Table S5. Significant genes ($p < 0.05$, FC* > 1.5) at 37°C in all studies

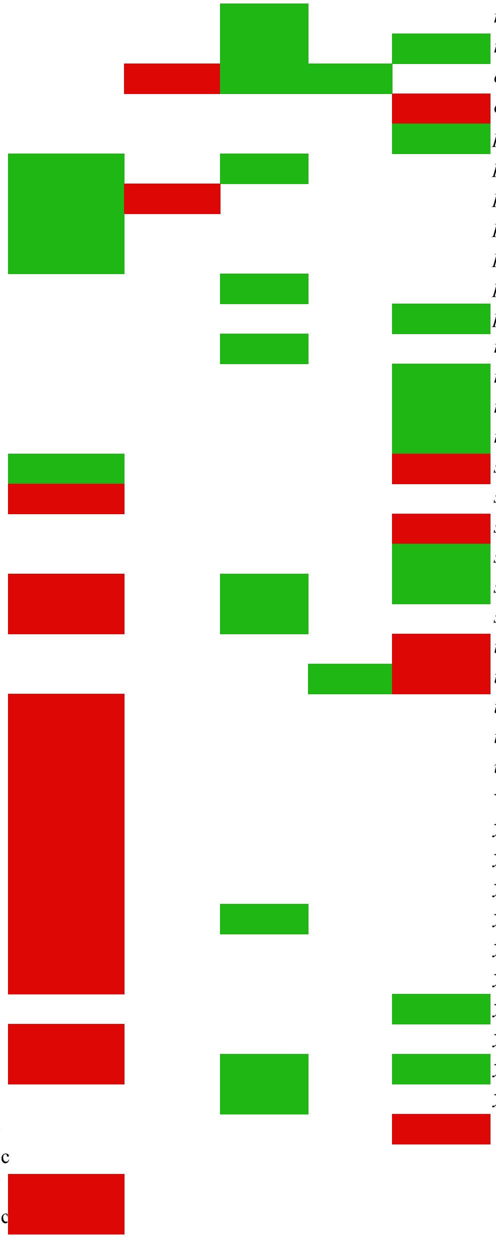
ID	**30°C vs 37°C**	**3 signals addition**	***ΔypeIR ΔyspIR ΔluxS***	**AI-2 addition**	***ΔluxS***	**Gene**	**Gene function**	**Process**
acnA					🟥	*acnA*	Aconitate hydratase 1	Tricarboxylic acid cycle
acpS					🟥	*acpS*	Holo-[acyl-carrier protein] syntl	Fatty acid biosynthesis
agaY			🟥		🟥	*agaY*	Putative aldolase	Degradation of carbon compounds
bfr			🟩			*bfr*	Bacterioferritin	Iron uptake
bglA	🟩					*bglA*	6-phospho-beta-glucosidase	Degradation of carbon compounds
caf1	🟥					*caf1*	Putative F1 capsule antigen, caf	
caf1A	🟥		🟩		🟩	*caf1A*	Putative F1 capsule anchoring p	
caf1M	🟥		🟩			*caf1M*	Putative F1 chaperone protein, c	
caf1R	🟥					*caf1R*	Putative F1 operon positive regu	
cstA	🟩					*cstA*	Putative carbon starvation prote	Adaptions and atypical conditions
dctA					🟥	*dctA*	C4-dicarboxylate transport prot	Transport/binding Carbohydrates,organic acids and alcohols
dnaJ	🟩					*dnaJ*	Chaperone protein DnaJ	Chaperones, chaperonins, heat shock
exuT						*exuT*	ExuT transport protein	Transport/binding Carbohydrates,organic acids and alcohols
feoA	🟩		🟩			*feoA*	Hypothetical ferrous iron transp	Unknown
focA				🟩		*focA*	Putative formate transporter 1	Transport/binding Carbohydrates,organic acids and alcohols
fruA		🟥		🟩	🟩	*fruA*	PTS system, fructose-specific II	Transport/binding Carbohydrates,organic acids and alcohols
gshA	🟩					*gshA*	Glutamate--cysteine ligase	Thioredoxin Biosynthesis
hmuS	🟩					*hmuS*	Hemin transport protein	Transport/binding proteins
hslR					🟩	*hslR*	Heat shock protein 15	Adaptions and atypical conditions
hutH	🟩					*hutH*	Histidine ammonia-lyase	Degradation of amino acids
ihfA	🟩					*ihfA*	Integration host factor alpha-sul	DNA replication, restriction/modification, recombination and repair
intA					🟩	*intA*	Phage integrase (partial)	
ipk					🟩	*ipk*	Putative 4-diphosphocytidyl-2-C	Menaquinone and ubiquinine Biosynthesis
lcrD	🟥		🟩			*lcrD*		Low calcium response
lcrF	🟥		🟩			*lcrF*		Low calcium response
lcrG	🟥					*lcrG*	Antiphagocytosis	Low calcium response
lcrH	🟥					*lcrH*		Low calcium response
lcrR	🟥					*lcrR*		Low calcium response
lcrV	🟥					*lcrV*	Antiphagocytosis	Low calcium response
lpxD	🟥					*lpxD*	UDP-3-o-[3-hydroxymyristoyl]	Surface polysaccharides, lipopolysaccharides and antigens
malF	🟩		🟥		🟥	*malF*	Maltose transport system perme	Maltose operon
malG	🟩		🟥		🟥	*malG*	Maltose transport system perme	Maltose operon
malK	🟩		🟥			*malK*	Maltose,maltodextrin transport ,	Maltose operon
metG					🟩	*metG*	Methionyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
msbA					🟩	*msbA*	Probable transport ATP-binding	Transport/binding proteins

Legend

up-regulated in control	🟥
down-regulated in control	🟩

* colors are reversed for AI-2 and three signal treatments

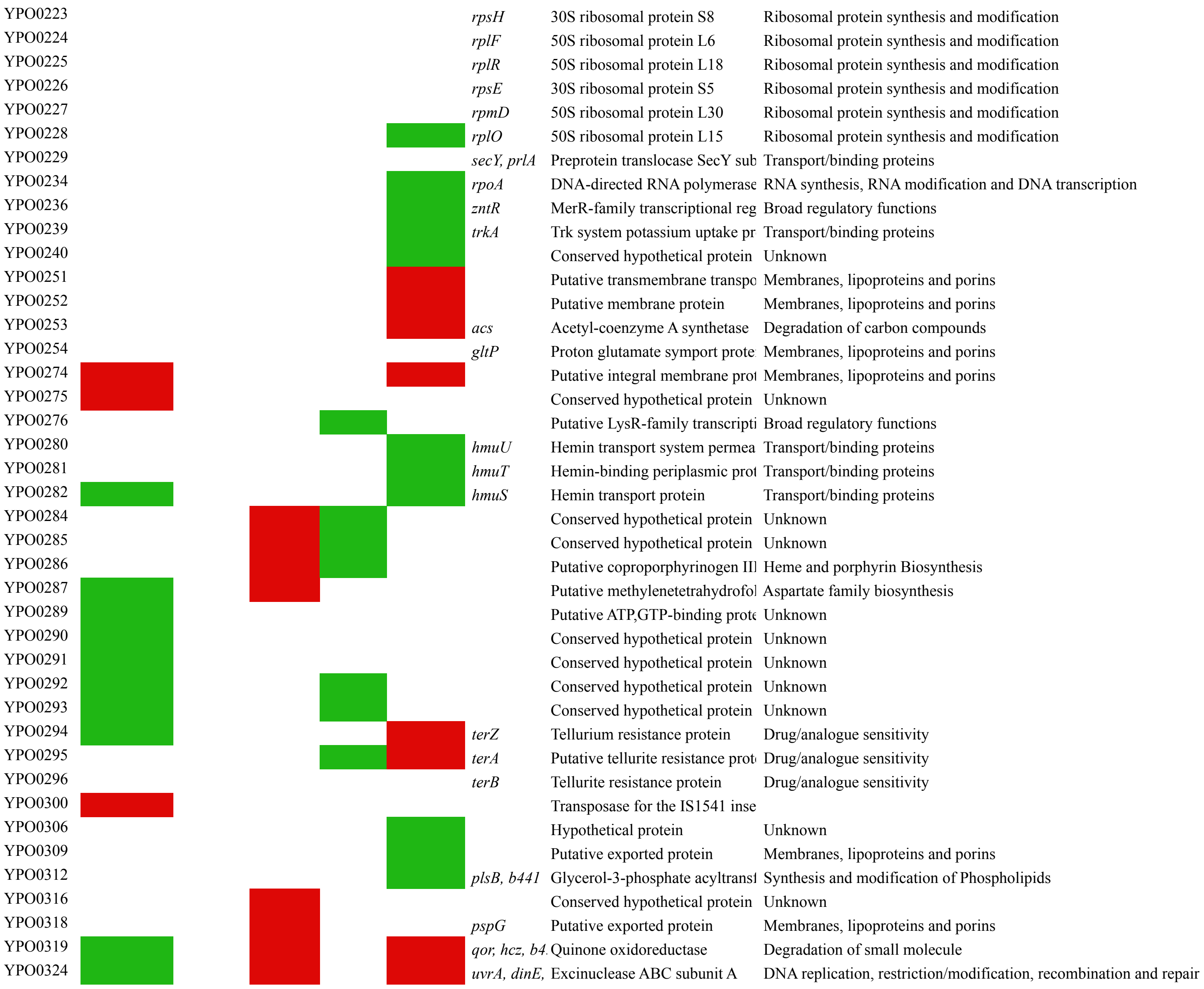
up-regulated in treated	🟥
down-regulated in treated	🟩



mtlA			🟩			*mtlA*	PTS system, mannitol-specific I	Transport/binding Carbohydrates,organic acids and alcohols
nusG			🟩		🟩	*nusG*	Transcription antitermination pr	RNA synthesis, RNA modification and DNA transcription
ompC		🟥	🟩	🟩		*ompC*	Outer membrane protein C, pori	Cell envelop
ompW					🟥	*ompW*	Putative exported protein	Membranes, lipoproteins and porins
pheS					🟩	*pheS*	Phenylalanyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
pim	🟩		🟩			*pim*		
pla	🟩	🟥				*pla*		
psiF	🟩					*psiF*	Putative starvation-inducible pr	Central intermediary metabolism
pspA	🟩					*pspA*	Phage shock protein A	Adaptions and atypical conditions
pstB			🟩			*pstB*	Putative phosphate transport AT	Transport/binding proteins
ptsI					🟩	*ptsI*	PTS sytem, enzyme I componen	Transport/binding Carbohydrates,organic acids and alcohols
rffE			🟩			*rffE*	UDP-N-acetylglucosamine 2-ep	Surface polysaccharides, lipopolysaccharides and antigens
rnpA					🟩	*rnpA*	Ribonuclease P protein	Degradation of RNA
rplK					🟩	*rplK*	50S ribosomal protein L11	Ribosomal protein synthesis and modification
rpsC					🟩	*rpsC*	30S ribosomal protein S3	Ribosomal protein synthesis and modification
sfuA	🟩				🟥	*sfuA*	Iron(III)-binding periplasmic pr	Transport/binding Cations
ssuA	🟥					*ssuA*	Putative aliphatic sulfonates bin	Transport/binding proteins
sucD					🟥	*sucD*	Succinyl-CoA synthetase alpha	Tricarboxylic acid cycle
sufI					🟩	*sufI*	Putative cell division protein	Cell division
sycE	🟥		🟩		🟩	*sycE*	Putative yopE chaperone	
sycN	🟥		🟩			*sycN*	Putative type III secretion prote	Type III Secretion System
tdh					🟥	*tdh*	Threonine 3-dehydrogenase	Degradation of amino acids
terA				🟩	🟥	*terA*	Putative tellurite resistance prot	Drug/analogue sensitivity
tnp	🟥					*tnp*		
tyeA	🟥					*tyeA*		
uhpB	🟥					*uhpB*	Two-component system, sensor	Broad regulatory functions
virG	🟥					*virG*		
ylpA	🟥					*ylpA*		
yopB	🟥					*yopB*		
yopD	🟥					*yopD*		
yopE	🟥		🟩			*yopE*		
yopH	🟥					*yopH*		
yopK	🟥					*yopK*		
yopM					🟩	*yopM*		
yopN	🟥					*yopN*		
yopP	🟥		🟩		🟩	*yopP*		
yopT			🟩			*yopT*		
YPCD1.02					🟥			
YPCD1.05c							Secretion chaperone	
YPCD1.07	🟥						Hypothetical protein	
YPCD1.08c	🟥						Hypothetical protein	

YPCD1.09c	🟥					Hypothetical protein	
YPCD1.14c	🟥						
YPCD1.15c	🟥					Hypothetical protein	
YPCD1.16c	🟥					Hypothetical protein	
YPCD1.18c	🟥		🟩				
YPCD1.23	🟥					Hypothetical protein	
YPCD1.31c						Secreted Effector Protein	
YPCD1.40						Type III Secretion System Atpas	
YPCD1.50					*yscA*	Hypothetical Protein	
YPCD1.51					*yscB*	Type III Secretion Apparatus C	Type III Secretion System
YPCD1.52							
YPCD1.69	🟥						
YPCD1.73c	🟥		🟩			Hypothetical Protein	
YPCD1.75c	🟥						
YPCD1.81	🟥						
YPCD1.82c	🟥						
YPCD1.83c	🟥						
YPCD1.85	🟥						
ypeI					*ypeI*	N-acylhomoserine lactone synth	AHL
ypkA	🟥		🟩		*ypkA*		
YPMT1.29c				🟥		Hypothetical Protein	
YPMT1.32	🟥					Putative Lipoprotein	
YPMT1.42				🟥		Putative Periplasmic Protein	
YPMT1.45c						Hypothetical Protein	
YPMT1.68c				🟥	*parA*	Partitioning Protein A	
YPMT1.69				🟩		Hypothetical Protein	
YPMT1.72c				🟥		Hypothetical Protein	
YPMT1.74			🟥			Murine toxin Protein	
YPMT1.81c						Putative F1 Operon Positive Re	
YPO0003		🟥		🟩	*asnA*	Aspartate-ammonia ligase	Aspartate family biosynthesis
YPO0007				🟥		Ribose permease	Transport/binding Carbohydrates,organic acids and alcohols
YPO0024	🟩				*glnA*	Glutamine synthetase	Glutamate family biosynthesis
YPO0026					*bipA, typA*	Putative GTPase	Pathogenicity
YPO0027	🟩					Conserved hypothetical protein	Unknown
YPO0028	🟩				*rbn*	Ribonuclease BN	Aminoacyl tRNA synthetases and their modification
YPO0029	🟩					Conserved hypothetical protein	Unknown
YPO0037				🟩	*trmH, spoU*	tRNA (guanosine-2'-O-)-methyl	Aminoacyl tRNA synthetases and their modification
YPO0042				🟩		Putative membrane protein	Membranes, lipoproteins and porins
YPO0044					*rph*	Ribonuclease PH	Degradation of RNA
YPO0045					*pyrE*	Orotate phosphoribosyltransfera	Pyrimidine ribonucleotide biosynthesis
YPO0050				🟩	*rpmB*	50S ribosomal protein L28	Ribosomal protein synthesis and modification

