Table S2. Significant differentially expressed genes ($p < 0.05$; FC* > 1.5): R88 vs ISM1980 (R88 Δ*luxS::Kan*), 37°C.

ID	*p* value	*q* value	FC	qRT-PCR	Gene	Gene function	Process	COG	COG function categories
YPO1507	0.016358457	0.035390695	13.3058		*mglB*	Galactose-binding protein	Transport/binding Carbohydrates,organic acids and alcohols	COG1879	G
YPO3300	1.25979E-06	0.000752186	12.78535		*luxS*	Autoinducer-2 production protein	AI-2	COG1854	T
YPO1137	0.014673728	0.034956394	8.774063		*galK, g*	Galactokinase	Galactose operon	COG0153	G
YPO3023	0.015798625	0.035091878	8.216136			Conserved hypothetical protein	Unknown	COG3010	G
YPO3786	0.008263472	0.032332443	7.70986		*udp*	Uridine phosphorylase	Salvage of nucleosides and nucleotides	COG2820	F
YPO0408	0.008112265	0.032332443	7.49323		*lsrF*	Putative aldolase	Degradation of carbon compounds	COG1830	G
YPO3279	0.008275862	0.032332443	7.438729	6.9	*yfiA*	Putative sigma 54 modulation protein	Broad regulatory functions	COG1544	J
YPO0409	0.012431201	0.034349747	7.366185		*lsrB*	AI-2 receptor, periplasmic protein	AI-2	COG1879	G
YPO1858	0.007158411	0.031529203	6.805969			Putative exported protein	Membranes, lipoproteins and porins	COG3055	S
YPO0407	0.006429163	0.030434909	6.738922		*lsrG*	Cleavage of P-DPD cleavage producing 2 phosphoglycoli	AI-2	COG1359	S
YPO3024	0.01101479	0.03336898	6.505838		*nanA, n*	Probable N-acetylneuraminate lyase	Surface structures	COG0329	EM
YPO1139	0.014157285	0.034834517	6.486999		*galE, g*	UDP-glucose 4-epimerase	Galactose operon	COG1087	M
YPO1508	0.020289444	0.037798026	6.470155		*mglA*	Galactoside transport ATP-binding protein	Transport/binding Carbohydrates,organic acids and alcohols	COG1129	G
YPO1423a	0.002674344	0.022752142	6.288358		*rmf*	Putative ribosome modulation factor	Ribosome maturation and modification	COG3130	J
YPO1138	0.020051	0.037744385	6.243869		*galT, ga*	Galactose-1-phosphate uridylyltransferase	Galactose operon	COG1085	C
YPO3020	0.028246324	0.040733399	5.204377			Putative sugar kinase	Unknown	COG1940	KG
YPO2774	0.011188172	0.033373987	5.130484		*hisJ*	Histidine-binding periplasmic protein	Transport/binding Amino acids and amines	COG0834	ET
YPO2012	0.013171971	0.034490359	4.941159			Putative membrane protein	Membranes, lipoproteins and porins		
YPO3714	0.004199769	0.026949058	4.910128	5	*malE*	Maltose-binding periplasmic protein precursor	Maltose operon	COG2182	G
YPO3016	0.027526909	0.040446181	4.890038		*nanT*	Putative sugar transporter	Transport/binding Carbohydrates,organic acids and alcohols	COG0477	GEPR
YPO2595	0.014240365	0.034834517	4.885639		*cspE*	Putative cold shock protein	Adaptions and atypical conditions	COG1278	K
YPO0439	0.004684303	0.027745502	4.880267	2	*deoB, d*	Phosphopentomutase	Salvage of nucleosides and nucleotides	COG1015	G
YPO3767	0.023681279	0.039017462	4.729881		*fadA, ol*	3-ketoacyl-CoA thiolase	Degradation of small molecule	COG0183	I
YPO3019	0.02398355	0.039017462	4.642254			Conserved hypothetical protein	Unknown	COG2731	G
YPO0149	0.025901041	0.039776249	4.54442			Putative membrane protein	Membranes, lipoproteins and porins		
