970	R		aldo/keto reductase family oxidoreductase, MYPE4720 paralog
CDS	MYPE7980	-		hypothetical protein
CDS	MYPE7990	M	*gidB*	glucose-inhibited division protein
CDS	MYPE8000	D		conserved hypothetical protein
CDS	MYPE8010	J	*proS*	prolyl aminoacyl-tRNA synthetase
CDS	MYPE8020	S		conserved hypothetical protein
CDS	MYPE8030	R	*deaD*	ATP-dependent RNA helicase
CDS	MYPE8040	S		conserved hypothetical protein
CDS	MYPE8050	-		conserved hypothetical protein
CDS	MYPE8060	L	*recR*	recombinational DNA repair protein
CDS	MYPE8070	S		conserved hypothetical protein
CDS	MYPE8080	L	*dnaX*	DNA polymerase III gamma-tau subunits
CDS	MYPE8090	-		hypothetical protein
CDS	MYPE8100	-		hypothetical protein

CDS	MYPE8110	L		conserved hypothetical protein, similar to hydrolase of Mycoplasma pneumoniae AE000016 Expect=7.5e-42, Identities=37%, containing Pfam domain TatD related DNase Accession number: PF01026
CDS	MYPE8120	R	*thdF*	thiophene and furan oxidation protein-related GTPase
CDS	MYPE8130	L		predicted DNA polymerase
CDS	MYPE8140	F	*tmk*	thymidylate kinase
CDS	MYPE8150	R		conserved hypothetical protein
CDS	MYPE8160	G	*pgk*	phosphoglycerate kinase
CDS	MYPE8170	G	*gap*	glyceraladehyde-3-phosphate dehydrogenase
CDS	MYPE8180	L		integrase/recombinase
CDS	MYPE8190	L	*hsdS*	type I restriction-modification system S subunit
CDS	MYPE8200	L	*hsdS*	type I restriction-modification system S subunit
CDS	MYPE8210	L	*hsdM*	type I restriction-modification system M subunit
CDS	MYPE8220	L	*hsdR*	type I restriction-modification system R subunit
CDS	MYPE8230	L	*hsdR*	type I restriction-modification system R subunit, partial
CDS	MYPE8250	J	*trmD*	tRNA-(5-methylaminomethyl-2-thiouridylate) methyltransferase
CDS	MYPE8260	-		hypothetical protein
CDS	MYPE8270	-		hypothetical protein, paralog family
CDS	MYPE8280	-		hypothetical protein, paralog of MYPE8270
CDS	MYPE8290	-		hypothetical protein, paralog of MYPE8270
CDS	MYPE8300	-		hypothetical protein, paralog of MYPE8270
CDS	MYPE8310	-		hypothetical protein, predicted integral membrane protein
CDS	MYPE8320	-		conserved hypothetical protein, predicted integral membrane protein
CDS	MYPE8330	R	*pip*	prolyl aminopeptidase
CDS	MYPE8340	S		conserved hypothetical protein
CDS	MYPE8350	R		conserved hypothetical protein
CDS	MYPE8360	K	*sigA*	RNA polymerase sigma factor, contains similarity to Pfam domain Sigma-70
CDS	MYPE8370	D	*ftsZ*	cell division protein FtsZ
CDS	MYPE8380	-		conserved hypothetical protein
CDS	MYPE8390	-		conserved hypothetical protein
CDS	MYPE8400	-		conserved hypothetical protein
CDS	MYPE8410	-		conserved hypothetical protein
CDS	MYPE8420	J	*lysS*	lysyl-tRNA synthetase
CDS	MYPE8430	N		conserved hypothetical protein, MYPE8450 paralog