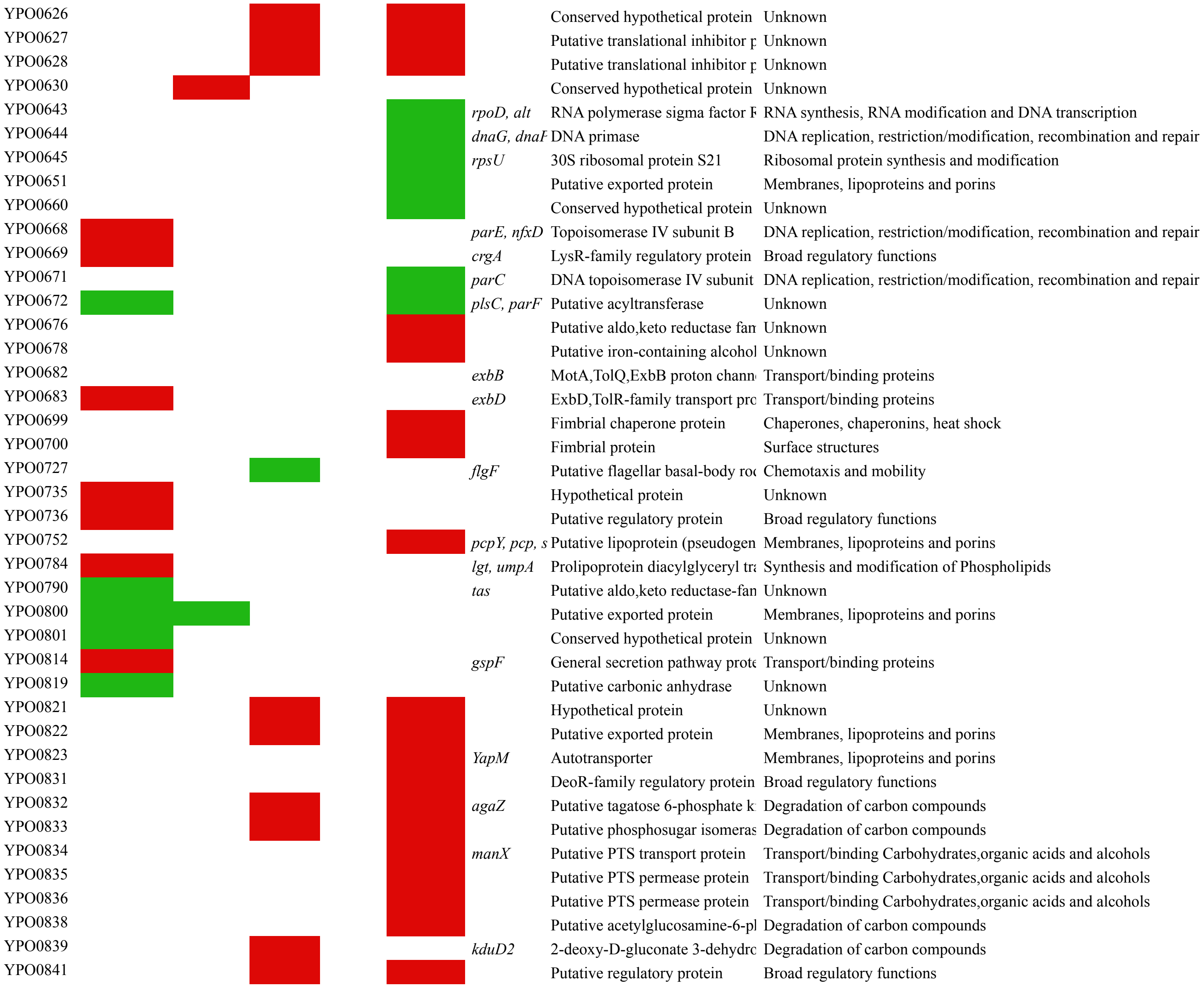
YPO0051				*rpmG*	50S ribosomal protein L33	Ribosomal protein synthesis and modification
YPO0052				*mutM, fpg*	Formamidopyrimidine-DNA gly	DNA replication, restriction/modification, recombination and repair
YPO0059			🟥	*kbl*	Amino-3-ketobutyrate coenzym	Fatty acid biosynthesis
YPO0060			🟥	*tdh*	Threonine 3-dehydrogenase	Degradation of amino acids
YPO0089			🟥	*glpX*	GlpX protein (pseudogene)	Central intermediary metabolism
YPO0091	🟩	🟥		*glpF*	Glycerol uptake facilitator prote	Membranes, lipoproteins and porins
YPO0100	🟩				Hypothetical protein	Unknown
YPO0102	🟩				Putative exported protein	Membranes, lipoproteins and porins
YPO0111	🟥			*rpmE*	50S ribosomal protein L31	Ribosomal protein synthesis and modification
YPO0112			🟩		Conserved hypothetical protein	Unknown
YPO0114			🟥	*metJ*	Ranscriptional repressor protein	Broad regulatory functions
YPO0120			🟩	*glpR*	Glycerol-3-phosphate repressor	Broad regulatory functions
YPO0130					Putative exported protein	Membranes, lipoproteins and porins
YPO0138	🟩			*pckA, pck*	Phosphoenolpyruvate carboxyki	Gluconeogenesis
YPO0149			🟥		Putative membrane protein	Membranes, lipoproteins and porins
YPO0152			🟥	*aroB*	3-dehydroquinate synthase	Aromatic amino acid family biosynthesis
YPO0155			🟩	*rpe*	Ribulose-phosphate 3-epimeras	Degradation of Polysaccharides
YPO0157			🟥	*trpS*	Tryptophanyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
YPO0158	🟩		🟥	*cysG*	Siroheme synthase	Heme and porphyrin Biosynthesis
YPO0159	🟩		🟥	*nirC*	Putative nitrite transporter	Transport/binding Anions
YPO0160	🟩		🟥	*nirD*	Nitrite reductase [NAD	Anaerobic respiration
YPO0164	🟥				Putative membrane receptor pro	Cell envelop
YPO0165	🟥		🟩		LacI-family transcriptional regu	Broad regulatory functions
YPO0177			🟩		Putative membrane protein	Membranes, lipoproteins and porins
YPO0180					Conserved hypothetical protein	Unknown
YPO0184				*tauC, ssiC*	Putative taurine transport systen	Transport/binding Carbohydrates,organic acids and alcohols
YPO0199	🟥				Conserved hypothetical protein	Unknown
YPO0205				*bfd*	Putative bacterioferritin-associa	Iron uptake
YPO0209				*rpsJ, nusE*	30S ribosomal protein S10	Ribosomal protein synthesis and modification
YPO0210	🟩			*rplC*	50S ribosomal protein L3	Ribosomal protein synthesis and modification
YPO0211			🟩	*rplD, eryA*	50S ribosomal protein L4	Ribosomal protein synthesis and modification
YPO0212				*rplW*	50S ribosomal protein L23	Ribosomal protein synthesis and modification
YPO0213	🟩			*rplB*	50S ribosomal protein l2	Ribosomal protein synthesis and modification
YPO0214	🟩			*rpsS*	30S ribosomal protein S19	Ribosomal protein synthesis and modification
YPO0215	🟩		🟩	*rplV, eryB*	50S ribosomal protein L22	Ribosomal protein synthesis and modification
YPO0216	🟩		🟩	*rpsC*	30S ribosomal protein S3	Ribosomal protein synthesis and modification
YPO0217	🟩		🟩	*rplP*	50S ribosomal protein L16	Ribosomal protein synthesis and modification
YPO0218	🟩		🟩	*rpmC*	50S ribosomal protein L29	Ribosomal protein synthesis and modification
YPO0219			🟩	*rpsQ, neaA*	30S ribosomal protein S17	Ribosomal protein synthesis and modification
YPO0220			🟩	*rplN*	50S ribosomal protein L14	Ribosomal protein synthesis and modification
YPO0222				*rplE*	50S ribosomal protein L5	Ribosomal protein synthesis and modification



YPO0223						*rpsH*	30S ribosomal protein S8	Ribosomal protein synthesis and modification
YPO0224						*rplF*	50S ribosomal protein L6	Ribosomal protein synthesis and modification
YPO0225						*rplR*	50S ribosomal protein L18	Ribosomal protein synthesis and modification
YPO0226						*rpsE*	30S ribosomal protein S5	Ribosomal protein synthesis and modification
YPO0227						*rpmD*	50S ribosomal protein L30	Ribosomal protein synthesis and modification
YPO0228					🟩	*rplO*	50S ribosomal protein L15	Ribosomal protein synthesis and modification
YPO0229						*secY, prlA*	Preprotein translocase SecY sub	Transport/binding proteins
YPO0234					🟩	*rpoA*	DNA-directed RNA polymerase	RNA synthesis, RNA modification and DNA transcription
YPO0236					🟩	*zntR*	MerR-family transcriptional reg	Broad regulatory functions
YPO0239					🟩	*trkA*	Trk system potassium uptake pr	Transport/binding proteins
YPO0240					🟩		Conserved hypothetical protein	Unknown
YPO0251					🟥		Putative transmembrane transpo	Membranes, lipoproteins and porins
YPO0252					🟥		Putative membrane protein	Membranes, lipoproteins and porins
YPO0253					🟥	*acs*	Acetyl-coenzyme A synthetase	Degradation of carbon compounds
YPO0254						*gltP*	Proton glutamate symport prote	Membranes, lipoproteins and porins
YPO0274	🟥				🟥		Putative integral membrane prot	Membranes, lipoproteins and porins
YPO0275	🟥						Conserved hypothetical protein	Unknown
YPO0276				🟩			Putative LysR-family transcripti	Broad regulatory functions
YPO0280					🟩	*hmuU*	Hemin transport system permea	Transport/binding proteins
YPO0281					🟩	*hmuT*	Hemin-binding periplasmic prot	Transport/binding proteins
YPO0282	🟩				🟩	*hmuS*	Hemin transport protein	Transport/binding proteins
YPO0284			🟥	🟩			Conserved hypothetical protein	Unknown
YPO0285			🟥	🟩			Conserved hypothetical protein	Unknown
YPO0286			🟥	🟩			Putative coproporphyrinogen III	Heme and porphyrin Biosynthesis
YPO0287	🟩		🟥				Putative methylenetetrahydrofol	Aspartate family biosynthesis
YPO0289	🟩						Putative ATP,GTP-binding prote	Unknown
YPO0290	🟩						Conserved hypothetical protein	Unknown
YPO0291	🟩						Conserved hypothetical protein	Unknown
YPO0292	🟩			🟩			Conserved hypothetical protein	Unknown
YPO0293	🟩			🟩			Conserved hypothetical protein	Unknown
YPO0294	🟩				🟥	*terZ*	Tellurium resistance protein	Drug/analogue sensitivity
YPO0295				🟩	🟥	*terA*	Putative tellurite resistance prot	Drug/analogue sensitivity
YPO0296						*terB*	Tellurite resistance protein	Drug/analogue sensitivity
YPO0300	🟥						Transposase for the IS1541 inse	
YPO0306					🟩		Hypothetical protein	Unknown
YPO0309					🟩		Putative exported protein	Membranes, lipoproteins and porins
YPO0312					🟩	*plsB, b441*	Glycerol-3-phosphate acyltransf	Synthesis and modification of Phospholipids
YPO0316			🟥				Conserved hypothetical protein	Unknown
YPO0318			🟥			*pspG*	Putative exported protein	Membranes, lipoproteins and porins
YPO0319	🟩		🟥		🟥	*qor, hcz, b4.*	Quinone oxidoreductase	Degradation of small molecule
YPO0324	🟩		🟥		🟥	*uvrA, dinE,*	Excinuclease ABC subunit A	DNA replication, restriction/modification, recombination and repair

YPO0325	🟩	🟥	🟥	*ssb, exrB, l*	Single-strand binding protein	DNA replication, restriction/modification, recombination and repair
YPO0326		🟩			Conserved hypothetical protein	Unknown
YPO0332	🟩	🟩		*rhaS, rhaC*	L-rhamnose operon regulatory p	Broad regulatory functions
YPO0336	🟥				Insertion element protein (fragm	
YPO0337	🟩		🟥		Putative exported protein	Membranes, lipoproteins and porins
YPO0338			🟩		Hypothetical protein	Unknown
YPO0354				*efp, b4147*	Elongation factor P	Protein translation and modification
YPO0363	🟥				Putative membrane transport pr	Membranes, lipoproteins and porins
YPO0365			🟥		Conserved hypothetical protein	Unknown
YPO0366				*orn, b4162*	Oligoribonuclease	Degradation of RNA
YPO0370	🟥				Putative N-acetylmuramoyl-L-a	Unknown
YPO0372	🟩		🟥	*miaA, trpX,*	tRNA delta(2)-isopentenylpyrop	Aminoacyl tRNA synthetases and their modification
YPO0397	🟥	🟥			Hypothetical protein	Unknown
YPO0398	🟥				Peptidase family protein	Membranes, lipoproteins and porins
YPO0401		🟥			Putative transcriptional regulato	Broad regulatory functions
YPO0404		🟩			PTS system, IIC component	Transport/binding Carbohydrates,organic acids and alcohols
YPO0407			🟥	*lsrG*	Cleavage of P-DPD cleavage pr	Lsr operon
YPO0408			🟥	*lsrF*	Putative aldolase	Lsr operon
YPO0409			🟥	*lsrB*	AI-2 receptor, periplasmic prote	Lsr operon
YPO0410			🟥	*lsrD*	Putative ABC transporter perme	Lsr operon
YPO0411			🟥	*lsrC*	Putative ABC transporter perme	Lsr operon
YPO0412			🟥	*lsrA*	Putative ABC transporter ATP-b	Lsr operon
YPO0414			🟥	*lsrR*	Pesudogene, repressor binds spe	Lsr operon
YPO0415		🟥	🟥	*lsrK*	Kinase phosphorylates carbon-5	Lsr operon
YPO0416	🟥		🟩	*rfaQ, waaQ*	Putative lipopolysaccharide cor	Surface polysaccharides, lipopolysaccharides and antigens
YPO0417			🟩	*waaL*	Putative O-antigen biosynthesis	Membranes, lipoproteins and porins
YPO0426					Putative membrane protein	Membranes, lipoproteins and porins
YPO0431	🟩			*osmY, b437*	Osmotically inducible protein Y	Unknown
YPO0435	🟩				Putative Na+ dependent nucleos	Transport/binding proteins
YPO0436			🟥	*deoC, dra,*	Deoxyribose-phosphate aldolas	Serine family biosynthesis
YPO0437			🟥	*deoA, tpp, t*	Thymidine phosphorylase (pseu	Salvage of nucleosides and nucleotides
YPO0439			🟥	*deoB, drm,*	Phosphopentomutase	Salvage of nucleosides and nucleotides
YPO0440			🟥	*deoD, pup,*	Purine nucleoside phosphoryla	Salvage of nucleosides and nucleotides
YPO0442			🟩	*serB, b438*	Phosphoserine phosphatase	Serine family biosynthesis
YPO0445		🟩	🟩		Conserved hypothetical protein	Unknown
YPO0455			🟥		Putative phosphoglycerate muta	
YPO0463			🟥	*talB*	Transaldolase B	Pentose phosphate pathway
YPO0467			🟩	*yaaH*	Putative membrane protein	Membranes, lipoproteins and porins
YPO0468	🟩			*dnaK, grpF,*	Chaperone protein DnaK	Chaperones, chaperonins, heat shock
YPO0472			🟩	*rpsT, b23*	30S ribosomal protein S20	Ribosomal protein synthesis and modification
YPO0473					Hypothetical protein	Unknown