YPO3766	0.033655827	0.044043591	4.523111		*fadB, ol*	Fatty acid oxidation complex alpha subunit	Degradation of small molecule	COG1250	I
YPO0410	0.04830817	0.048944781	4.496503		*lsrD*	Putative ABC transporter permease protein	AI-2	COG1172	G
YPO0436	0.014120499	0.034834517	4.486173		*deoC, d*	Deoxyribose-phosphate aldolase	Serine family biosynthesis	COG0274	F
YPO0845	3.35315E-05	0.007931073	4.390311			ThiJ,PfpI-family thiamine biogenesis protein	Thiamine Biosynthesis	COG0693	R
YPO0623	0.008284936	0.032332443	4.202166			Putative aminotransferase	Unknown	COG0436	E
YPO0624	0.008402765	0.032332443	4.172853			Putative membrane protein	Membranes, lipoproteins and porins	COG1757	C
YPO3788	0.00124827	0.019738662	4.100463		*metE*	5-methyltetrahydropteroyltriglutamate--homocyst eine me	Aspartate family biosynthesis	COG0620	E
YPO0832	0.00230563	0.021602417	4.096775		*agaZ*	Putative tagatose 6-phosphate kinase	Degradation of carbon compounds		
YPO0844	0.00115403	0.019298639	4.084094		*agaY, k*	Putative aldolase	Degradation of carbon compounds	COG0191	G
YPO1303	0.000740891	0.017718588	4.028524	5.67	*psaA*	pH 6 antigen precursor (antigen 4) (adhesin)	Surface polysaccharides, lipopolysaccharides and antigens		
YPO3725	0.000429881	0.01718606	3.88802	6.34	*aceA, ic*	Isocitrate lyase	Glyoxylate bypass	COG2224	C
YPO1509	0.043332818	0.047568566	3.79468		*mglC*	Galactoside permease	Transport/binding Carbohydrates,organic acids and alcohols	COG1172	G
YPO3200	0.005731756	0.029973848	3.787477		*malZ*	Putative maltodextrin glucosidase	Maltose operon	COG0366	G
YPO0414	0.010939991	0.03336898	3.727359		*lsrR*	Repressor binds specifically to the P-DPD(pseudogene)	AI-2		
YPO3244	0.00528406	0.029198545	3.720284		*yafH*	Probable acyl-CoA dehydrogenase	Degradation of small molecule	COG1960	I
YPO3726	0.000285712	0.016712285	3.693225		*aceB, m*	Malate synthase A	Glyoxylate bypass	COG2225	C
YPO3681	0.000126442	0.012919226	3.67407			Putative insecticial toxin	Pathogenicity	COG1196	D
YPO1645	0.003878347	0.026026647	3.670398			Conserved hypothetical protein	Unknown	COG0702	MG
YPO3711	0.013585818	0.034748073	3.625166		*lamB, m*	Maltoporin	Maltose operon		
YPO2444	0.013016153	0.034490359	3.577986			Conserved hypothetical protein	Unknown	COG3001	G
YPO0907	0.014709352	0.034956394	3.469117		*gcvT*	Aminomethyltransferase	Degradation of amino acids	COG0404	E

YPO0625	0.014832857	0.034956394	3.370294		Hypothetical protein	Unknown		
YPO0906	0.01094286	0.03336898	3.361207	*gcsH*	Glycine cleavage system H protein	glycine	COG0509	E
YPO1512	0.008339601	0.032332443	3.346784	*cdd*	Cytidine deaminase	Salvage of nucleosides and nucleotides	COG0295	F
YPO2264	0.00069757	0.017718588	3.30521	*fumC*	Fumarate hydratase, class II	Tricarboxylic acid cycle	COG0114	C
malF	0.020120924	0.037744385	3.234906	*malF*	Maltose transport system permease protein MalF	Maltose operon		
YPO0337	0.034443007	0.044527354	3.234906		Putative exported protein	Membranes, lipoproteins and porins		