CDS	MYPE8440	-		conserved hypothetical protein, MYPE8450 paralog
CDS	MYPE8450	-		conserved hypothetical protein, paralog family
CDS	MYPE8460	L		predicted ATP/GTP-binding protein
CDS	MYPE8470	-		conserved hypothetical protein, MYPE8480 paralog
CDS	MYPE8480	-		conserved hypothetical protein, paralog family
CDS	MYPE8490	-		conserved hypothetical protein, MYPE8450 paralog
CDS	MYPE8500	O		protease
CDS	MYPE8510	O		protease
CDS	MYPE8520	-		predicted O-methyltransferase
CDS	MYPE8530	L		conserved hypothetical protein
CDS	MYPE8540	J	*alaS*	alanyl-tRNA synthetase
CDS	MYPE8550	E		putative lipoprotein, MYPE8600 paralog
CDS	MYPE8560	R		haloacid dehalogenase-like hydrolase
CDS	MYPE8570	G	*potA*	spermidine/putrescine transport ATP-binding protein PotA
CDS	MYPE8580	E	*potB*	spermidine/putrescine transport system permease PotB
CDS	MYPE8590	E	*potC*	spermidine/putrescine transport system permease PotC
CDS	MYPE8600	E		putative lipoprotein, paralog family

CDS	MYPE8610	O	*gcp*	o-sialoglycoprotein endopeptidase
CDS	MYPE8620	-		conserved hypothetical protein
CDS	MYPE8630	-		hypothetical protein
CDS	MYPE8640	-		predicted permease, predicted integral membrane protein
CDS	MYPE8650	H	*lplA*	lipoate protein ligase A
CDS	MYPE8660	P		Trk-type cation transport protein, predicted integral membrane protein
CDS	MYPE8670	-		hypothetical protein
CDS	MYPE8680	D		conserved hypotheticalprotein
CDS	MYPE8690	F		formate-tetrahydrofolate ligase
CDS	MYPE8700	O		endopeptidase
CDS	MYPE8710	P		heavy-metal transporting P-type ATPase
CDS	MYPE8720	P		heavy-metal transporting ATPase, partial
CDS	MYPE8730	-		hypothetical protein
CDS	MYPE8750	R	*oppF*	oligopeptide ABC transporter ATP-binding protein
CDS	MYPE8760	R	*oppD*	oligopeptide ABC transporter ATP-binding protein
CDS	MYPE8770	E	*oppC*	oligopeptide ABC transporter permease protein
CDS	MYPE8780	E	*oppB*	oligopeptide ABC transporter permease protein
CDS	MYPE8790	-		hypothetical protein
CDS	MYPE8800	-		hypothetical protein
CDS	MYPE8810	-		hypothetical protein
CDS	MYPE8820	J	*ileS*	isoleucyl-tRNA synthetase
CDS	MYPE8830	M		putative glycosyltransferase
CDS	MYPE8840	K	*nusG*	transcription antitermination factor
CDS	MYPE8850	N	*secE*	predicted preprotein translocase subunit SecE
CDS	MYPE8860	-		conserved hypothetical protein
CDS	MYPE8870	S		conserved hypothetical protein
CDS	MYPE8880	R		conserved hypothetical protein
CDS	MYPE8890	L	*uvrB*	excinuclease ABC subunit B
CDS	MYPE8900	S		conserved hypothetical protein
CDS	MYPE8910	L		ATP-dependent DNA helicase
CDS	MYPE8920	-		conserved hypothetical protein
CDS	MYPE8930	M		glycosyltransferase
CDS	MYPE8940	-		hypothetical protein
CDS	MYPE8950	E		cytosol aminopeptidase
CDS	MYPE8960	O	*grpE*	heat shock protein GrpE