YPO0481			🟩	*carA, pyrA,*	Carbamoyl-phosphate synthase	Glutamate family biosynthesis
YPO0483	🟥				Putative LysE type translocator	Transport/binding Amino acids and amines
YPO0490	🟥			*apaH, b49*	Bis(5'nucleosyl)-tetraphosphata	Miscellaneous nucleoside/nucleotide reactions
YPO0495	🟥			*imp, ostA, b*	Organic solvent tolerance protei	Adaptions and atypical conditions
YPO0498	🟩				Hypothetical protein	Unknown
YPO0499	🟩				Hypothetical protein	Unknown
YPO0500	🟩				Conserved hypothetical protein	Unknown
YPO0501	🟩				Conserved hypothetical protein	Unknown
YPO0502	🟩				Conserved hypothetical protein	Unknown
YPO0503	🟩				Conserved hypothetical protein	Unknown
YPO0504	🟩				Conserved hypothetical protein	Unknown
YPO0505	🟩				Conserved hypothetical protein	Unknown
YPO0506	🟩			*clpB, htpM*	Putative Clp ATPase	Degradation of Proteins, peptides and glycopeptides
YPO0507	🟩				Conserved hypothetical protein	Unknown
YPO0508	🟩				Hypothetical protein	Unknown
YPO0509	🟩				Hypothetical protein	Unknown
YPO0510	🟩				Hypothetical protein	Unknown
YPO0511	🟩				Hypothetical protein	Unknown
YPO0511a	🟩				Hypothetical protein	Unknown
YPO0512	🟩				Putative lipoprotein	Membranes, lipoproteins and porins
YPO0513	🟩				Conserved hypothetical protein	Unknown
YPO0514	🟩				Putative OmpA-family membra	Membranes, lipoproteins and porins
YPO0516	🟩				Hypothetical protein	Unknown
YPO0525		🟥			Hypothetical protein	
YPO0552	🟥			*mraY, murX*	Phospho-N-acetylmuramoyl-pe	Murein sacculus and peptidoglycan
YPO0553	🟥			*murD*	UDP-N-acetylmuramoylalanine	Murein sacculus and peptidoglycan
YPO0557	🟥			*ddlB, ddl*	D-alanine--D-alanine ligase B	Murein sacculus and peptidoglycan
YPO0560			🟥	*ftsZ, sfiB, s*	Cell division protein FtsZ	Cell division
YPO0562					Conserved hypothetical protein	Unknown
YPO0563			🟥		Putative exported protein	Membranes, lipoproteins and porins
YPO0568			🟥		Putative membrane protein	Membranes, lipoproteins and porins
YPO0569a		🟥	🟥		Conserved hypothetical protein	Unknown
YPO0570	🟩		🟥	*yqjD*	Putative membrane protein	Membranes, lipoproteins and porins
YPO0571	🟩				Hypothetical protein	Unknown
YPO0584			🟥		Putative symporter protein	Transport/binding proteins
YPO0589			🟥	*fadH, fadH*	2,4-dienoyl-CoA reductase	Degradation of small molecule
YPO0590	🟩		🟥	*hdeD*	Putative membrane protein	Membranes, lipoproteins and porins
YPO0609					Putative transporter ATP-bindin	Transport/binding proteins
YPO0623			🟥		Putative aminotransferase	Unknown
YPO0624			🟥		Putative membrane protein	Membranes, lipoproteins and porins
YPO0625			🟥		Hypothetical protein	Unknown

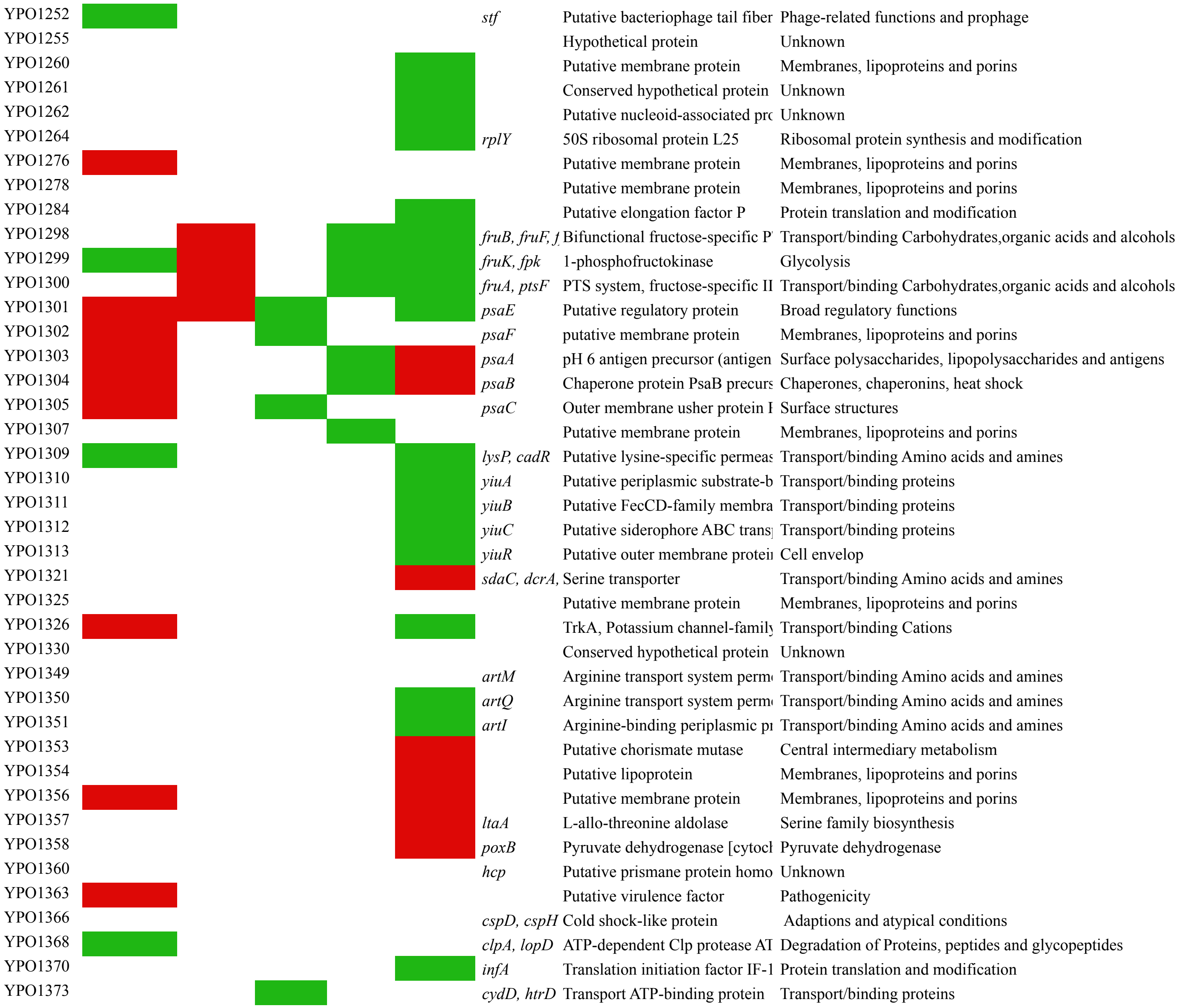


YPO0626			🟥	🟥		Conserved hypothetical protein	Unknown
YPO0627			🟥	🟥		Putative translational inhibitor p	Unknown
YPO0628			🟥	🟥		Putative translational inhibitor p	Unknown
YPO0630		🟥				Conserved hypothetical protein	Unknown
YPO0643				🟩	*rpoD, alt*	RNA polymerase sigma factor R	RNA synthesis, RNA modification and DNA transcription
YPO0644				🟩	*dnaG, dnaF*	DNA primase	DNA replication, restriction/modification, recombination and repair
YPO0645				🟩	*rpsU*	30S ribosomal protein S21	Ribosomal protein synthesis and modification
YPO0651				🟩		Putative exported protein	Membranes, lipoproteins and porins
YPO0660				🟩		Conserved hypothetical protein	Unknown
YPO0668	🟥				*parE, nfxD*	Topoisomerase IV subunit B	DNA replication, restriction/modification, recombination and repair
YPO0669	🟥				*crgA*	LysR-family regulatory protein	Broad regulatory functions
YPO0671				🟩	*parC*	DNA topoisomerase IV subunit	DNA replication, restriction/modification, recombination and repair
YPO0672	🟩			🟩	*plsC, parF*	Putative acyltransferase	Unknown
YPO0676				🟥		Putative aldo,keto reductase fan	Unknown
YPO0678				🟥		Putative iron-containing alcohol	Unknown
YPO0682					*exbB*	MotA,TolQ,ExbB proton chann	Transport/binding proteins
YPO0683	🟥				*exbD*	ExbD,TolR-family transport prc	Transport/binding proteins
YPO0699				🟥		Fimbrial chaperone protein	Chaperones, chaperonins, heat shock
YPO0700				🟥		Fimbrial protein	Surface structures
YPO0727			🟩		*flgF*	Putative flagellar basal-body roc	Chemotaxis and mobility
YPO0735	🟥					Hypothetical protein	Unknown
YPO0736	🟥					Putative regulatory protein	Broad regulatory functions
YPO0752				🟥	*pcpY, pcp, s*	Putative lipoprotein (pseudogen	Membranes, lipoproteins and porins
YPO0784	🟥				*lgt, umpA*	Prolipoprotein diacylglyceryl tra	Synthesis and modification of Phospholipids
YPO0790	🟩				*tas*	Putative aldo,keto reductase-fan	Unknown
YPO0800	🟩	🟩				Putative exported protein	Membranes, lipoproteins and porins
YPO0801	🟩					Conserved hypothetical protein	Unknown
YPO0814	🟥				*gspF*	General secretion pathway prote	Transport/binding proteins
YPO0819	🟩					Putative carbonic anhydrase	Unknown
YPO0821			🟥	🟥		Hypothetical protein	Unknown
YPO0822			🟥	🟥		Putative exported protein	Membranes, lipoproteins and porins
YPO0823				🟥	*YapM*	Autotransporter	Membranes, lipoproteins and porins
YPO0831				🟥		DeoR-family regulatory protein	Broad regulatory functions
YPO0832			🟥	🟥	*agaZ*	Putative tagatose 6-phosphate k	Degradation of carbon compounds
YPO0833			🟥	🟥		Putative phosphosugar isomeras	Degradation of carbon compounds
YPO0834				🟥	*manX*	Putative PTS transport protein	Transport/binding Carbohydrates,organic acids and alcohols
YPO0835				🟥		Putative PTS permease protein	Transport/binding Carbohydrates,organic acids and alcohols
YPO0836				🟥		Putative PTS permease protein	Transport/binding Carbohydrates,organic acids and alcohols
YPO0838				🟥		Putative acetylglucosamine-6-pl	Degradation of carbon compounds
YPO0839			🟥		*kduD2*	2-deoxy-D-gluconate 3-dehydrc	Degradation of carbon compounds
YPO0841			🟥	🟥		Putative regulatory protein	Broad regulatory functions

YPO0842			🟥	🟥		Putative sulfatase	Sulphur metabolism
YPO0844			🟥	🟥	*agaY, kba*	Putative aldolase	Degradation of carbon compounds
YPO0845			🟥	🟥		ThiJ,PfpI-family thiamine bioge	Thiamine Biosynthesis
YPO0862				🟩		Putative exported protein	Membranes, lipoproteins and porins
YPO0881			🟩	🟩		Conserved hypothetical protein	Unknown
YPO0882	🟩		🟩			Conserved hypothetical protein	Unknown
YPO0889	🟥				*prfB, supK*	Peptide chain release factor 2	Protein translation and modification
YPO0900	🟩					Putative hemolysin III	Pathogenicity
YPO0904						Hypothetical protein	Unknown
YPO0905				🟥	*gcvP*	Glycine dehydrogenase	glycine
YPO0906				🟥	*gcsH*	Glycine cleavage system H prot	glycine
YPO0907				🟥	*gcvT*	Aminomethyltransferase	Degradation of amino acids
YPO0913				🟥		Putative 5-formyltetrahydrofola	Unknown
YPO0917	🟩			🟥	*yggE*	Putative exported protein	Membranes, lipoproteins and porins
YPO0928						Putative Rieske protein	Unknown
YPO0929					*speA*	Biosynthetic arginine decarboxy	Polyamine synthesis
YPO0931	🟩		🟥	🟥	*metK*	S-adenosylmethionine synthetas	Central intermediary metabolism
YPO0934				🟩		Conserved hypothetical protein	Unknown
YPO0936				🟩		Conserved hypothetical protein	Unknown
YPO0937	🟥					Conserved hypothetical protein	Unknown
YPO0941	🟥					Conserved hypothetical protein	Unknown
YPO0943	🟥			🟩	*yggT*	Putative membrane protein	Membranes, lipoproteins and porins
YPO0944	🟥			🟩		Conserved hypothetical protein	Unknown
YPO0945	🟥					Conserved hypothetical protein	Unknown
YPO0946	🟥					Putative oxygen-independent co	Heme and porphyrin Biosynthesis
YPO0948	🟥		🟥			Conserved hypothetical protein	Unknown
YPO0950				🟩		Conserved hypothetical protein	Unknown
YPO0951				🟩		Putative methyltransferase	Unknown
YPO0952				🟩	*mutY, mutB*	A,G-specific adenine glycosylas	DNA replication, restriction/modification, recombination and repair
YPO0954				🟩	*mltC*	Membrane-bound lytic murein t	Murein sacculus and peptidoglycan
YPO0955				🟩		Hypothetical protein	Unknown
YPO0956				🟩		Putative hydroxamate-type ferri	Iron uptake
YPO0983						Putative membrane protein	Membranes, lipoproteins and porins
YPO0984	🟩				*yspI*	N-acylhomoserine lactone synth	AHL
YPO0985					*yspR*	Quorum-sensing transcriptional	AHL
YPO0986						Putative exported protein	Membranes, lipoproteins and porins
YPO0987	🟩					Putative exported protein	Membranes, lipoproteins and porins
YPO0992		🟩			*iucC*	Putative siderophore biosynthes	Iron uptake
YPO0993					*iucD*	Putative siderophore biosynthes	Iron uptake
YPO1011					*ynp1*	Putative TonB-dependent outer	Cell envelop
YPO1014a						Prepilin peptidase (partial)	Surface structures

YPO1023			🟩		N-acetylmuramoyl-L-alanine an	Murein sacculus and peptidoglycan
YPO1025			🟩		Membrane-bound lytic murein t	Murein sacculus and peptidoglycan
YPO1030			🟩		Conserved hypothetical protein	Unknown
YPO1031			🟩		Conserved hypothetical protein	Unknown
YPO1037			🟩		Conserved hypothetical protein	Unknown
YPO1038	🟥				Conserved hypothetical protein	Unknown
YPO1040			🟥		Conserved hypothetical protein	Unknown
YPO1041			🟥	*dapD*	2,3,4,5-tetrahydropyridine-2-car	Aspartate family biosynthesis
YPO1044			🟩	*rpsB*	30S ribosomal protein S2	Ribosomal protein synthesis and modification
YPO1045			🟩	*tsf*	Elongation factor Ts	Protein translation and modification
YPO1049			🟩	*uppS, rth*	Undecaprenyl pyrophosphate sy	Sugar nucleotides metabolism
YPO1051	🟥				Putative membrane protein	Membranes, lipoproteins and porins
YPO1054	🟥			*lpxD, firA,*	UDP-3-o-[3-hydroxymyristoyl]	Surface polysaccharides, lipopolysaccharides and antigens
YPO1055	🟥			*fabZ, sefA*	(3R)-hydroxymyristoyl-(acyl ca	Fatty acid biosynthesis
YPO1056	🟥			*lpxA*	Acyl-[acyl-carrier-protein]--UD	Surface polysaccharides, lipopolysaccharides and antigens
YPO1057	🟥			*lpxB, pgsB*	Lipid-A-disaccharide synthase	Surface polysaccharides, lipopolysaccharides and antigens
YPO1058	🟥			*rnhB, b183*	Ribonuclease HII	Degradation of RNA
YPO1068			🟩	*proS, drpA*	Prolyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
YPO1071	🟩				Putative lipoprotein	Membranes, lipoproteins and porins
YPO1072	🟩	🟥			ABC transporter permease prote	Transport/binding proteins
YPO1078			🟩	*mltD, dniR*	Membrane-bound lytic murein t	Murein sacculus and peptidoglycan
YPO1086a			🟩		Phage integrase (partial)	
YPO1092		🟩			Putative DNA-binding prophage	Phage-related functions and prophage
YPO1098		🟥	🟩		Putative prophage integrase	
YPO1104	🟥				Conserved hypothetical protein	Unknown
YPO1107			🟩	*grpE*	Heat shock protein GrpE	Adaptions and atypical conditions
YPO1108		🟥	🟥	*gltA, gluT, i*	Citrate synthase GltA	Tricarboxylic acid cycle
YPO1111			🟥	*sdhA*	Succinate dehydrogenase flavop	Tricarboxylic acid cycle
YPO1112			🟥	*sdhB*	Succinate dehydrogenase iron-s	Tricarboxylic acid cycle
YPO1113			🟥	*sucA*	2-oxoglutarate dehydrogenase E	Tricarboxylic acid cycle
YPO1114			🟥	*sucB*	Dihydrolipoamide succinyltrans	Tricarboxylic acid cycle
YPO1115			🟥	*sucC, b728*	Succinyl-CoA synthetase beta c	Tricarboxylic acid cycle
YPO1116			🟥	*sucD*	Succinyl-CoA synthetase alpha	Tricarboxylic acid cycle
YPO1117			🟥	*cydA*	Cytochrome D ubiquinol oxidas	Electron transport
YPO1118			🟥	*cydB*	Cytochrome D ubiquinol oxidas	Electron transport
YPO1120	🟥				Conserved hypothetical protein	Unknown
YPO1121		🟩		*tolQ*	TolQ colicin import protein	Colicin-related functions
YPO1127			🟩	*nadA, nicA*	Quinolinate synthetase A	Pyridine nucleotide Biosynthesis
YPO1133				*gpmA, gpm*	Phosphoglycerate mutase 1	Glycolysis
YPO1137			🟥	*galK, galA*	Galactokinase	Galactose operon
YPO1138			🟥	*galT, galB*	Galactose-1-phosphate uridylylt	Galactose operon