YPO3724	0.001639004	0.02045638	3.186426	*aceK*	Isocitrate dehydrogenase kinase,phosphatase	Glyoxylate bypass		
YPO3527	0.002065279	0.021431731	3.045606		Conserved hypothetical protein	Unknown		
YPO1321	0.04630615	0.048690731	3.042562	*sdaC, d*	Serine transporter	Transport/binding Amino acids and amines	COG0814	E
YPO0252	0.010708534	0.033239226	3.02769		Putative membrane protein	Membranes, lipoproteins and porins	COG3162	S
YPO2666	0.00694063	0.031357403	3.007172	*ureB, ye*	Urease beta subunit	Pathogenicity	COG0832	E
YPO0253	0.008612943	0.032332443	3.001463	*acs*	Acetyl-coenzyme A synthetase	Degradation of carbon compounds	COG0365	I
YPO0412	0.028199496	0.040733399	2.994568	*lsrA*	Putative ABC transporter ATP-binding protein	AI-2	COG1129	G
YPO4080	0.016077332	0.035297758	2.985896	*malS*	Alpha-amylase protein	Maltose operon	COG0366	G
YPO1383	0.001357595	0.019849387	2.919756	*pflB, pfl*	Formate acetyltransferase 1	Anaerobic respiration	COG1882	C
YPO0821	0.00807808	0.032332443	2.909555		Hypothetical protein	Unknown	COG0086	K
YPO0833	0.011996999	0.034195991	2.870252		Putative phosphosugar isomerase	Degradation of carbon compounds	COG2222	M
YPO2744	0.022810804	0.039017462	2.85908	*fadL, ttr*	Putative long-chain fatty acid transport protein	Transport/binding Carbohydrates,organic acids and alcohols	COG2067	I
YPO2665	0.007183757	0.031529203	2.826955	*ureA, ye*	Urease gamma subunit	Pathogenicity	COG0831	E
YPO3970	0.020688739	0.03822026	2.824129	*uspA*	Universal stress protein A	Adaptions and atypical conditions	COG0589	T
YPO3687	0.005184109	0.028811426	2.819614		Putative succinate-semialdehyde dehydrogenase (pseudog	Central intermediary metabolism		
YPO0325	0.001907325	0.021336704	2.797707	*ssb, exr*	Single-strand binding protein	DNA replication, restriction/modification, recombination and r	COG0629	L
YPO2675	0.002201657	0.021479969	2.795469		Putative potassium channel protein	Transport/binding Cations	COG1226	P
YPO2577	0.018247956	0.03641551	2.789605		Putative aldehyde dehydrogenase	Degradation of carbon compounds	COG1012	C
YPO0437	0.038460339	0.045450147	2.777635	*deoA, tp*	Thymidine phosphorylase (pseudogene)	Salvage of nucleosides and nucleotides		
YPO1235	0.040787512	0.046904392	2.761848		Conserved hypothetical protein	Unknown	COG3395	S
YPO0440	0.023796246	0.039017462	2.738472	*deoD, p*	Purine nucleoside phosphorylase	Salvage of nucleosides and nucleotides	COG0813	F
YPO3319	0.016959696	0.035522094	2.704724	*katY*	Catalase-peroxidase	Oxidative stress	COG0376	P
YPMT1.72	0.008310071	0.032332443	2.688276					
YPO0584	0.041640127	0.047031976	2.678615		Putative symporter protein	Transport/binding proteins	COG3633	E
YPO2255	0.007688786	0.03221144	2.652493	*araF*	L-arabinose-binding periplasmic protein precursor	Arabinose operon	COG1879	G
YPO0834	0.041899666	0.047124761	2.650902	*manX*	Putative PTS transport protein	Transport/binding Carbohydrates,organic acids and alcohols	COG3444	G
YPO2074	0.013479909	0.034748073	2.623476	*fadD*	Long-chain-fatty-acid-CoA ligase	Degradation of small molecule	COG0318	IQ
malG	0.023319444	0.039017462	2.621116	*malG*	Maltose transport system permease protein MalG	Maltose operon		