CDS	MYPE8970	O	*dnaJ*	heat shock protein DnaJ
CDS	MYPE8980	T		phosphotyrosine protein phosphatase
CDS	MYPE8990	C		NADH-dependent flavin oxidoreductase
CDS	MYPE9000	Q		conserved hypothetical protein
CDS	MYPE9010	-		hypothetical protein
CDS	MYPE9020	-		conserved hypothetical protein
CDS	MYPE9030	J	*cysS*	cysteinyl-tRNA synthetase
CDS	MYPE9040	L		helicase with SNF2 domain
CDS	MYPE9050	R		conserved hypothetical protein
CDS	MYPE9060	T		serine/threonine protein kinase
CDS	MYPE9070	-		hypothetical protein, MYPE950 paralog
CDS	MYPE9080	-		hypothetical protein, MYPE950 paralog
CDS	MYPE9090	-		hypothetical protein
CDS	MYPE9100	L	*uvrA*	excinuclease ABC subunit A
CDS	MYPE9110	-		conserved hypothetical protein, similar to Pfam domain pertussis toxin subunit S1, PF02917
CDS	MYPE9120	C		flavodoxin
CDS	MYPE9130	-		hypothetical protein
CDS	MYPE9150	J	*rpLT*	ribosomal protein L20
CDS	MYPE9160	J	*infC*	translation initiation factor IF3

CDS	MYPE9170	L	*polC*	DNA polymerase III subunit alpha
CDS	MYPE9180	J	*rpsU*	ribosomal protein S21
CDS	MYPE9190	-		hypothetical protein
CDS	MYPE9200	J	*rpmF*	ribosomal protein L32
rRNA	MYPE20000			5S ribosomal RNA gene, putative 3'-end
rRNA	MYPE20010			23S ribosomal RNA gene, putative 3'-end
rRNA	MYPE20020			16S ribosomal RNA gene, reported
CDS	MYPE9240	-		hypothetical protein
CDS	MYPE9250	-		hypothetical protein
CDS	MYPE9260	J	*pheT*	phenylalanyl-tRNA synthetase subunit beta
CDS	MYPE9270	J	*pheS*	phenylalanyl-tRNA synthetase subunit alpha
CDS	MYPE9280	J	*truB*	tRNA pseudouridine 5S synthase
CDS	MYPE9290	-		hypothetical protein
CDS	MYPE9300	R		esterase/lipase 2
CDS	MYPE9310	H		riboflavin kinase/FAD synthetase
CDS	MYPE9320	-		hypothetical protein
CDS	MYPE9330	O	*trxB*	thioredoxin reductase
CDS	MYPE9340	P	*phoU*	phosphate transport system regulatory protein
CDS	MYPE9350	P	*pstB*	phosphate ABC transporter permease PstB, MYPE3080 paralog
CDS	MYPE9360	P	*pstA*	phosphate ABC transporter permease PstA
CDS	MYPE9370	P		predicted phosphate binding protein PstS
CDS	MYPE9380	J	*metS*	methionyl-tRNA synthetase
CDS	MYPE9390	C		phosphoenolpyruvate carboxylase
CDS	MYPE9400	M		peptidoglycan acetylation
CDS	MYPE9410	R		conserved hypothetical protein
CDS	MYPE9420	H		conserved hypothetical protein
CDS	MYPE9430	R		conserved hypothetical protein
CDS	MYPE9440	L		predicted nucleotidyltransferase
CDS	MYPE9450	F		phosphoribosylpyrophosphate synthetase
CDS	MYPE9460	R		ribonuclease H-related protein
CDS	MYPE9470	-		conserved hypothetical protein
CDS	MYPE9480	-		predicted choline kinase
CDS	MYPE9490	O	*dnaK*	chaperone protein DnaK/ heat shock protein 70
CDS	MYPE9500	R		oxidoreductase, aldo/keto reductase family, MYPE4720 paralog
CDS	MYPE9510	-		hypothetical protein