YPO1139					🟥	*galE, galD*	UDP-glucose 4-epimerase	Galactose operon
YPO1145						*modA*	Molybdate-binding periplasmic	Transport/binding Anions
YPO1149					🟥		Conserved hypothetical protein	Unknown
YPO1151						*bioB*	Biotin synthase	Biotin Biosynthesis
YPO1152	🟥					*bioF*	8-amino-7-oxononanoate syntha	Biotin Biosynthesis
YPO1158					🟩		Conserved hypothetical protein	Unknown
YPO1160	🟥					*moaC, chlA*	Molybdenum cofactor biosynthe	Molybdopterin Biosynthesis
YPO1161	🟥					*moaD, chlA*	Molybdopterin [mpt] converting	Molybdopterin Biosynthesis
YPO1162	🟥					*moaE, chlA*	Molybdopterin [mpt] converting	Molybdopterin Biosynthesis
YPO1168	🟩					*betT*	High-affinity choline transport p	Adaptions and atypical conditions
YPO1174							Hypothetical protein	Unknown
YPO1176	🟥		🟩			*pbpG*	Penicillin-binding protein 7 prec	Murein sacculus and peptidoglycan
YPO1177	🟩					*dld*	D-lactate dehydrogenase	Aerobic respiration
YPO1181	🟩						Putative membrane protein	Membranes, lipoproteins and porins
YPO1186					🟩		Conserved hypothetical protein	Unknown
YPO1192	🟩						Conserved hypothetical protein	Unknown
YPO1193	🟩						Putative pyridoxal-dependent de	Degradation of amino acids
YPO1200	🟩						Putative amino acid permease	
YPO1201	🟩						Putative amino acid decarboxyla	Degradation of amino acids
YPO1203					🟩		Putative membrane protein	Membranes, lipoproteins and porins
YPO1207	🟩				🟥	*katA*	Catalase	Oxidative stress
YPO1208					🟩		Putative exported protein	Membranes, lipoproteins and porins
YPO1212					🟩		Putative iron-sulphur binding pr	Unknown
YPO1218					🟩	*rcsB*	Probable two component respon	Broad regulatory functions
YPO1221	🟥						Putative membrane protein	Membranes, lipoproteins and porins
YPO1222		🟥	🟩	🟩		*ompC, meo.*	Outer membrane protein C, pori	Cell envelop
YPO1224	🟩					*ampH*	Putative penicillin-binding prote	Murein sacculus and peptidoglycan
YPO1235					🟥		Conserved hypothetical protein	Unknown
YPO1236					🟥		Putative class II aldolase-family	Unknown
YPO1239	🟩						Putative bacteriophage protein	Phage-related functions and prophage
YPO1240	🟩		🟥				Putative ATP-binding protein	Unknown
YPO1241	🟩		🟥				Putative bacteriophage protein	Phage-related functions and prophage
YPO1242	🟩		🟥				Putative bacteriophage tail shea	Phage-related functions and prophage
YPO1243	🟩						Hypothetical protein	Unknown
YPO1244	🟩		🟥				Hypothetical protein	Unknown
YPO1245	🟩						Putative bacteriophage coat prot	Phage-related functions and prophage
YPO1246	🟩						Putative bacteriophage protein	Phage-related functions and prophage
YPO1248	🟩						Putative bacteriophage (basepla	Phage-related functions and prophage
YPO1249	🟩						Putative bacteriophage protein (	Phage-related functions and prophage
YPO1250	🟩						Putative bacteriophage protein	Phage-related functions and prophage
YPO1251	🟩						Putative bacteriophage protein	Phage-related functions and prophage



YPO1252	🟩					*stf*	Putative bacteriophage tail fiber	Phage-related functions and prophage
YPO1255							Hypothetical protein	Unknown
YPO1260					🟩		Putative membrane protein	Membranes, lipoproteins and porins
YPO1261					🟩		Conserved hypothetical protein	Unknown
YPO1262					🟩		Putative nucleoid-associated prc	Unknown
YPO1264					🟩	*rplY*	50S ribosomal protein L25	Ribosomal protein synthesis and modification
YPO1276	🟥						Putative membrane protein	Membranes, lipoproteins and porins
YPO1278							Putative membrane protein	Membranes, lipoproteins and porins
YPO1284					🟩		Putative elongation factor P	Protein translation and modification
YPO1298		🟥		🟩	🟩	*fruB, fruF, f*	Bifunctional fructose-specific P	Transport/binding Carbohydrates,organic acids and alcohols
YPO1299	🟩	🟥		🟩	🟩	*fruK, fpk*	1-phosphofructokinase	Glycolysis
YPO1300		🟥		🟩	🟩	*fruA, ptsF*	PTS system, fructose-specific II	Transport/binding Carbohydrates,organic acids and alcohols
YPO1301	🟥	🟥	🟩		🟩	*psaE*	Putative regulatory protein	Broad regulatory functions
YPO1302	🟥		🟩			*psaF*	putative membrane protein	Membranes, lipoproteins and porins
YPO1303	🟥			🟩	🟥	*psaA*	pH 6 antigen precursor (antigen	Surface polysaccharides, lipopolysaccharides and antigens
YPO1304	🟥			🟩	🟥	*psaB*	Chaperone protein PsaB precurs	Chaperones, chaperonins, heat shock
YPO1305	🟥		🟩			*psaC*	Outer membrane usher protein I	Surface structures
YPO1307				🟩			Putative membrane protein	Membranes, lipoproteins and porins
YPO1309	🟩				🟩	*lysP, cadR*	Putative lysine-specific permeas	Transport/binding Amino acids and amines
YPO1310					🟩	*yiuA*	Putative periplasmic substrate-b	Transport/binding proteins
YPO1311					🟩	*yiuB*	Putative FecCD-family membra	Transport/binding proteins
YPO1312					🟩	*yiuC*	Putative siderophore ABC trans	Transport/binding proteins
YPO1313					🟩	*yiuR*	Putative outer membrane protei	Cell envelop
YPO1321					🟥	*sdaC, dcrA,*	Serine transporter	Transport/binding Amino acids and amines
YPO1325							Putative membrane protein	Membranes, lipoproteins and porins
YPO1326	🟥				🟩		TrkA, Potassium channel-family	Transport/binding Cations
YPO1330							Conserved hypothetical protein	Unknown
YPO1349						*artM*	Arginine transport system perm	Transport/binding Amino acids and amines
YPO1350					🟩	*artQ*	Arginine transport system perm	Transport/binding Amino acids and amines
YPO1351					🟩	*artI*	Arginine-binding periplasmic pı	Transport/binding Amino acids and amines
YPO1353					🟥		Putative chorismate mutase	Central intermediary metabolism
YPO1354					🟥		Putative lipoprotein	Membranes, lipoproteins and porins
YPO1356	🟥				🟥		Putative membrane protein	Membranes, lipoproteins and porins
YPO1357					🟥	*ltaA*	L-allo-threonine aldolase	Serine family biosynthesis
YPO1358					🟥	*poxB*	Pyruvate dehydrogenase [cytocl	Pyruvate dehydrogenase
YPO1360						*hcp*	Putative prismane protein homo	Unknown
YPO1363	🟥						Putative virulence factor	Pathogenicity
YPO1366						*cspD, cspH*	Cold shock-like protein	Adaptions and atypical conditions
YPO1368	🟩					*clpA, lopD*	ATP-dependent Clp protease AT	Degradation of Proteins, peptides and glycopeptides
YPO1370					🟩	*infA*	Translation initiation factor IF-1	Protein translation and modification
YPO1373			🟩			*cydD, htrD*	Transport ATP-binding protein	Transport/binding proteins

YPO1380	🟥						Putative membrane protein	Membranes, lipoproteins and porins
YPO1383			🟥	🟩	🟥	*pflB, pfl*	Formate acetyltransferase 1	Anaerobic respiration
YPO1384				🟩		*focA*	Putative formate transporter 1	Transport/binding Carbohydrates,organic acids and alcohols
YPO1385					🟩		Conserved hypothetical protein	Unknown
YPO1386	🟥				🟥	*ansB*	Putative L-asparaginase II precu	Degradation of amino acids
YPO1395					🟩	*msbA*	Probable transport ATP-binding	Transport/binding proteins
YPO1398		🟥			🟩	*cspB*	Cold shock-like protein	Adaptions and atypical conditions
YPO1404					🟩	*mukE, kicA*	Conserved hypothetical protein	Unknown
YPO1405					🟩	*mukB*	Cell division protein	Cell division
YPO1407	🟩						Putative exported protein	Membranes, lipoproteins and porins
YPO1408	🟥						Putative exported protein	Membranes, lipoproteins and porins
YPO1409	🟥						Metallo-beta-lactamase superfa	Unknown
YPO1411	🟩						Putative outer membrane porin	Cell envelop
YPO1412					🟩	*asnS, tss*	Asparaginyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
YPO1417							Putative iron-sulfur binding pro	Unknown
YPO1418					🟩		Conserved hypothetical protein	Unknown
YPO1420					🟩	*pqiA*	Putative paraquat-inducible prot	Membranes, lipoproteins and porins
YPO1423a					🟥	*rmf*	Putative ribosome modulation f	Ribosome maturation and modification
YPO1430					🟩	*fabA*	3-hydroxydecanoyl-[acyl-carrie	Fatty acid biosynthesis
YPO1431					🟩		Putative Lon protease	Unknown
YPO1435	🟩	🟥	🟩		🟩	*ompA, tolG,*	Putative outer membrane porin	Cell envelop
YPO1443							Conserved hypothetical protein	Unknown
YPO1444					🟩		Conserved hypothetical protein	Unknown
YPO1445					🟩		Conserved hypothetical protein	Unknown
YPO1447							Putative sulfite reductase subun	Sulphur metabolism
YPO1463							Putative acyl transferase	Fatty acid biosynthesis
YPO1474							Putative exported protein	Membranes, lipoproteins and porins
YPO1491						*ybiT*	ABC transporter ATP-binding p	Transport/binding proteins
YPO1499		🟩					Putative membrane protein	Membranes, lipoproteins and porins
YPO1501			🟥		🟥		Putative esterase	Unknown
YPO1505					🟩	*folE*	GTP cyclohydrolase I	Folic acid Biosynthesis
YPO1507					🟥	*mglB*	Galactose-binding protein	Transport/binding Carbohydrates,organic acids and alcohols
YPO1508	🟥				🟥	*mglA*	Galactoside transport ATP-bindi	Transport/binding Carbohydrates,organic acids and alcohols
YPO1509					🟥	*mglC*	Galactoside permease	Transport/binding Carbohydrates,organic acids and alcohols
YPO1511					🟥	*sfcA, maeA*	NAD-dependent malic enzyme	Gluconeogenesis
YPO1512				🟩	🟥	*cdd*	Cytidine deaminase	Salvage of nucleosides and nucleotides
YPO1513			🟩			*yohK*	Putative membrane protein	Membranes, lipoproteins and porins
YPO1517	🟩						Putative sugar ABC transporter	Transport/binding Carbohydrates,organic acids and alcohols
YPO1522					🟩	*metG*	Methionyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
YPO1524					🟩	*udk, b266*	Uridine kinase	Miscellaneous nucleoside/nucleotide reactions
YPO1525					🟩	*dcd, dus, pa*	Deoxycytidine triphosphate dea	2 -deoxyribonucleotide biosynthesis

YPO1528					*ysuF, fhuF*	Putative ferric iron reductase	Electron transport
YPO1531				🟩	*alcB*	Putative siderophore biosyntheti	Iron uptake
YPO1537				🟩	*ysuR*	Putative iron-siderophore recept	Iron uptake
YPO1540	🟥				*galF*	UTP-glucose-1-phosphate uridy	Galactose operon
YPO1541	🟥				*gnd*	6-phosphogluconate dehydroger	Pentose phosphate pathway
YPO1547			🟥		*hisC*	Histidinol-phosphate aminotran	Histidine biosynthesis
YPO1548			🟥		*hisD*	Histidinol dehydrogenase	Histidine biosynthesis
YPO1551				🟥		Putative exported protein	Membranes, lipoproteins and porins
YPO1557					*yeeF*	Amino acid permease	Transport/binding Amino acids and amines
YPO1559	🟥					Hypothetical protein	Unknown
YPO1563						Putative transmembrane transpo	Transport/binding proteins
YPO1566				🟥		Putative hydrolase	Unknown
YPO1567				🟥		Putative racemase	Unknown
YPO1570			🟥		*argG*	Argininosuccinate synthase	Glutamate family biosynthesis
YPO1573				🟥		Putative polysaccharide deacety	Unknown
YPO1575				🟩		225 conserved hypothetical prot	Unknown
YPO1584				🟥		Conserved hypothetical protein	Unknown
YPO1594	🟩			🟩		Conserved hypothetical protein	Unknown
YPO1595				🟩	*rpmF*	Ribosomal protein L32	Ribosomal protein synthesis and modification
YPO1596	🟥				*plsX*	Fatty acid,phospholipid synthes	Synthesis and modification of Phospholipids
YPO1597				🟩	*fabH*	3-oxoacyl-[acyl-carrier-protein]	Fatty acid biosynthesis
YPO1601				🟩	*fabF, fabJ*	3-oxoacyl-[acyl-carrier-protein]	Fatty acid biosynthesis
YPO1603	🟥				*pabC*	4-amino-4-deoxychorismate lya	Folic acid Biosynthesis
YPO1607	🟥					Putative deoxyribonuclease	Unknown
YPO1608	🟥		🟩		*ptsG, glcA,*	PTS system, glucose-specific II	Transport/binding Carbohydrates,organic acids and alcohols
YPO1618		🟥				Hypothetical protein	Unknown
YPO1626				🟩	*lolC*	Lipoprotein releasing system, tr	Membranes, lipoproteins and porins
YPO1627				🟩	*lolD*	Lipoprotein releasing system, A	Membranes, lipoproteins and porins
YPO1628				🟩	*lolE*	Lipoprotein releasing system, tr	Membranes, lipoproteins and porins
YPO1630				🟩	*cobB*	Putative Sir2 family protein	Unknown
YPO1636				🟩	*purB*	Adenylosuccinate lyase	Purine ribonucleotide biosynthesis
YPO1637						Conserved hypothetical protein	Unknown
YPO1638					*trmU, asuE*	tRNA (5-methylaminomethyl-2-	Aminoacyl tRNA synthetases and their modification
YPO1641			🟥	🟥	*icdA, icd, ic*	Isocitrate dehydrogenase [NAD	Tricarboxylic acid cycle
YPO1645	🟥			🟥		Conserved hypothetical protein	Unknown
YPO1649	🟩		🟩	🟩		Conserved hypothetical protein	Unknown
YPO1650				🟥		Hypothetical protein	Unknown
YPO1652	🟩				*ylaC*	Putative membrane protein	Membranes, lipoproteins and porins
YPO1654			🟥		*lacZ*	Beta-galactosidase	Lactose operon
YPO1655				🟩	*cspC, msm*	Cold shock protein	Adaptions and atypical conditions
YPO1659		🟥				Hypothetical protein	Unknown