YPO3716	0.002228149	0.021479969	2.595295	*malG*	Maltose transport system permease protein MalG	Maltose operon	COG0395	G
YPO4003	0.026865588	0.040256329	2.592701	*dppA*	Periplasmic dipeptide transport protein	Transport/binding proteins	COG0747	E
agaY	0.000111683	0.012514977	2.587003	*agaY, kb*	Putative aldolase	Degradation of carbon compounds		
YPO1115	0.001832234	0.021162725	2.572813	*sucC, b*	Succinyl-CoA synthetase beta chain	Tricarboxylic acid cycle	COG0045	C
YPO3034	0.005812179	0.030095594	2.558958	*maeB*	NADP-dependent malic enzyme	Gluconeogenesis	COG0281	C
YPO1041	0.007236625	0.031553633	2.546449	*dapD*	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltrans	Aspartate family biosynthesis	COG2171	E
YPO1207	0.001183719	0.019298639	2.539583	*katA*	Catalase	Oxidative stress	COG0753	P
YPO0831	0.030408591	0.041986505	2.532482		DeoR-family regulatory protein	Broad regulatory functions	COG1349	KG
YPO2615	0.018153749	0.03641551	2.508538	*glnH*	Putative amino acid-binding protein precursor	Transport/binding Amino acids and amines	COG0834	ET
YPO3199	0.045444242	0.048392859	2.485565		Probable short-chain dehydrogenase	Unknown	COG1028	IQR
sucD	0.024191028	0.039097379	2.442202	*sucD*	Succinyl-CoA synthetase alpha chain	Tricarboxylic acid cycle		
YPO3648	0.013067495	0.034490359	2.43781		Putative 2-hydroxy-3-oxopropionate reductase	Degradation of carbon compounds	COG2084	I
YPO0823	0.011525788	0.03357332	2.40488	*yapM*	Autotransporter	Membranes, lipoproteins and porins	COG2931	Q
YPO3649	0.008994435	0.032612957	2.401035		Putative gamma carboxymuconolactone decarboxylase	Degradation of small molecule	COG0599	S
YPO1112	0.007388566	0.031595575	2.396238	*sdhB*	Succinate dehydrogenase iron-sulfur protein	Tricarboxylic acid cycle	COG0479	C
YPO1116	0.005890983	0.030095594	2.394561	*sucD*	Succinyl-CoA synthetase alpha chain	Tricarboxylic acid cycle	COG0074	C
YPO0626	0.004878701	0.027776406	2.390494		Conserved hypothetical protein	Unknown	COG2964	S

YPO1996	0.007785382	0.032332443	2.388343		Hypothetical protein	Unknown	COG2812	L
YPO2667	0.014633648	0.034956394	2.379761	*ureC, y*	Urease alpha subunit	Pathogenicity	COG0804	E
YPO1040	0.031079325	0.042303438	2.363633		Conserved hypothetical protein	Unknown	COG1196	D
YPO0060	0.003833637	0.026026647	2.362688	*tdh*	Threonine 3-dehydrogenase	Degradation of amino acids	COG1063	ER
YPO0415	0.02471714	0.039115715	2.35514	*lsrK*	Kinase phosphorylates carbon-5 of the open form of DPD	AI-2	COG1070	G
YPO0822	0.02736267	0.040338726	2.346911		Putative exported protein	Membranes, lipoproteins and porins		
YPO3715	0.02189188	0.038668179	2.344096	*malF*	Maltose transport system permease protein MalF	Maltose operon	COG1175	G
YPO1114	0.002128869	0.021479969	2.334972	*sucB*	Dihydrolipoamide succinyltransferase component of 2-ox	Tricarboxylic acid cycle	COG0508	C
YPO1358	0.000834542	0.019104257	2.326581	*poxB*	Pyruvate dehydrogenase [cytochrome]	Pyruvate dehydrogenase	COG0028	EH
YPO2386	1.33734E-05	0.004440893	2.317757	*sodB*	Superoxide dismutase [Fe]	Detoxification	COG0605	P