CDS	MYPE9520	D		hypothetical protein
CDS	MYPE9530	L		probable DNA polymerase III
CDS	MYPE9540	I		CDP-diglyceride synthetase
CDS	MYPE9550	I		undecaprenyl diphosphate synthase
CDS	MYPE9560	J	*frr*	ribosome releasing/ recycling factor
CDS	MYPE9570	F	*pyrH*	uridylate kinase
CDS	MYPE9580	J	*tsf*	elongation factor Ts
CDS	MYPE9600	-		hypothetical protein, predicted integral membrane protein, paralog family
CDS	MYPE9610	-		hypothetical protein, paralog of MYPE9600 (C-terminal)
CDS	MYPE9620	L		transposase
CDS	MYPE9630	-		hypothetical protein, paralog of MYPE9600 (N-terminal)
CDS	MYPE9640	C		L-lactate dehydrogenase
CDS	MYPE9650	H		putative lipopolysaccharide biosynthesis enzyme KdtB
CDS	MYPE9660	J	*rpsB*	ribosomal protein S2
CDS	MYPE9670	K		transcription regulation proteins GntR
CDS	MYPE9680	G		PTS system sucrose-specific IIABC component
CDS	MYPE9690	G		sucrose-6-phosphate hydrolase
CDS	MYPE9700	K		ROK family-glucose kinase or transcriptional regulator

CDS	MYPE9710	R		conserved hypothetical protein
CDS	MYPE9720	-		hypothetical protein
CDS	MYPE9730	-		hypothetical protein
CDS	MYPE9740	J	*hisT*	tRNA pseudouridine synthase
CDS	MYPE9750	P		cobalt transport membrane protein
CDS	MYPE9760	P		cobalt transport ATP-binding protein
CDS	MYPE9770	P		cobalt transport ATP-binding protein, MYPE3080 paralog
CDS	MYPE9780	L		transposase for IS1630-like insertion sequence element
CDS	MYPE9790	-		hypothetical protein, similar to endonuclease
CDS	MYPE9800	L		cytosine-specific DNA methylase
CDS	MYPE9810	-		hypothetical protein
CDS	MYPE9820	-		conserved hypothetical protein
CDS	MYPE9830	-		hypothetical protein
CDS	MYPE9840	-		hypothetical protein, paralog of MYPE9860 and MYPE8270
CDS	MYPE9850	-		hypothetical protein, paralog of MYPE9860 and MYPE8270
CDS	MYPE9860	-		hypothetical protein, MYPE8270 paralog
CDS	MYPE9870	Q		short-chain alcohol dehydrogenase family enzyme
CDS	MYPE9880	-		hypothetical protein
CDS	MYPE9890	E	*pepC*	aminopeptidase C
CDS	MYPE9900	E	*pepC*	aminopeptidase C
CDS	MYPE9910	J	*rpsQ*	ribosomal protein L17
CDS	MYPE9920	K	*rpoA*	RNA polymerase subunit alpha
CDS	MYPE9930	J	*rpsK*	ribosomal protein S11
CDS	MYPE9940	J	*rpsM*	ribosomal protein S13
CDS	MYPE9950	J	*infA*	translation initiation factor IF-1
CDS	MYPE9960	J	*map*	methionine aminopeptidase
CDS	MYPE9970	F	*adk*	adenylate kinase
CDS	MYPE9980	N	*secY*	preprotein translocase SecY
CDS	MYPE9990	J	*rplO*	ribosomal protein L15
CDS	MYPE10000	J	*rpsE*	ribosomal protein S5
CDS	MYPE10010	J	*rplR*	ribosomal protein L18
CDS	MYPE10020	J	*rplF*	ribosomal protein L6
CDS	MYPE10030	J	*rpsH*	ribosomal protein S8
CDS	MYPE10040	J	*rpsN*	ribosomal protein S14
CDS	MYPE10050	J	*rplE*	ribosomal protein L5