YPO1660					*mgtC*	Mg(2+) transport ATPase protei	Pathogenicity
YPO1661			🟩		*mgtB*	Mg(2+) transport ATPase protei	Pathogenicity
YPO1683	🟩	🟥				Probable N-acetylmuramoyl-L-a	Degradation of Proteins, peptides and glycopeptides
YPO1684	🟩					Putative membrane protein (pse	Membranes, lipoproteins and porins
YPO1686	🟩					Putative exported protein	Membranes, lipoproteins and porins
YPO1688				🟩		Hypothetical protein	Unknown
YPO1694						Conserved hypothetical protein	Unknown
YPO1702				🟩	*yebS*	Putative membrane protein	Membranes, lipoproteins and porins
YPO1705	🟥				*prc, tsp*	Tail-specific protease precursor	Degradation of Proteins, peptides and glycopeptides
YPO1706	🟩	🟩			*htpX*	Putative heat shock protein	Adaptions and atypical conditions
YPO1713					*ogl*	Oligogalacturonate lyase	Degradation of Proteins, peptides and glycopeptides
YPO1714	🟩				*kdgR*	IclR-family transcriptional regu	Broad regulatory functions
YPO1715				🟩	*ybjR, b867*	Probable N-acetylmuramoyl-L-a	Murein sacculus and peptidoglycan
YPO1718						Putative exported protein	Membranes, lipoproteins and porins
YPO1735				🟩		Putative ABC transporter (ATP-	Transport/binding proteins
YPO1743				🟩	*aroP*	Aromatic amino acid transport p	Transport/binding Amino acids and amines
YPO1744				🟩	*pagP*	Putative exported protein	Membranes, lipoproteins and porins
YPO1753				🟩	*fcuA*	Ferrichrome receptor protein	Cell envelop
YPO1754	🟥	🟩			*yebN*	Putative membrane protein	Membranes, lipoproteins and porins
YPO1755				🟩	*yobD*	Putative membrane protein	Membranes, lipoproteins and porins
YPO1757	🟩				*manY, ptsP,*	PTS system, mannose-specific I	Transport/binding Carbohydrates,organic acids and alcohols
YPO1758	🟩				*manX, ptsL,*	PTS system, mannose-specific I	Transport/binding Carbohydrates,organic acids and alcohols
YPO1764	🟩				*hpaD*	3,4-dihydroxyphenylacetate 2,3-	Degradation of carbon compounds
YPO1765	🟩				*hpaF*	5-carboxymethyl-2-hydroxymuc	Degradation of carbon compounds
YPO1770				🟥	*hpaC*	4-hydroxyphenylacetate 3-mono	Degradation of carbon compounds
YPO1773				🟩	*pabB*	Para-aminobenzoate synthase co	Folic acid Biosynthesis
YPO1778				🟥		Conserved hypothetical protein	Unknown
YPO1779				🟥		Putative exported protein	Membranes, lipoproteins and porins
YPO1783					*ftnA, ftn, rsg*	Ferritin	Iron uptake
YPO1784	🟩					Putative copper resistance prote	Detoxification
YPO1828			🟥		*fliH, fla BII*	Flagellar assembly protein FliH	Chemotaxis and mobility
YPO1847		🟩			*yecS*	Putative amino-acid ABC transp	Transport/binding Amino acids and amines
YPO1848		🟩			*yecC*	Putative amino-acid ABC transp	Transport/binding Amino acids and amines
YPO1849	🟩					Conserved hypothetical protein	Unknown
YPO1850	🟩					Hypothetical protein	Unknown
YPO1851	🟩				*putA, poaA*	Bifunctional PutA protein [inclu	Degradation of amino acids
YPO1852	🟩					Putative membrane protein	Membranes, lipoproteins and porins
YPO1853	🟩				*putP*	Proline permease	Transport/binding Amino acids and amines
YPO1854		🟩		🟩		Putative membrane protein	Membranes, lipoproteins and porins
YPO1855		🟩		🟩		Putative exported protein	Membranes, lipoproteins and porins
YPO1856		🟩		🟩		Conserved hypothetical protein	Unknown

YPO1857	🟩				🟥	*wrbA*	Trp repressor binding protein	Broad regulatory functions
YPO1858					🟥		Putative exported protein	Membranes, lipoproteins and porins
YPO1866			🟩			*uvrC*	Excinuclease ABC subunit C	DNA replication, restriction/modification, recombination and repair
YPO1867	🟥					*pgsA*	CDP-diacylglycerol--glycerol-3	Synthesis and modification of Phospholipids
YPO1871							Hypothetical protein	Unknown
YPO1883	🟩						Hypothetical protein (pseudoger	Unknown
YPO1917	🟥						Integrase	
YPO1921							Probable pili assembly chaperor	Chaperones, chaperonins, heat shock
YPO1926						*ripA*	Putative 4-hydroxybutyrate coe	Fatty acid biosynthesis
YPO1932							Putative sugar transporter	Transport/binding Carbohydrates,organic acids and alcohols
YPO1942							Putative exported protein	Membranes, lipoproteins and porins
YPO1956							Hypothetical protein	Unknown
YPO1968					🟥		Transposase for insertion seque	
YPO1969					🟥		Putative IS100 transposase	
YPO1986							Putative exported protein	Membranes, lipoproteins and porins
YPO1992	🟥		🟩				Conserved hypothetical protein	Unknown
YPO1993	🟥	🟥	🟩				Putative dehydrogenase	Unknown
YPO1994	🟥	🟥	🟩				Hypothetical protein	Unknown
YPO1995	🟥	🟥	🟩		🟥		Hypothetical protein	Unknown
YPO1996	🟥				🟥		Hypothetical protein	Unknown
YPO2010					🟩	*ychF*	Conserved hypothetical protein	Unknown
YPO2011					🟩	*pth*	Peptidyl-tRNA hydrolase	Aminoacyl tRNA synthetases and their modification
YPO2012	🟩			🟩	🟥		Putative membrane protein	Membranes, lipoproteins and porins
YPO2013					🟩	*prsA, prs*	Ribose-phosphate pyrophosphol	Sugar nucleotides metabolism
YPO2018	🟥						Putative protoporphyrinogen ox	Heme and porphyrin Biosynthesis
YPO2038	🟥						Conserved hypothetical protein	Unknown
YPO2040	🟥						Putative membrane protein	Membranes, lipoproteins and porins
YPO2047					🟩		Conserved hypothetical protein	Unknown
YPO2053						*aspS, tls*	Aspartyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
YPO2056					🟩	*ruvC*	Crossover junction endodeoxyri	DNA replication, restriction/modification, recombination and repair
YPO2061	🟥				🟩	*znuA*	Exported high-affinity zinc upta	Transport/binding Cations
YPO2073					🟥		Putative lipoprotein	Membranes, lipoproteins and porins
YPO2074					🟥	*fadD*	Long-chain-fatty-acid-CoA liga:	Degradation of small molecule
YPO2075					🟩	*rnd*	Ribonuclease D	Degradation of RNA
YPO2076	🟩					*minE*	Cell division topological specifi	Cell division
YPO2077	🟩					*minD*	Septum site-determining proteir	Cell division
YPO2078	🟩					*minC*	Cell division inhibitor	Cell division
YPO2087a							Putative phage protein	Phage-related functions and prophage
YPO2145	🟩						Conserved hypothetical protein	Unknown
YPO2152	🟩				🟥		Conserved hypothetical protein	Unknown
YPO2153	🟩				🟥		Conserved hypothetical protein	Unknown

YPO2158				🟥		Conserved hypothetical protein	Unknown
YPO2162			🟥		*sppA*	Protease IV	Degradation of Proteins, peptides and glycopeptides
YPO2174	🟥			🟩	*pmrE*	Putative nucleotide sugar dehyd	Sugar nucleotides metabolism
YPO2180		🟥			*adhE, ana*	Aldehyde-alcohol dehydrogenas	Fermentation
YPO2191						Hypothetical protein	Unknown
YPO2201				🟥	*ompW*	Putative exported protein	Membranes, lipoproteins and porins
YPO2218				🟩	*topA, supX*	DNA topoisomerase I	DNA replication, restriction/modification, recombination and repair
YPO2229	🟩				*osmB*	Osmotically inducible lipoprote	Adaptions and atypical conditions
YPO2233	🟩					Conserved hypothetical protein	Unknown
YPO2234	🟩			🟥	*cstA*	Putative carbon starvation prote	Adaptions and atypical conditions
YPO2235				🟩	*rnb*	Exoribonuclease II	Degradation of RNA
YPO2244	🟥			🟩		Putative iron-sulfur binding NA	Unknown
YPO2245				🟩		Putative iron-sulfur protein	Unknown
YPO2246				🟩		Putative membrane protein	Membranes, lipoproteins and porins
YPO2255				🟥	*araF*	L-arabinose-binding periplasmi	Arabinose operon
YPO2256				🟥	*araG*	L-arabinose transport ATP-bind	Arabinose operon
YPO2257				🟥	*araH*	L-arabinose transport system pe	Arabinose operon
YPO2262	🟩					Putative exported protein	Membranes, lipoproteins and porins
YPO2264				🟥	*fumC*	Fumarate hydratase, class II	Tricarboxylic acid cycle
YPO2267			🟩			LysR-family transcriptional regu	Broad regulatory functions
YPO2269					*bioD*	Putative dethiobiotin synthetase	Biotin Biosynthesis
YPO2270			🟥			Putative membrane protein	Membranes, lipoproteins and porins
YPO2271	🟩					Phage hypothetical protein	Unknown
YPO2272	🟩					Phage hypothetical protein	Unknown
YPO2273	🟩			🟩		Phage hypothetical protein	Unknown
YPO2279						Putative phage-related membran	Membranes, lipoproteins and porins
YPO2282						Hypothetical protein	Unknown
YPO2293	🟩				*ilvB*	Putative acetolactate synthase la	Pyruvate family biosynthesis
YPO2295				🟩		Haloacid dehalogenase-like hyd	Unknown
YPO2299				🟥	*ogt*	Putative methylated-DNA--prot	DNA replication, restriction/modification, recombination and repair
YPO2301	🟩			🟥		Putative stress protein	Unknown
YPO2315	🟩			🟩		Putative exported protein	Membranes, lipoproteins and porins
YPO2323	🟥			🟥	*acpD*	Acyl carrier protein phosphodie	Fatty acid biosynthesis
YPO2325				🟥	*dalD*	Putative mannitol dehydrogenas	Degradation of carbon compounds
YPO2329	🟩				*ldhA, hslI, l*	D-lactate dehydrogenase	Fermentation
YPO2330	🟩				*hslJ*	Putative heat shock protein	Adaptions and atypical conditions
YPO2333					*qacE*	Quaternary ammonium compou	Drug/analogue sensitivity
YPO2335				🟩		Conserved hypothetical protein	Unknown
YPO2339	🟩				*mppA*	Putative periplasmic murein pep	Transport/binding proteins
YPO2344	🟩				*tyrR*	Transcriptional regulatory prote	Broad regulatory functions
YPO2362				🟥		Putative membrane protein	Membranes, lipoproteins and porins

YPO2363			🟥		Conserved hypothetical protein	Unknown
YPO2364			🟥		Insertion sequence IS100, ATP-	
YPO2367			🟥	*gst*	Glutathione S-transferase	Thioredoxin Biosynthesis
YPO2368			🟩	*pdxY*	Pyridoxamine kinase	Central intermediary metabolism
YPO2369			🟩	*tyrS*	Tyrosyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
YPO2370			🟩	*pdxH*	Pyridoxamine 5'-phosphate oxi	Pyridoxine Biosynthesis
YPO2374	🟩			*slyA, rovA*	MarR-family transcriptional reg	Broad regulatory functions
YPO2386			🟥	*sodB*	Superoxide dismutase [Fe]	Detoxification
YPO2387			🟩	*purR*	Purine nucleotide synthesis repr	Broad regulatory functions
YPO2390		🟩		*cfa, cdfA*	Cyclopropane-fatty-acyl-phosp	Fatty acid biosynthesis
YPO2394		🟩		*lpp, mlpA*	Major outer membrane lipoprot	Membranes, lipoproteins and porins
YPO2398			🟩		Putative exported protein (pseu	Membranes, lipoproteins and porins
YPO2399			🟩	*sufE*	Conserved hypothetical protein	Unknown
YPO2400			🟩	*sufS*	Putative selenocysteine lyase	Central intermediary metabolism
YPO2401			🟩	*sufD*	Conserved hypothetical protein	Unknown
YPO2402			🟩	*sufC*	Putative ATP-dependent transpo	Transport/binding proteins
YPO2403			🟩	*sufB*	Conserved hypothetical protein	Unknown
YPO2404			🟩	*sufA*	Conserved hypothetical protein	Unknown
YPO2416			🟩		Putative membrane protein	Membranes, lipoproteins and porins
YPO2421	🟥			*pmrF*	Probable glycosyl transferase	Unknown
YPO2427	🟩			*ihfA, himA,*	Integration host factor alpha-su	DNA replication, restriction/modification, recombination and repair
YPO2428			🟩	*pheT*	Phenylalanyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
YPO2429			🟩	*pheS*	Phenylalanyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
YPO2430			🟩	*rplT, pdzA*	50S ribosomal protein L20	Ribosomal protein synthesis and modification
YPO2436					Hypothetical protein	Unknown
YPO2439			🟩	*yfeA*	Periplasmic-binding protein	Transport/binding Cations
YPO2440			🟩	*yfeB*	ATP-binding transport protein	Transport/binding Cations
YPO2441			🟩	*yfeC*	Chelated iron transport system	Transport/binding Cations
YPO2442			🟩	*yfeD*	Chelated iron transport system	Transport/binding Cations
YPO2443			🟩		Putative membrane protein	Membranes, lipoproteins and porins
YPO2444	🟩		🟥		Conserved hypothetical protein	Unknown
YPO2448			🟩	*solA, soxA*	Putative sarcosine oxidase	Unknown
YPO2449			🟩		Putative LuxR-family regulator	Broad regulatory functions
YPO2452			🟩		Hypothetical protein	Unknown
YPO2456				*ypeI*	N-acylhomoserine lactone synt	AHL
YPO2457				*ypeR*	Quorum-sensing transcriptional	AHL
YPO2486	🟥				Conserved hypothetical protein	Unknown
YPO2501				*rbsB*	Sugar binding protein precursor	Transport/binding Carbohydrates,organic acids and alcohols
YPO2502	🟥		🟥	*gutB*	Putative zinc-binding dehydrog	Unknown
YPO2506			🟩	*ompX, omp*	Putative outer membrane protei	Cell envelop
YPO2510	🟩		🟥	*dps*	Putative DNA-binding protein	Adaptions and atypical conditions