YPO3785	0.004625876	0.027612645	2.300209		Conserved hypothetical protein	Unknown	COG2365	T
YPO1779	0.016680859	0.035480778	2.29745		Putative exported protein	Membranes, lipoproteins and porins		
YPO1304	0.000991296	0.019298639	2.280056	*psaB*	Chaperone protein PsaB precursor	Chaperones, chaperonins, heat shock	COG3121	NU
YPO0324	0.000439996	0.01718606	2.263246	*uvrA, d*	Excinuclease ABC subunit A	DNA replication, restriction/modification, recombination and r	COG0178	L
YPO1995	0.007077255	0.031503233	2.254662		Hypothetical protein	Unknown		
YPO1113	0.021693559	0.038632787	2.244988	*sucA*	2-oxoglutarate dehydrogenase E1 component	Tricarboxylic acid cycle	COG0567	C
YPO0905	0.047674435	0.048838565	2.229105	*gcvP*	Glycine dehydrogenase	glycine	COG1003	E
YPO1236	0.023535042	0.039017462	2.225096		Putative class II aldolase-family protein	Unknown	COG0235	G
YPO3650	0.031698639	0.042659127	2.170158		Putative metabolite transport protein	Transport/binding proteins	COG0477	GEPR
YPO3647	0.033520717	0.043953387	2.169507		Conserved hypothetical protein	Unknown	COG0491	R
YPO0836	0.008456176	0.032332443	2.157176		Putative PTS permease protein	Transport/binding Carbohydrates,organic acids and alcohols	COG0477	GEPR
tdh	0.028694632	0.040972496	2.154589	*tdh*	Threonine 3-dehydrogenase	Degradation of amino acids		
YPO3712	0.023816915	0.039017462	2.149854	*malK*	Maltose,maltodextrin transport ATP-binding protein	Maltose operon	COG1130	G
YPO3070	0.012542289	0.034349747	2.137635	*yfgD*	Putative arsenate reductase	Drug/analogue sensitivity	COG1393	P
YPO1108	0.005107508	0.028504972	2.128888	*gltA, gl*	Citrate synthase GltA	Tricarboxylic acid cycle	COG0372	C
YPO2905	0.002212996	0.021479969	2.126123	*ail*	Attachment invasion locus protein	Ail	COG3637	M
YPO2301	0.02186698	0.038668179	2.119542		Putative stress protein	Unknown	COG0589	T
YPO0411	0.021563768	0.038632787	2.114673	*lsrC*	Putative ABC transporter permease protein	AI-2	COG1172	G
YPO2854	0.024984009	0.039180251	2.107916		Conserved hypothetical protein	Unknown	COG3422	S
YPO0059	0.009602608	0.032670333	2.073629	*kbl*	Amino-3-ketobutyrate coenzyme A ligase	Fatty acid biosynthesis	COG0156	H
YPO1111	0.023901309	0.039017462	2.063905	*sdhA*	Succinate dehydrogenase flavoprotein subunit	Tricarboxylic acid cycle	COG1053	C
YPO0570	0.002476038	0.022045547	2.046846	*yqjD*	Putative membrane protein	Membranes, lipoproteins and porins	COG1196	D
YPO1354	0.00993294	0.032901973	2.046232		Putative lipoprotein	Membranes, lipoproteins and porins		
YPO3583	0.008651768	0.032332443	2.04051	*yhbH*	Probable sigma (54) modulation protein (pseudogene)	RNA synthesis, RNA modification and DNA transcription		
acnA	0.000473518	0.01718606	2.033178	*acnA, a*	Aconitate hydratase 1	Tricarboxylic acid cycle		
YPO1353	0.001509315	0.019849387	2.026479		Putative chorismate mutase	Central intermediary metabolism	COG1605	E
YPO0159	0.014354938	0.034956394	2.023037	*nirC*	Putative nitrite transporter	Transport/binding Anions	COG2116	P
YPO0676	0.015658982	0.034956394	2.020813		Putative aldo,keto reductase family protein	Unknown	COG0656	R