CDS	MYPE10060	J	*rplX*	ribosomal protein L24
CDS	MYPE10070	J	*rplN*	ribosomal protein L14
CDS	MYPE10080	J	*rpsQ*	ribosomal protein S17
CDS	MYPE10090	J	*rpsC*	ribosomal protein S3
CDS	MYPE10100	J	*rpmC*	ribosomal protein L29
CDS	MYPE10110	J	*rplP*	ribosomal protein L16
CDS	MYPE10120	J	*rplV*	ribosomal protein L22
CDS	MYPE10130	J	*rpsS*	ribosomal protein S19
CDS	MYPE10150	J	*rplB*	ribosomal protein L2
CDS	MYPE10160	J	*rplW*	ribosomal protein L23
CDS	MYPE10170	J	*rplD*	ribosomal protein L4
CDS	MYPE10180	J	*rplC*	ribosomal protein L3
CDS	MYPE10190	J	*rpsJ*	ribosomal protein S10
CDS	MYPE10200	R		haloacid dehalogenase-like hydrolase
CDS	MYPE10210	K		predicted transcriptional regulator, similar to Pfam domain Bvg accessory factor PF03309
CDS	MYPE10220	L	*rnhB*	ribonuclease HII
CDS	MYPE10230	F	*apt*	adenine phosphoribosyltransferase
CDS	MYPE10240	N		predicted protein-export membrane protein SecD
CDS	MYPE10250	O	*ftsH*	cell division protein FtsH
CDS	MYPE10260	F	*hpt*	hypoxanthine-guanine phosphoribosyltransferase

CDS	MYPE10270	I		putative enzyme of deoxy-xylulose pathway YgbB, similar to YacN of Bacillus subtilis
CDS	MYPE10280	R		ABC transporter ATP-binding protein, MYPE3080 paralog
CDS	MYPE10290	R		probably ABC transporter membrane protein
CDS	MYPE10300	F	*upp*	uracil phosphoribosyltransferase
CDS	MYPE10310	F		GMP reductase, guanosine 5'-monophosphate oxidoreductase
CDS	MYPE10320	F	*tdk*	thymidine kinase
CDS	MYPE10330	R		GTP-binding protein
CDS	MYPE10340	G		fructose-bisphosphate aldolase
CDS	MYPE10350	K	*rpoE*	DNA-directed RNA polymerase subunit delta
CDS	MYPE10360	R		conserved hypothetical protein
CDS	MYPE10370	J	*gltX*	glutamyl-tRNA synthetase
CDS	MYPE10380	I		putative GHMP kinases ATP-binding protein
CDS	MYPE10390	J	*ksgA*	dimethyladenosine transferase
CDS	MYPE10400	N		similar to SpoIIIJ of Bacillus subtilis
CDS	MYPE10410	J	*rnpA*	ribonuclease P protein component
CDS	MYPE10420	J	*rpmH*	ribosomal protein L34
tRNA	MYPE20030			tRNA-Arg
tRNA	MYPE20040			tRNA-Asn
tRNA	MYPE20050			tRNA-Glu
tRNA	MYPE20060			tRNA-Val
tRNA	MYPE20070			tRNA-Thr
tRNA	MYPE20080			tRNA-Lys
tRNA	MYPE20090			tRNA-Leu
tRNA	MYPE20100			tRNA-Ser
tRNA	MYPE20110			tRNA-Ile
tRNA	MYPE20120			tRNA-Ala
tRNA	MYPE20130			tRNA-Arg
tRNA	MYPE20140			tRNA-Cys
tRNA	MYPE20150			tRNA-Arg
tRNA	MYPE20160			tRNA-Pro
tRNA	MYPE20170			tRNA-Met
tRNA	MYPE20180			tRNA-Met
tRNA	MYPE20190			tRNA-Ser
tRNA	MYPE20200			tRNA-Met
tRNA	MYPE20210			tRNA-Asp
tRNA	MYPE20220			tRNA-Phe
tRNA	MYPE20230			tRNA-Tyr
tRNA	MYPE20240			tRNA-Gln
tRNA	MYPE20250			tRNA-Lys
tRNA	MYPE20260			tRNA-Leu
tRNA	MYPE20270			tRNA-Gly
tRNA	MYPE20280			tRNA-Leu
tRNA	MYPE20290			tRNA-Gly
tRNA	MYPE20300			tRNA-Trp
tRNA	MYPE20310			tRNA-His
tRNA	MYPE20320			tRNA-SeC