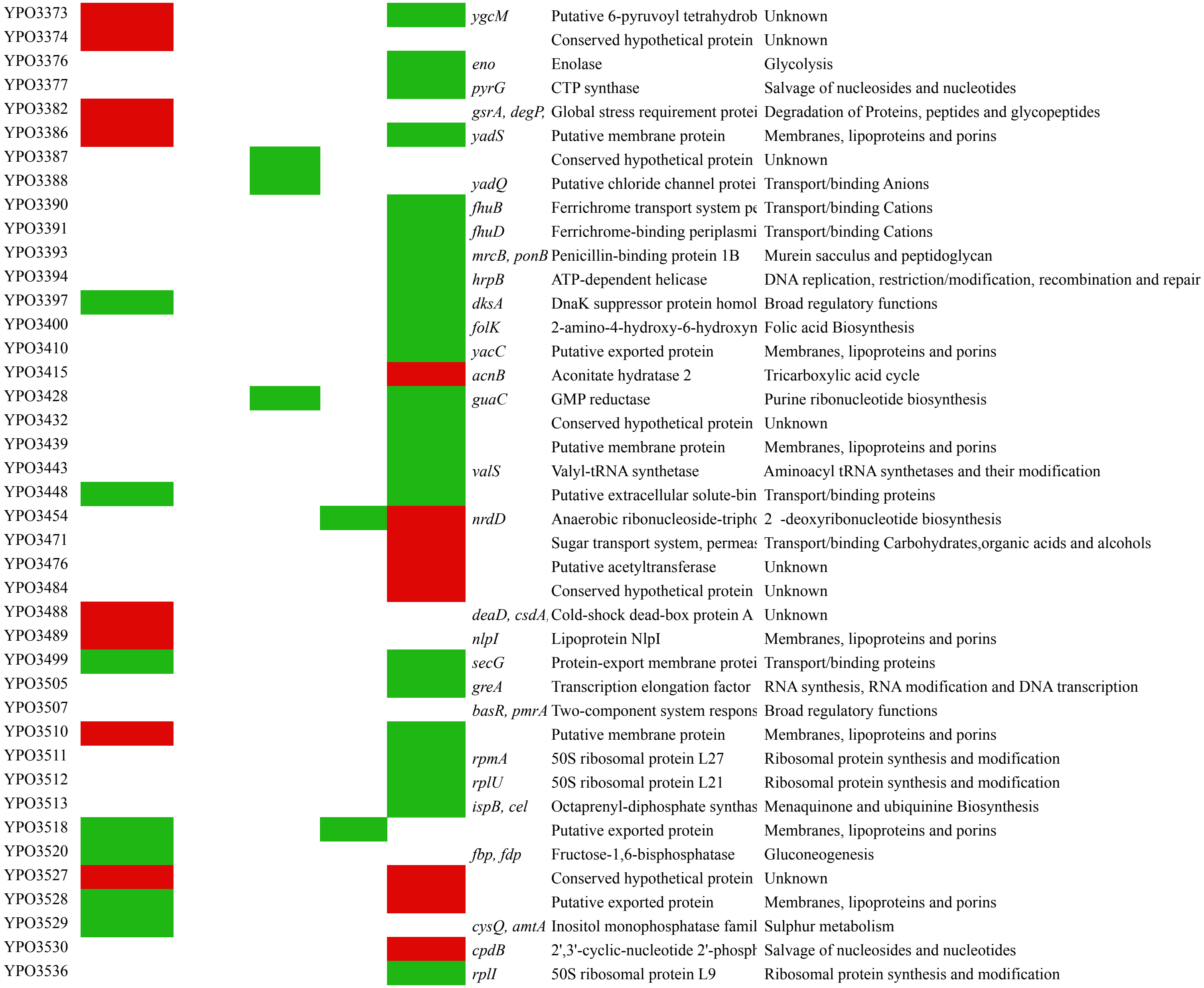
YPO2512	🟩				*glnH*	Putative glutamine-binding peri	Transport/binding Amino acids and amines
YPO2531	🟩				*elaB*	Putative membrane protein	Membranes, lipoproteins and porins
YPO2536	🟥					Putative D-isomer specific 2-hy	Unknown
YPO2539	🟥				*idnO*	Gluconate 5-dehydrogenase	Degradation of carbon compounds
YPO2540	🟥				*idnK, gntV*	Putative thermosensitive glucon	Degradation of carbon compounds
YPO2541	🟥					Conserved hypothetical protein	Unknown
YPO2558				🟩	*aat*	Probable aminotransferase	Unknown
YPO2559				🟩		Conserved hypothetical protein	Unknown
YPO2565				🟩		Hypothetical protein	Unknown
YPO2574			🟩			Putative membrane protein	Membranes, lipoproteins and porins
YPO2577	🟥			🟥		Putative aldehyde dehydrogenas	Unknown
YPO2578	🟥					Putative thiamine pyrophosphat	Degradation of carbon compounds
YPO2579	🟥					Putative myo-inositol dehydrog	Degradation of carbon compounds
YPO2590						Hypothetical protein	Unknown
YPO2595	🟩			🟥	*cspE*	Putative cold shock protein	Adaptions and atypical conditions
YPO2597				🟥	*tatE*	Sec-independent protein translo	Transport/binding proteins
YPO2604	🟥				*pbpA, mrdA*	Penicillin-binding protein 2	Murein sacculus and peptidoglycan
YPO2605	🟥					Conserved hypothetical protein	Unknown
YPO2606	🟥					Conserved hypothetical protein	Unknown
YPO2607	🟥			🟩	*nadD*	Putative nicotinate-nucleotide a	Unknown
YPO2611				🟥		Conserved hypothetical protein	Unknown
YPO2615				🟥	*glnH*	Putative amino acid-binding pr	Transport/binding Amino acids and amines
YPO2616	🟥				*cutE, lnt*	Putative apolipoprotein N-acylt	Membranes, lipoproteins and porins
YPO2623			🟥		*asnB*	Asparagine synthetase B	Aspartate family biosynthesis
YPO2626	🟩				*nagA*	Putative N-acetylglucosamine-6	Amino sugars metabolism
YPO2635				🟩	*fldA*	Flavodoxin 1	Electron transport
YPO2637				🟩		Conserved hypothetical protein	Unknown
YPO2645	🟩				*proX, proU*	Glycine betaine-binding peripla	Transport/binding Amino acids and amines
YPO2646	🟩				*proW*	Glycine betaine,L-proline transp	Transport/binding Amino acids and amines
YPO2647	🟩				*proV*	Glycine betaine,L-proline transp	Transport/binding Amino acids and amines
YPO2648				🟩	*nrdF*	Ribonucleoside-diphosphate red	Sugar nucleotides metabolism
YPO2649				🟩	*nrdE*	Ribonucleoside-diphosphate red	Sugar nucleotides metabolism
YPO2650				🟩	*nrdI*	NrdI protein homologue	Unknown
YPO2651					*nrdH*	Putative glutaredoxin	Sugar nucleotides metabolism
YPO2659		🟥		🟩	*cspB*	Cold shock protein	Adaptions and atypical conditions
YPO2665				🟥	*ureA, yeuA*	Urease gamma subunit	Pathogenicity
YPO2666				🟥	*ureB, yeuB*	Urease beta subunit	Pathogenicity
YPO2667				🟥	*ureC, yeuC*	Urease alpha subunit	Pathogenicity
YPO2668				🟥	*ureE*	Urease accessory protein	Pathogenicity
YPO2669				🟥	*ureF*	Urease accessory protein	Pathogenicity
YPO2670				🟥	*ureG*	Urease accessory protein	Membranes, lipoproteins and porins

YPO2671		🟩		🟥	*ureD*	Urease accessory protein (pseud	Pathogenicity
YPO2672	🟩			🟥		Putative urea transporter	Transport/binding Amino acids and amines
YPO2674	🟩	🟩				Putative exported protein	Membranes, lipoproteins and porins
YPO2675				🟥		Putative potassium channel prot	Transport/binding Cations
YPO2676	🟩					Putative membrane protein	Membranes, lipoproteins and porins
YPO2693			🟩		*ybfA*	Putative membrane protein	Membranes, lipoproteins and porins
YPO2695				🟥	*phrB, phr*	Putative deoxyribodipyrimidine	DNA replication, restriction/modification, recombination and repair
YPO2696	🟩					Putative 3',5'-cyclic-nucleotide I	Degradation of small molecule
YPO2699	🟩					Conserved hypothetical protein	Unknown
YPO2703		🟩			*pcp*	Putative pyrrolidone-carboxylat	Degradation of Proteins, peptides and glycopeptides
YPO2704				🟩	*ung*	Putative uracil-DNA glycosylas	DNA replication, restriction/modification, recombination and repair
YPO2705	🟩		🟩	🟥		Conserved hypothetical protein	Unknown
YPO2708				🟩	*srmB, rbaB*	ATP-dependent RNA helicase	RNA synthesis, RNA modification and DNA transcription
YPO2710	🟥				*nadB, nicB*	L-aspartate oxidase	Pyridine nucleotide Biosynthesis
YPO2711	🟥				*rpoE, sigE*	RNA polymerase sigma E factor	RNA synthesis, RNA modification and DNA transcription
YPO2712	🟥				*rseA, mclA*	Sigma E factor negative regulat	Broad regulatory functions
YPO2713	🟥				*rseB*	Sigma E factor regulatory protei	Broad regulatory functions
YPO2714	🟥				*rseC*	Sigma E factor regulatory protei	Broad regulatory functions
YPO2720	🟥				*recO*	DNA repair protein	DNA replication, restriction/modification, recombination and repair
YPO2731	🟩			🟩		Putative membrane protein	Membranes, lipoproteins and porins
YPO2740					*ccmG, dsbE*	Thiol:disulfide interchange prot	Heme and porphyrin Biosynthesis
YPO2744				🟥	*fadL, ttr*	Putative long-chain fatty acid tr	Transport/binding Carbohydrates,organic acids and alcohols
YPO2745				🟥		Conserved hypothetical protein	Unknown
YPO2746				🟥		Putative 3-ketoacyl-CoA thiolas	Degradation of small molecule
YPO2748	🟥				*sixA*	Putative phosphohistidine phosp	Broad regulatory functions
YPO2753				🟩	*yfcA*	Putative membrane protein	Membranes, lipoproteins and porins
YPO2755				🟩		Conserved hypothetical protein	Unknown
YPO2757	🟩			🟩	*fabB, fabC*	3-oxoacyl-[acyl-carrier-protein]	Fatty acid biosynthesis
YPO2767	🟥				*dedA*	Putative membrane protein	Membranes, lipoproteins and porins
YPO2771					*cvpA, dedE*	Putative colicin V production pr	Colicin-related functions
YPO2772				🟩	*purF*	Amidophosphoribosyltransferas	Purine ribonucleotide biosynthesis
YPO2774				🟥	*hisJ*	Histidine-binding periplasmic p	Transport/binding Amino acids and amines
YPO2775	🟥				*hisQ*	Histidine transport system perm	Transport/binding Amino acids and amines
YPO2778	🟩			🟥		Conserved hypothetical protein	Unknown
YPO2780				🟩		Conserved hypothetical protein	Unknown
YPO2795						Hypothetical protein	Unknown
YPO2804				🟥		Hypothetical protein	Unknown
YPO2805	🟩			🟥		Putative aldo,keto reductase	Unknown
YPO2806				🟥		Putative aldo,keto reductase	Unknown
YPO2815		🟥				Putative acyltransferase	Unknown
YPO2827					*upp, uraP*	Uracil phosphoribosyltransferas	Salvage of nucleosides and nucleotides

YPO2830	🟥				*speG*	Spermidine acetyltransferase	Polyamine synthesis
YPO2836	🟩				*ppk*	Polyphosphate kinase	Central intermediary metabolism
YPO2844				🟥	*goaG, gabT*	Putative aminobutyrate aminotr	Central intermediary metabolism
YPO2854	🟩			🟥		Conserved hypothetical protein	Unknown
YPO2855			🟩			Putative protease	Degradation of Proteins, peptides and glycopeptides
YPO2857	🟥				*ykfE, ivy*	Putative exported protein	Membranes, lipoproteins and porins
YPO2868						Conserved hypothetical protein	Unknown
YPO2870					*guaA*	Putative GMP synthase	Purine ribonucleotide biosynthesis
YPO2878				🟩	*hisS*	Histidyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
YPO2893		🟩				Chaperone protein HscB	
YPO2894		🟩			*iscA/yfhF*	Conserved hypothetical protein	Unknown
YPO2895		🟩			*nifU,iscU/yj*	NifU family protein	Unknown
YPO2896		🟩			*iscS, nifS, y*	Putative aminotransferase	Unknown
YPO2897		🟩			*yfhP*	Conserved hypothetical protein	Unknown
YPO2899					*suhB*	Putative inositol monophosphat	Unknown
YPO2904		🟩			*hcaT*	Putative transport permease pro	Transport/binding Carbohydrates,organic acids and alcohols
YPO2905				🟥	*ail*	Attachment invasion locus prote	Ail
YPO2907		🟥			*glyA*	Serine hydroxymethyltransferas	Central intermediary metabolism
YPO2908				🟩	*hmp, hmpA,*	Flavohemoprotein	Aerobic respiration
YPO2909						Conserved hypothetical protein	Unknown
YPO2922				🟩		Putative membrane protein	Murein sacculus and peptidoglycan
YPO2929				🟥	*acpS, dpj*	Holo-[acyl-carrier protein] synt	Fatty acid biosynthesis
YPO2930				🟥	*pdxJ*	Pyridoxal phosphate biosyntheti	Pyridoxine Biosynthesis
YPO2958	🟩			🟥	*sfuA, yfuA*	Iron(III)-binding periplasmic pr	Transport/binding Cations
YPO2969						Putative iron-sulphur protein	Unknown
YPO2974		🟥				Putative B-type cytochrome	Electron transport
YPO2975		🟥		🟥		Putative aminotransferase	Unknown
YPO2976	🟩					Conserved hypothetical protein	Unknown
YPO2978						Putative membrane protein	Membranes, lipoproteins and porins
YPO2983	🟥				*nupC, cru*	Nucleoside permease	Transport/binding proteins
YPO2984	🟥				*gltX*	Lutamyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
YPO2990	🟩				*zipA*	Putative cell division protein	Cell division
YPO2991				🟩	*cysZ*	Putative membrane protein	Membranes, lipoproteins and porins
YPO2993				🟩	*ptsH, hpr*	PTS system, phosphocarrier pro	Transport/binding Carbohydrates,organic acids and alcohols
YPO2994				🟩	*ptsI*	PTS sytem, enzyme I componer	Transport/binding Carbohydrates,organic acids and alcohols
YPO3001						Putative pyridine nucleotide-dis	Electron transport
YPO3010				🟩		Hypothetical protein	Unknown
YPO3013		🟩		🟩	*cysW*	Sulfate transport system permea	Transport/binding Anions
YPO3016				🟥	*nanT*	Putative sugar transporter	Transport/binding Carbohydrates,organic acids and alcohols
YPO3019				🟥		Conserved hypothetical protein	Unknown
YPO3020				🟥		Putative sugar kinase	Unknown

YPO3023			🟥		Conserved hypothetical protein	Unknown
YPO3024			🟥	*nanA, npl*	Probable N-acetylneuraminate l	Surface structures
YPO3026			🟩	*yfeY*	Putative lipoprotein	Membranes, lipoproteins and porins
YPO3027				*ygiW*	Putative exported protein	Membranes, lipoproteins and porins
YPO3034			🟥	*maeB*	NADP-dependent malic enzyme	Gluconeogenesis
YPO3041	🟩			*narP*	Nitrate,nitrite response regulato	Broad regulatory functions
YPO3047			🟥	*ydeN*	Putative sulfatase	Sulphur metabolism
YPO3048	🟩				Probable ABC-transporter, ATP-	Transport/binding proteins
YPO3049	🟩	🟥			Putative binding protein-depend	Transport/binding proteins
YPO3050	🟩	🟥			Putative exported protein	Membranes, lipoproteins and porins
YPO3052			🟩		Conserved hypothetical protein	Unknown
YPO3057			🟩	*yeaL*	Putative membrane protein	Membranes, lipoproteins and porins
YPO3069		🟥			Putative exported protein	Membranes, lipoproteins and porins
YPO3070	🟥	🟥	🟥	*yfgD*	Putative arsenate reductase	Drug/analogue sensitivity
YPO3077			🟩	*purK*	Phosphoribosylaminoimidazole	Purine ribonucleotide biosynthesis
YPO3079			🟩	*ybbA*	Putative ABC transporter ATP-b	Transport/binding proteins
YPO3086				*ybaR*	Putative cation-transporting AT	Transport/binding Cations
YPO3094			🟩	*rosB, ybaL*	Putative potassium antiporter	Transport/binding Cations
YPO3118			🟩	*adk, plsA, d*	Adenylate kinase	Purine ribonucleotide biosynthesis
YPO3120			🟩	*recR*	Recombination protein RecR	DNA replication, restriction/modification, recombination and repair
YPO3123	🟥		🟩	*apt*	Adenine phosphoribosyltransfer	Salvage of nucleosides and nucleotides
YPO3128			🟥		Conserved hypothetical protein	Unknown
YPO3137		🟩	🟩		Conserved hypothetical protein	Unknown
YPO3138		🟩	🟩	*ymoA*	Modulating protein YmoA (hist	Broad regulatory functions
YPO3140			🟥	*ybaY*	Putative lipoprotein	Membranes, lipoproteins and porins
YPO3142				*amtB*	Probable ammonium transporter	Transport/binding Cations
YPO3143				*glnK*	Nitrogen regulatory protein P-II	Broad regulatory functions
YPO3151					Conserved hypothetical protein	Unknown
YPO3153			🟩	*ppiD*	Peptidyl-prolyl cis-trans isomera	Protein translation and modification
YPO3154			🟩	*hupB, hopD*	DNA-binding protein HU-beta	Adaptions and atypical conditions
YPO3158			🟩	*tig*	Trigger factor	Cell division
YPO3159			🟩		Hypothetical protein	Unknown
YPO3163				*yfeN*	Putative exported protein	Membranes, lipoproteins and porins
YPO3164	🟩			*cyoA*	Cytochrome O ubiquinol oxidas	Aerobic respiration
YPO3170			🟩		Conserved hypothetical protein	Unknown
YPO3173			🟩	*thiI*	Thiamine biosynthesis protein	Thiamine Biosynthesis
YPO3189			🟩	*secD*	Protein-export membrane protei	Transport/binding proteins
YPO3190			🟩	*yajC*	Putative membrane protein	Membranes, lipoproteins and porins
YPO3199	🟩		🟥		Probable short-chain dehydroge	Unknown
YPO3200	🟩	🟥	🟥	*malZ*	Putative maltodextrin glucosida	Maltose operon
YPO3203		🟩		*pstS*	Phosphate binding protein	Transport/binding Anions