YPO1778	0.016045875	0.035287018	2.020207		Conserved hypothetical protein	Unknown	COG3097	S
YPO2975	0.013969373	0.034834517	2.016171		Putative aminotransferase	Unknown	COG0436	E
YPO2256	0.012530845	0.034349747	2.013954	*araG*	L-arabinose transport ATP-binding protein	Arabinose operon	COG1129	G
YPO3471	0.010156495	0.03304557	2.006918		Sugar transport system, permease protein	Transport/binding Carbohydrates,organic acids and alcohols	COG1175	G
YPO3991	0.001093603	0.019298639	2.004711		Putative insulinase family protease	Degradation of Proteins, peptides and glycopeptides	COG0612	R
YPMT1.4	0.012490386	0.034349747	2.001907				COG0715	P
YPO3476	0.006547687	0.030706792	1.989732		Putative acetyltransferase	Unknown	COG3153	R
YPO3484	0.004489408	0.026982691	1.981591		Conserved hypothetical protein	Unknown	COG2141	C
YPO0835	0.004370997	0.026955851	1.977829		Putative PTS permease protein	Transport/binding Carbohydrates,organic acids and alcohols	COG0477	GEPR
YPO2668	0.020486289	0.038057981	1.974273	*ureE*	Urease accessory protein	Pathogenicity	COG0803	P
YPO3820	0.021704261	0.038632787	1.966195	*zntA*	Putative P-type cation-translocating membrane ATPase	Transport/binding Cations	COG2217	P
YPO3582	0.004888509	0.027776406	1.964819	*rpoN, g*	RNA polymerase sigma-54 factor	RNA synthesis, RNA modification and DNA transcription	COG1508	K
YPO3977	0.018420537	0.036508093	1.963837	*gor*	Glutathione reductase	Oxidative stress	COG1249	C

YPO3992	0.026984393	0.040256329	1.960501	*dctA*	C4-dicarboxylate transport protein	Transport/binding Carbohydrates,organic acids and alcohols	COG1301	C
YPO3047	0.047011827	0.048690731	1.95541	*ydeN*	Putative sulfatase	Sulphur metabolism	COG3119	P
YPO0842	0.006040236	0.030310453	1.933245		Putative sulfatase	Sulphur metabolism	COG3119	P
YPO0569a	0.009659239	0.032670333	1.915541		Conserved hypothetical protein	Unknown		
YPO2695	0.014875297	0.034956394	1.915158	*phrB, p*	Putative deoxyribodipyrimidine photolyase	DNA replication, restriction/modification, recombination and r	COG0415	L
YPO3710	0.038954407	0.045911468	1.914775	*malM, r*	Maltose operon periplasmic protein	Maltose operon		
YPO2844	0.015529225	0.034956394	1.909612	*goaG, g*	Putative aminobutyrate aminotransferase	Central intermediary metabolism	COG0160	E
YPO3689	0.003425151	0.024960851	1.896481		Putative ribonuclease	Degradation of RNA		
YPO3696	0.013537557	0.034748073	1.88891	*treC, ol*	Putative trehalose-6-phosphate hydrolase	Degradation of carbon compounds	COG0366	G
YPO3682	0.002337924	0.021602417	1.880617		Putative lysR-family transcriptional regulatory protein	Broad regulatory functions	COG0583	K
YPO2669	0.003343794	0.02457963	1.876672	*ureF*	Urease accessory protein	Pathogenicity	COG0830	O
YPO0627	0.035890728	0.044847424	1.875921		Putative translational inhibitor protein	Unknown	COG0251	J
YPO3140	0.002393942	0.021618465	1.867499	*ybaY*	Putative lipoprotein	Membranes, lipoproteins and porins	COG3126	S
YPMT1.2	0.023286439	0.039017462	1.863208				COG1475	K