YPO3206					🟩	*sbcD*	Exonuclease SbcD	Degradation of DNA
YPO3212	🟩				🟩	*rdgC*	Recombination associated prote	DNA replication, restriction/modification, recombination and repair
YPO3225					🟩	*gpt, gpp, gx*	Xanthine-guanine phosphoribos	Salvage of nucleosides and nucleotides
YPO3235			🟥			*nqrF, nqr6*	NADH-uniquinone oxidoreduct	Electron transport
YPO3237			🟥			*nqrD, nqr4*	Na+-translocating NADH-quinc	Electron transport
YPO3244					🟥	*yafH*	Probable acyl-CoA dehydrogena	Degradation of small molecule
YPO3254					🟥		Putative amino acid ABC transp	Transport/binding Amino acids and amines
YPO3260	🟩						Hypothetical protein	Unknown
YPO3261	🟩						Probable amidase	Degradation of small molecule
YPO3272					🟥	*yfiQ*	Putative acetyltransferase	Unknown
YPO3278	🟥					*yfiO*	Putative lipoprotein	Membranes, lipoproteins and porins
YPO3279	🟩			🟩	🟥	*yfiA*	Putative sigma 54 modulation p	Broad regulatory functions
YPO3290						*ydiY*	Putative exported protein	Membranes, lipoproteins and porins
YPO3292					🟩	*rplS*	50S ribosomal protein L19	Ribosomal protein synthesis and modification
YPO3293					🟩	*trmD*	tRNA (guanine-N1)-methyltrans	Aminoacyl tRNA synthetases and their modification
YPO3294					🟩	*rimM*	16S rRNA processing protein	Ribosome maturation and modification
YPO3295					🟩	*rpsP*	30S ribosomal protein S16	Ribosomal protein synthesis and modification
YPO3300	🟩		🟥		🟥	*luxS*	Autoinducer-2 production prote	AI-2
YPO3301	🟩					*gshA, gsh-I,*	Glutamate--cysteine ligase	Thioredoxin Biosynthesis
YPO3302	🟩				🟩	*yqaA*	Putative membrane protein	Membranes, lipoproteins and porins
YPO3303	🟩					*yqaB*	Putative hydrolase	Unknown
YPO3319	🟥				🟥	*katY*	Catalase-peroxidase	Oxidative stress
YPO3320	🟥		🟩		🟩	*cybC*	Putative cytochrome B562	Electron transport
YPO3321	🟥		🟩		🟩	*cybB*	Probable cytochrome B561	Electron transport
YPO3323						*dmsC*	Anaerobic dimethyl sulfoxide re	Anaerobic respiration
YPO3327					🟥	*fucR*	Putative deoR-family regulatory	Broad regulatory functions
YPO3335					🟥	*fumA, fumB*	Fumarate hydratase, class I	Tricarboxylic acid cycle
YPO3340							Putative exogenous ferric siderc	Iron uptake
YPO3348							Transcriptional regulatory prote	Broad regulatory functions
YPO3351							Putative dehydrogenase	Unknown
YPO3359			🟩				Conserved hypothetical protein	Unknown
YPO3360			🟩		🟩	*ispF, mecS,*	2C-methyl-D-erythritol 2,4-cycl	Central intermediary metabolism
YPO3361			🟩		🟩	*ispD, b274*	4-diphosphocytidyl-2C-methyl-	Central intermediary metabolism
YPO3362					🟩		Conserved hypothetical protein	Unknown
YPO3363			🟩			*ygbE*	Putative membrane protein	Membranes, lipoproteins and porins
YPO3364					🟩	*cysC*	Adenylylsulfate kinase	Sulphur metabolism
YPO3365			🟩		🟩	*cysN*	Sulfate adenylyltransferase subu	Sulphur metabolism
YPO3366			🟩		🟩	*cysD*	Sulfate adenylyltransferase subu	Sulphur metabolism
YPO3367			🟩		🟩	*cysG*	Siroheme synthase	Heme and porphyrin Biosynthesis
YPO3369			🟩				Conserved hypothetical protein	Unknown
YPO3372					🟩	*cysJ*	Sulfite reductase [NADPH] flav	Sulphur metabolism

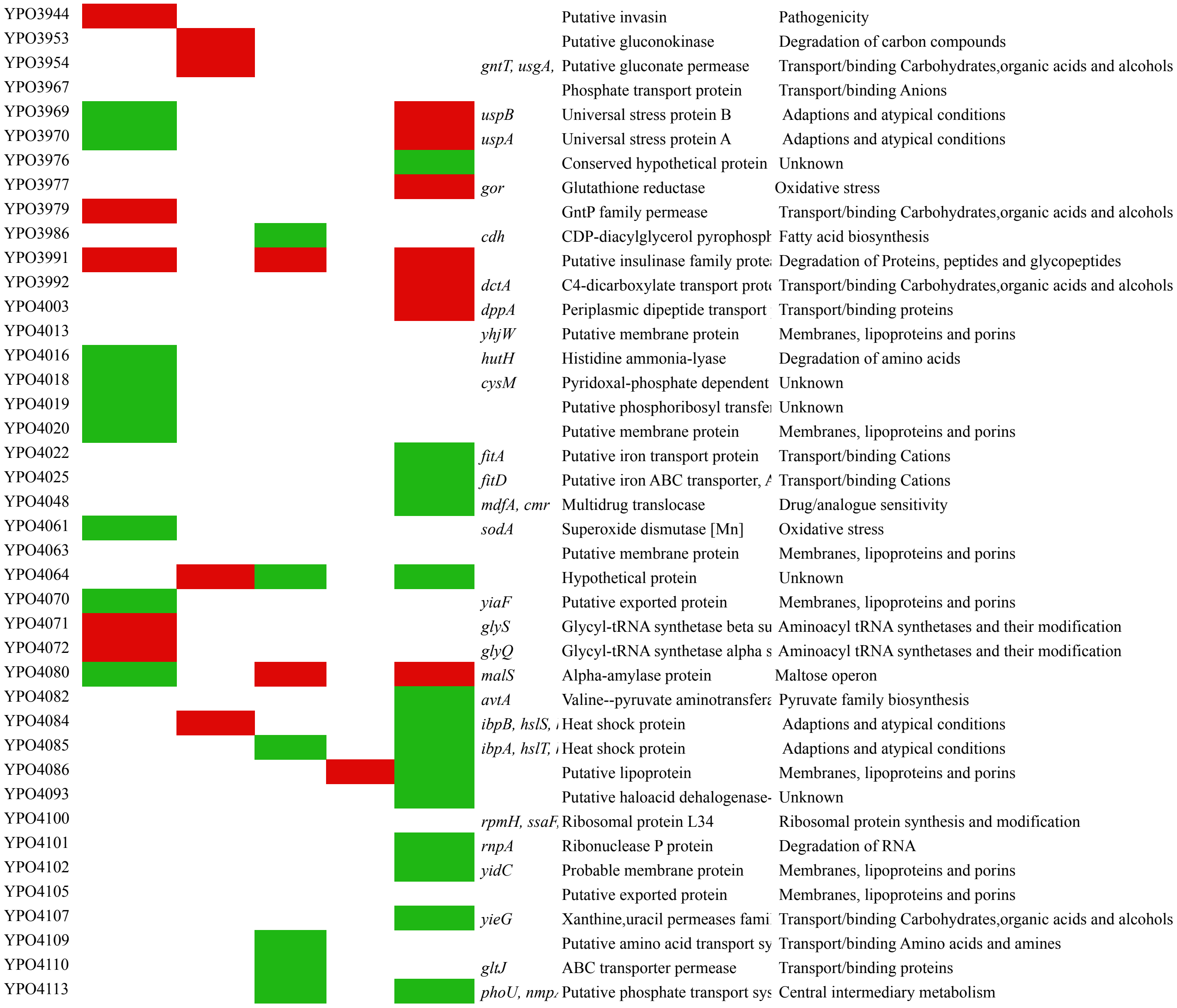


YPO3373	🟥			🟩	*ygcM*	Putative 6-pyruvoyl tetrahydrob	Unknown
YPO3374	🟥					Conserved hypothetical protein	Unknown
YPO3376				🟩	*eno*	Enolase	Glycolysis
YPO3377				🟩	*pyrG*	CTP synthase	Salvage of nucleosides and nucleotides
YPO3382	🟥				*gsrA, degP,*	Global stress requirement protei	Degradation of Proteins, peptides and glycopeptides
YPO3386	🟥			🟩	*yadS*	Putative membrane protein	Membranes, lipoproteins and porins
YPO3387		🟩				Conserved hypothetical protein	Unknown
YPO3388		🟩			*yadQ*	Putative chloride channel protei	Transport/binding Anions
YPO3390				🟩	*fhuB*	Ferrichrome transport system pe	Transport/binding Cations
YPO3391				🟩	*fhuD*	Ferrichrome-binding periplasmi	Transport/binding Cations
YPO3393				🟩	*mrcB, ponB*	Penicillin-binding protein 1B	Murein sacculus and peptidoglycan
YPO3394				🟩	*hrpB*	ATP-dependent helicase	DNA replication, restriction/modification, recombination and repair
YPO3397	🟩			🟩	*dksA*	DnaK suppressor protein homol	Broad regulatory functions
YPO3400				🟩	*folK*	2-amino-4-hydroxy-6-hydroxyn	Folic acid Biosynthesis
YPO3410				🟩	*yacC*	Putative exported protein	Membranes, lipoproteins and porins
YPO3415				🟥	*acnB*	Aconitate hydratase 2	Tricarboxylic acid cycle
YPO3428		🟩		🟩	*guaC*	GMP reductase	Purine ribonucleotide biosynthesis
YPO3432				🟩		Conserved hypothetical protein	Unknown
YPO3439				🟩		Putative membrane protein	Membranes, lipoproteins and porins
YPO3443				🟩	*valS*	Valyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification
YPO3448	🟩			🟩		Putative extracellular solute-bin	Transport/binding proteins
YPO3454			🟩	🟥	*nrdD*	Anaerobic ribonucleoside-triphc	2 -deoxyribonucleotide biosynthesis
YPO3471				🟥		Sugar transport system, permeas	Transport/binding Carbohydrates,organic acids and alcohols
YPO3476				🟥		Putative acetyltransferase	Unknown
YPO3484				🟥		Conserved hypothetical protein	Unknown
YPO3488	🟥				*deaD, csdA,*	Cold-shock dead-box protein A	Unknown
YPO3489	🟥				*nlpI*	Lipoprotein NlpI	Membranes, lipoproteins and porins
YPO3499	🟩			🟩	*secG*	Protein-export membrane protei	Transport/binding proteins
YPO3505				🟩	*greA*	Transcription elongation factor	RNA synthesis, RNA modification and DNA transcription
YPO3507					*basR, pmrA*	Two-component system respons	Broad regulatory functions
YPO3510	🟥			🟩		Putative membrane protein	Membranes, lipoproteins and porins
YPO3511				🟩	*rpmA*	50S ribosomal protein L27	Ribosomal protein synthesis and modification
YPO3512				🟩	*rplU*	50S ribosomal protein L21	Ribosomal protein synthesis and modification
YPO3513				🟩	*ispB, cel*	Octaprenyl-diphosphate synthas	Menaquinone and ubiquinine Biosynthesis
YPO3518	🟩		🟩			Putative exported protein	Membranes, lipoproteins and porins
YPO3520	🟩				*fbp, fdp*	Fructose-1,6-bisphosphatase	Gluconeogenesis
YPO3527	🟥			🟥		Conserved hypothetical protein	Unknown
YPO3528	🟩			🟥		Putative exported protein	Membranes, lipoproteins and porins
YPO3529	🟩				*cysQ, amtA*	Inositol monophosphatase famil	Sulphur metabolism
YPO3530				🟥	*cpdB*	2',3'-cyclic-nucleotide 2'-phospl	Salvage of nucleosides and nucleotides
YPO3536				🟩	*rplI*	50S ribosomal protein L9	Ribosomal protein synthesis and modification

YPO3537	🟩			🟩	*rpsR*	30S ribosomal protein S18	Ribosomal protein synthesis and modification
YPO3538	🟩			🟩	*priB*	Primosomal replication protein	DNA replication, restriction/modification, recombination and repair
YPO3539	🟩			🟩	*rpsF*	30S ribosomal protein S6	Ribosomal protein synthesis and modification
YPO3540	🟩					Hypothetical protein	Unknown
YPO3562				🟩	*rpsI*	30S ribosomal protein S9	Ribosomal protein synthesis and modification
YPO3563				🟩	*rplM*	50S ribosomal protein L13	Ribosomal protein synthesis and modification
YPO3565	🟩					Putative membrane protein	Membranes, lipoproteins and porins
YPO3566			🟥	🟥	*degQ, hhoA*	Protease	Degradation of Proteins, peptides and glycopeptides
YPO3569				🟩	*murA, mur*	UDP-N-acetylglucosamine 1-ca	Murein sacculus and peptidoglycan
YPO3570				🟩		BolA-like protein	Unknown
YPO3580	🟥					Conserved hypothetical protein	Unknown
YPO3581	🟥				*yhbG*	Probable ABC transporter ATP-	Transport/binding proteins
YPO3582				🟥	*rpoN, glnF,*	RNA polymerase sigma-54 fact	RNA synthesis, RNA modification and DNA transcription
YPO3583				🟥	*yhbH*	Probable sigma (54) modulation	RNA synthesis, RNA modification and DNA transcription
YPO3588	🟥			🟥	*pyrB*	Aspartate carbamoyltransferase	Pyrimidine ribonucleotide biosynthesis
YPO3589	🟥			🟥	*pyrI*	Aspartate carbamoyltransferase	Broad regulatory functions
YPO3606						Putative Rhs accessory genetic	Unknown
YPO3610						Conserved hypothetical protein	Unknown
YPO3612	🟩			🟩		Putative transcriptional regulato	Broad regulatory functions
YPO3624	🟥				*ssuA*	Putative aliphatic sulfonates bin	Transport/binding proteins
YPO3625	🟥				*ssuD*	Alkanesulfonate monooxygenas	Sulphur metabolism
YPO3626	🟥				*ssuC*	Putative aliphatic sulfonates tra	Transport/binding proteins
YPO3631			🟥			Putative exported protein	Membranes, lipoproteins and porins
YPO3632	🟥				*ddg, lpxP*	Putative membrane protein	Membranes, lipoproteins and porins
YPO3639				🟥	*yghU*	Putative glutathione S-transfera	Unknown
YPO3640						Putative exported protein	Membranes, lipoproteins and porins
YPO3643		🟥		🟩	*cspa2*	Major cold shock protein Cspa2	Adaptions and atypical conditions
YPO3644		🟥		🟩	*cspa1*	Major cold shock protein Cspa1	Adaptions and atypical conditions
YPO3645						Hypothetical protein	Unknown
YPO3646	🟩				*pcp, pcpY, s*	Outer membrane lipoprotein	Membranes, lipoproteins and porins
YPO3647				🟥		Conserved hypothetical protein	Unknown
YPO3648				🟥		Putative 2-hydroxy-3-oxopropi	Degradation of carbon compounds
YPO3649				🟥		Putative gamma carboxymucon	Degradation of small molecule
YPO3650				🟥		Putative metabolite transport pr	Transport/binding proteins
YPO3652	🟥					Hypothetical protein	Unknown
YPO3653	🟥					Putative colicin immunity prote	Colicin-related functions
YPO3654					*fiS*	DNA-binding protein Fis	DNA replication, restriction/modification, recombination and repair
YPO3655						Conserved hypothetical protein	Unknown
YPO3658			🟥		*accC, fabG*	Biotin carboxylase	Fatty acid biosynthesis
YPO3661			🟩			Putative membrane protein	Membranes, lipoproteins and porins
YPO3665	🟥				*mreB, envB*	Rod shape-determining protein	Murein sacculus and peptidoglycan

YPO3666	🟥		🟩	*mreC*	Rod shape-determining protein	Murein sacculus and peptidoglycan
YPO3667	🟥			*mreD*	Rod shape-determining protein	Murein sacculus and peptidoglycan
YPO3668	🟥			*yhdE*	Putative inhibitor of septum forı	Unknown
YPO3681		🟥	🟥		Putative insectician toxin	Pathogenicity
YPO3682	🟩	🟥	🟥		Putative lysR-family transcriptiı	Broad regulatory functions
YPO3686				*yhcP*	Putative membrane protein	Membranes, lipoproteins and porins
YPO3687			🟥		Putative succinate-semialdehydı	Central intermediary metabolism
YPO3689			🟥		Putative ribonuclease	Degradation of RNA
YPO3690			🟥		Putative ribonuclease inhibitor	Unknown
YPO3695				*rnk*	Regulator of nucleoside diphosț	Broad regulatory functions
YPO3696	🟩		🟥	*treC, olgH*	Putative trehalose-6-phosphate l	Degradation of carbon compounds
YPO3697	🟩		🟥	*treB*	PTS system, trehalose-specific I	Transport/binding Carbohydrates,organic acids and alcohols
YPO3705	🟩				Conserved hypothetical protein	Unknown
YPO3706	🟩				Conserved hypothetical protein	Unknown
YPO3707	🟩				Conserved hypothetical protein	Unknown
YPO3708	🟩				Conserved hypothetical protein	Unknown
YPO3710	🟩	🟥	🟥	*malM, mol*	Maltose operon periplasmic pro	Maltose operon
YPO3711	🟩	🟥	🟥	*lamB, malB*	Maltoporin	Maltose operon
YPO3712	🟩	🟥	🟥	*malK*	Maltose,maltodextrin transport	Maltose operon
YPO3713	🟩	🟥			Hypothetical protein	Unknown
YPO3714	🟩	🟥	🟥	*malE*	Maltose-binding periplasmic prı	Maltose operon
YPO3715	🟩	🟥	🟥	*malF*	Maltose transport system perme	Maltose operon
YPO3716	🟩	🟥	🟥	*malG*	Maltose transport system perme	Maltose operon
YPO3718	🟩			*pgi*	Glucose-6-phosphate isomerase	Glycolysis
YPO3722			🟩	*metH*	5-Methyltetrahydrofolate--homı	Aspartate family biosynthesis
YPO3724			🟥	*aceK*	Isocitrate dehydrogenase kinase	Glyoxylate bypass
YPO3725			🟥	*aceA, icl*	Isocitrate lyase	Glyoxylate bypass
YPO3726			🟥	*aceB, mas*	Malate synthase A	Glyoxylate bypass
YPO3727		🟥		*metA*	Homoserine O-succinyltransferı	Aspartate family biosynthesis
YPO3731	🟩			*hupA*	DNA-binding protein HU-alpha	Adaptions and atypical conditions
YPO3737	🟩			*rsd*	Regulator of sigma D	Broad regulatory functions
YPO3738		🟥			Hypothetical protein	Unknown
YPO3740		🟥		*thiE*	Thiamine-phosphate pyrophospl	Thiamine Biosynthesis
YPO3741		🟥		*thiF*	Thiamine biosynthesis protein T	Thiamine Biosynthesis
YPO3743	🟩			*thiH*	Thiamine biosynthesis protein T	Thiamine Biosynthesis
YPO3746			🟩	*rpoC, tabB*	DNA-directed RNA polymerase	RNA synthesis, RNA modification and DNA transcription
YPO3747				*rpoB, groN,*	DNA-directed RNA polymerase	RNA synthesis, RNA modification and DNA transcription
YPO3748			🟩	*rplL*	50S ribosomal protein L7,L12	Ribosomal protein synthesis and modification
YPO3749			🟩	*rplJ*	50S ribosomal protein L10	Ribosomal protein synthesis and modification
YPO3750			🟩	*rplA*	50S ribosomal protein L1	Ribosomal protein synthesis and modification
YPO3751			🟩	*rplK, relC*	50S ribosomal protein L11	Ribosomal protein synthesis and modification

YPO3752					🟩	*nusG*	Transcription antitermination pr	RNA synthesis, RNA modification and DNA transcription
YPO3753					🟩	*secE, prlG*	Preprotein translocase SecE sub	Transport/binding proteins
YPO3754	🟩				🟩	*tufA, tufB*	Elongation factor Tu	Protein translation and modification
YPO3760					🟩	*murB*	UDP-N-acetylenolpyruvoylgluc	Murein sacculus and peptidoglycan
YPO3766					🟥	*fadB, oldB*	Fatty acid oxidation complex al	Degradation of small molecule
YPO3767					🟥	*fadA, oldA*	3-ketoacyl-CoA thiolase	Degradation of small molecule
YPO3768					🟩	*fadI, fre, flr*	NAD(P)H-flavin reductase	Electron transport
YPO3769					🟩		Conserved hypothetical protein	Unknown
YPO3775	🟥					*tatD, mttC*	Deoxyribonuclease TatD (pseud	Degradation of DNA
YPO3776	🟥					*tatC, mttB*	Sec-independent protein translo	Transport/binding proteins
YPO3779					🟩	*aarF*	Ubiquinone biosynthesis protei	Menaquinone and ubiquinine Biosynthesis
YPO3783	🟥						Putative membrane protein	Membranes, lipoproteins and porins
YPO3784							Putative carbon starvation prote	Adaptions and atypical conditions
YPO3785					🟥		Conserved hypothetical protein	Unknown
YPO3786				🟩	🟥	*udp*	Uridine phosphorylase	Salvage of nucleosides and nucleotides
YPO3787					🟥		Putative carboxymethylenebute	Degradation of small molecule
YPO3788	🟩	🟩	🟥		🟥	*metE*	5-methyltetrahydropteroyltriglu	Aspartate family biosynthesis
YPO3789			🟥			*metR*	LysR-family transcriptional reg	Broad regulatory functions
YPO3797							Putative exported protein	Membranes, lipoproteins and porins
YPO3811					🟩	*rpoH, htpR,*	RNA polymerase sigma-32 fact	RNA synthesis, RNA modification and DNA transcription
YPO3817			🟩				Putative membrane protein	Membranes, lipoproteins and porins
YPO3819	🟩					*yhhN*	Putative membrane protein	Membranes, lipoproteins and porins
YPO3820					🟥	*zntA*	Putative P-type cation-transloca	Transport/binding Cations
YPO3829	🟥				🟩		Putative haloacid dehalogenase-	Unknown
YPO3834					🟩	*pldA*	Phospholipase A	Central intermediary metabolism
YPO3838	🟩						Conserved hypothetical protein	Unknown
YPO3839	🟩						Conserved hypothetical protein	Unknown
YPO3840	🟩						Putative TetR-family regulatory	Broad regulatory functions
YPO3864			🟩			*rffE, wecB,*	UDP-N-acetylglucosamine 2-ep	Surface polysaccharides, lipopolysaccharides and antigens
YPO3865			🟩			*wzzE, wzz, i*	Putative lipopolysaccharide bio	Surface polysaccharides, lipopolysaccharides and antigens
YPO3866					🟩	*rfe, b3784*	Putative undecaprenyl-phosphat	Surface polysaccharides, lipopolysaccharides and antigens
YPO3873					🟩	*ppiC*	Peptidyl-prolyl cis-trans isomer	Protein translation and modification
YPO3888	🟩				🟥	*ilvC*	Ketol-acid reductoisomerase	Pyruvate family biosynthesis
YPO3901		🟥				*ilvG*	Acetolactate synthase isozyme I	Pyruvate family biosynthesis
YPO3903					🟩		Conserved hypothetical protein	Unknown
YPO3911					🟩	*trmA*	tRNA (uracil-5)-methyltransfer	Aminoacyl tRNA synthetases and their modification
YPO3912					🟥	*yijD*	Putative membrane protein	Membranes, lipoproteins and porins
YPO3924						*argH*	Putative argininosuccinate lyase	Glutamate family biosynthesis
YPO3937	🟩					*glpD, glyD*	Aerobic glycerol-3-phosphate d	Central intermediary metabolism
YPO3938						*glgP, glgY*	Glycogen phosphorylase	Synthesis and modification of Polysaccharides (cytoplasmic)
YPO3940						*glgC*	Glucose-1-phosphate adenylyltr	Synthesis and modification of Polysaccharides (cytoplasmic)



YPO3944	🟥						Putative invasin	Pathogenicity
YPO3953		🟥					Putative gluconokinase	Degradation of carbon compounds
YPO3954		🟥				*gntT, usgA,*	Putative gluconate permease	Transport/binding Carbohydrates,organic acids and alcohols
YPO3967							Phosphate transport protein	Transport/binding Anions
YPO3969	🟩				🟥	*uspB*	Universal stress protein B	Adaptions and atypical conditions
YPO3970	🟩				🟥	*uspA*	Universal stress protein A	Adaptions and atypical conditions
YPO3976					🟩		Conserved hypothetical protein	Unknown
YPO3977					🟥	*gor*	Glutathione reductase	Oxidative stress
YPO3979	🟥						GntP family permease	Transport/binding Carbohydrates,organic acids and alcohols
YPO3986			🟩			*cdh*	CDP-diacylglycerol pyrophosph	Fatty acid biosynthesis
YPO3991	🟥		🟥		🟥		Putative insulinase family prote	Degradation of Proteins, peptides and glycopeptides
YPO3992					🟥	*dctA*	C4-dicarboxylate transport prot	Transport/binding Carbohydrates,organic acids and alcohols
YPO4003					🟥	*dppA*	Periplasmic dipeptide transport	Transport/binding proteins
YPO4013						*yhjW*	Putative membrane protein	Membranes, lipoproteins and porins
YPO4016	🟩					*hutH*	Histidine ammonia-lyase	Degradation of amino acids
YPO4018	🟩					*cysM*	Pyridoxal-phosphate dependent	Unknown
YPO4019	🟩						Putative phosphoribosyl transfe	Unknown
YPO4020	🟩						Putative membrane protein	Membranes, lipoproteins and porins
YPO4022					🟩	*fitA*	Putative iron transport protein	Transport/binding Cations
YPO4025					🟩	*fitD*	Putative iron ABC transporter,	Transport/binding Cations
YPO4048					🟩	*mdfA, cmr*	Multidrug translocase	Drug/analogue sensitivity
YPO4061	🟩					*sodA*	Superoxide dismutase [Mn]	Oxidative stress
YPO4063							Putative membrane protein	Membranes, lipoproteins and porins
YPO4064		🟥	🟩		🟩		Hypothetical protein	Unknown
YPO4070	🟩					*yiaF*	Putative exported protein	Membranes, lipoproteins and porins
YPO4071	🟥					*glyS*	Glycyl-tRNA synthetase beta su	Aminoacyl tRNA synthetases and their modification
YPO4072	🟥					*glyQ*	Glycyl-tRNA synthetase alpha s	Aminoacyl tRNA synthetases and their modification
YPO4080	🟩		🟥		🟥	*malS*	Alpha-amylase protein	Maltose operon
YPO4082					🟩	*avtA*	Valine--pyruvate aminotransfer	Pyruvate family biosynthesis
YPO4084		🟥			🟩	*ibpB, hslS,*	Heat shock protein	Adaptions and atypical conditions
YPO4085			🟩		🟩	*ibpA, hslT,*	Heat shock protein	Adaptions and atypical conditions
YPO4086				🟥	🟩		Putative lipoprotein	Membranes, lipoproteins and porins
YPO4093					🟩		Putative haloacid dehalogenase-	Unknown
YPO4100						*rpmH, ssaF,*	Ribosomal protein L34	Ribosomal protein synthesis and modification
YPO4101					🟩	*rnpA*	Ribonuclease P protein	Degradation of RNA
YPO4102					🟩	*yidC*	Probable membrane protein	Membranes, lipoproteins and porins
YPO4105							Putative exported protein	Membranes, lipoproteins and porins
YPO4107					🟩	*yieG*	Xanthine,uracil permeases fami	Transport/binding Carbohydrates,organic acids and alcohols
YPO4109			🟩				Putative amino acid transport sy	Transport/binding Amino acids and amines
YPO4110			🟩			*gltJ*	ABC transporter permease	Transport/binding proteins
YPO4113			🟩		🟩	*phoU, nmp*	Putative phosphate transport sys	Central intermediary metabolism

YPO4114		🟩		*pstB, phoT*	Putative phosphate transport AT	Transport/binding Anions
YPO4115		🟩	🟩	*pstA, phoT*	Putative phosphate transport sys	Transport/binding Anions
YPO4116		🟩		*pstC, phoW*	Putative phosphate transport sys	Transport/binding Anions
YPO4119			🟩	*glmU*	UDP-N-acetylglucosamine pyr	Sugar nucleotides metabolism
YPO4120	🟩			*atpC, uncC,*	ATP synthase epsilon subunit pr	ATP-proton motive force
YPO4122	🟩			*atpG, uncG*	ATP synthase gamma subunit p	ATP-proton motive force
YPO4124			🟩	*atpH, uncH*	ATP synthase delta subunit prot	ATP-proton motive force
YPO4125			🟩	*atpF, uncF,*	ATP synthase subunit B protein	ATP-proton motive force
YPO4127			🟩	*atpB, uncB,*	ATP synthase subunit B protein	ATP-proton motive force
YPO4128			🟩	*atpI, uncI*	ATP synthase protein I	ATP-proton motive force
YPO4130			🟩	*gidA*	Glucose inhibited division prote	Cell division
YPPCP1.08c			🟩		Putative Transcriptional Regula	
yscB	🟥	🟩	🟩	*yscB*	Type III Secretion Apparatus C	Type III Secretion System
yscC	🟥	🟩	🟩	*yscC*	Outer Membrane Secretin Precu	Type III Secretion System
yscD	🟥		🟩	*yscD*	Virulence Protein	Type III Secretion System
yscE	🟥		🟩	*yscE*	Type III Secretion Apparatus C	Type III Secretion System
yscF	🟥		🟩	*yscF*	Needle Complex Major Subunit	Type III Secretion System
yscG	🟥		🟩	*yscG*	Type III Secretion Apparatus C	Type III Secretion System
yscH	🟥		🟩	*yscH*		Type III Secretion System
yscI	🟥	🟩	🟩	*yscI*		Type III Secretion System
yscJ	🟥	🟩	🟩	*yscJ*		Type III Secretion System
yscK	🟥	🟩	🟩	*yscK*	Type III Secretion Apparatus C	Type III Secretion System
yscL	🟥	🟩	🟩	*yscL*	Type III Secretion System Prote	Type III Secretion System
yscM	🟥	🟩	🟩	*yscM*		Type III Secretion System
yscN	🟥	🟩		*yscN*	Type III Secretion System Atpa	Type III Secretion System
yscO	🟥	🟩		*yscO*	Type III Secretion Apparatus C	Type III Secretion System
yscP	🟥	🟩		*yscP*	Type III Secretion Apparatus C	Type III Secretion System
yscQ	🟥	🟩		*yscQ*	Type III Secretion System Prote	Type III Secretion System
yscR	🟥	🟩		*yscR*	Type III Secretion System Prote	Type III Secretion System
yscS	🟥	🟩	🟩	*yscS*	Needle Complex Export Protein	Type III Secretion System
yscT	🟥	🟩		*yscT*	Needle Complex Export Protein	Type III Secretion System
yscU	🟥			*yscU*	Needle Complex Export Protein	Type III Secretion System
yscX	🟥	🟩		*yscX*	Hypothetical Protein	Type III Secretion System
yscY	🟥	🟩		*yscY*	Hypothetical Protein	Type III Secretion System