YPO0568	0.003890661	0.026026647	1.8593		Putative membrane protein	Membranes, lipoproteins and porins	COG2259	S
YPO3272	0.003573592	0.025248501	1.85707	*yfiQ*	Putative acetyltransferase	Unknown	COG1042	C
YPO0251	0.043118175	0.047489934	1.848547		Putative transmembrane transport protein	Membranes, lipoproteins and porins	COG0591	ER
YPO2257	0.000528907	0.01725695	1.847993	*araH*	L-arabinose transport system permease protein	Arabinose operon	COG1172	G
YPO3969	0.01414622	0.034834517	1.844485	*uspB*	Universal stress protein B	Adaptions and atypical conditions		
YPO2323	0.044414849	0.048011847	1.843747	*acpD*	Acyl carrier protein phosphodiesterase	Fatty acid biosynthesis	COG1182	I
YPO2510	0.016694932	0.035480778	1.842826	*dps*	Putative DNA-binding protein	Broad regulatory functions	COG0783	P
YPO0678	0.016254137	0.035390695	1.825767		Putative iron-containing alcohol dehydrogenase	Unknown	COG1979	C
YPO0365	0.036694146	0.045055609	1.81957		Conserved hypothetical protein	Unknown	COG1162	R
YPO3589	0.016979616	0.035522094	1.818296	*pyrI*	Aspartate carbamoyltransferase regulatory chain	Broad regulatory functions	COG1781	F
YPO1357	0.038214936	0.045350365	1.817387	*ltaA*	L-allo-threonine aldolase	Serine family biosynthesis	COG2008	E
YPO0931	0.000681938	0.017718588	1.816842	*metK*	S-adenosylmethionine synthetase	Central intermediary metabolism	COG0192	H
YPO0628	0.015046866	0.034956394	1.816297		Putative translational inhibitor protein	Unknown	COG0251	J
YPO3415	0.005665834	0.029919034	1.811038	*acnB*	Aconitate hydratase 2	Tricarboxylic acid cycle	COG1049	C
YPO1770	0.021186851	0.038575491	1.798225	*hpaC*	4-hydroxyphenylacetate 3-monooxygenase coupling prote	Degradation of carbon compounds	COG1853	R
YPO2705	0.042896555	0.047359741	1.790151		Conserved hypothetical protein	Unknown	COG3445	R
YPO2672	0.001607498	0.02045638	1.785324		Putative urea transporter	Transport/binding Amino acids and amines	COG2814	G
YPO0007	0.017004115	0.035522094	1.783896		Ribose permease	Transport/binding Carbohydrates,organic acids and alcohols	COG1869	G
YPO3588	0.00334079	0.02457963	1.777131	*pyrB*	Aspartate carbamoyltransferase catalytic subunit	Pyrimidine ribonucleotide biosynthesis	COG0540	F
YPO0913	0.004450827	0.026955851	1.774289		Putative 5-formyltetrahydrofolate cyclo-ligase-family pro	Unknown	COG0212	H
YPO3327	0.023235078	0.039017462	1.767737	*fucR*	Putative deoR-family regulatory protein	Broad regulatory functions	COG1349	KG
YPO2670	0.001313525	0.019849387	1.765087	*ureG*	Urease accessory protein	Pathogenicity	COG0378	OK
YPO0160	0.034494811	0.044527354	1.765087	*nirD*	Nitrite reductase [NAD	Anaerobic respiration	COG2146	PR
YPO1356	0.008443903	0.032332443	1.763323		Putative membrane protein	Membranes, lipoproteins and porins	COG0702	MG
YPO3697	0.002683338	0.022752142	1.763147	*treB*	PTS system, trehalose-specific IIBC component	Transport/binding Carbohydrates,organic acids and alcohols	COG1263	G
YPO3566	0.017272445	0.03562513	1.762089	*degQ, h*	Protease	Degradation of Proteins, peptides and glycopeptides	COG0265	O
YPO0319	0.00871662	0.032341011	1.761913	*qor, hcz*	Quinone oxidoreductase	Degradation of small molecule	COG0604	CR
YPO0274	0.023882545	0.039017462	1.758568		Putative integral membrane protein	Membranes, lipoproteins and porins	COG2391	R
YPO3335	0.034146439	0.044466581	1.749098	*fumA, f*	Fumarate hydratase, class I	Tricarboxylic acid cycle	COG1951	C
YPO2153	0.002988757	0.023080789	1.733946		Conserved hypothetical protein	Unknown	COG2766	T
YPO1567	0.024734846	0.039115715	1.731694		Putative racemase	Unknown	COG1441	H
YPO2958	0.035620476	0.044730947	1.731521	*sfuA, yf*	Iron(III)-binding periplasmic protein	Transport/binding Cations	COG1840	P
YPO0699	0.02477705	0.039115715	1.730655		Fimbrial chaperone protein	Chaperones, chaperonins, heat shock	COG3121	NU
YPO1584	0.010846718	0.033350559	1.729444		Conserved hypothetical protein (pseudogene)	Unknown		
YPO2152	0.001888769	0.021336704	1.727025		Conserved hypothetical protein	Unknown	COG2718	S
acpS	0.001061499	0.019298639	1.725643	*acpS, d*	Holo-[acyl-carrier protein] synthase	Fatty acid biosynthesis		
YPO2671	0.011218531	0.033373987	1.719614	*ureD*	Urease accessory protein (pseudogene)	Pathogenicity		

YPO3530	0.025039809	0.039190458	1.719098	*cpdB*	2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor	Salvage of nucleosides and nucleotides	COG0737	F
YPO1857	0.022096827	0.038728348	1.716522	*wrbA*	Trp repressor binding protein	Broad regulatory functions	COG0655	R
sfuA	0.015405061	0.034956394	1.715149	*sfuA, yf*	Iron(III)-binding periplasmic protein	Transport/binding Cations		
YPO2611	0.000920492	0.019104257	1.71138		Conserved hypothetical protein	Unknown	COG0711	C
YPO1386	0.020587151	0.038191941	1.710867	*ansB*	Putative L-asparaginase II precursor	Degradation of amino acids	COG0252	EJ
YPO2804	0.021685309	0.038632787	1.709327		Hypothetical protein	Unknown		
YPO1969	0.015568807	0.034956394	1.708986		Putative IS1 transposase		COG1484	L
YPO0152	0.002945425	0.022898051	1.706253	*aroB*	3-dehydroquinate synthase	Aromatic amino acid family biosynthesis	COG0337	E
YPO0455	0.021002427	0.038543268	1.701142		Putative phosphoglycerate mutase		COG0406	G
YPO2201	0.008064333	0.032332443	1.680683	*ompW*	Putative exported protein	Membranes, lipoproteins and porins	COG3047	M
YPO2805	0.013724382	0.034748073	1.679506		Putative aldo,keto reductase	Unknown	COG0656	R
YPO0294	0.004118319	0.026694697	1.673136	*terZ*	Tellurium resistance protein	Drug/analogue sensitivity	COG2310	T
YPO0463	0.004853264	0.027776406	1.667624	*talB*	Transaldolase B	Pentose phosphate pathway	COG0176	G
YPO2367	0.015557898	0.034956394	1.662795	*gst*	Glutathione S-transferase	Thioredoxin Biosynthesis	COG0625	O
YPO2778	0.037228447	0.045242152	1.65566		Conserved hypothetical protein	Unknown	COG1090	R
dctA	0.034123836	0.044466581	1.65384	*dctA*	C4-dicarboxylate transport protein	Transport/binding Carbohydrates,organic acids and alcohols		
YPO2597	0.015041211	0.034956394	1.653675	*tatE*	Sec-independent protein translocase protein	Transport/binding proteins	COG1826	U
YPO2929	0.004041925	0.02644726	1.653179	*acpS, d*	Holo-[acyl-carrier protein] synthase	Fatty acid biosynthesis	COG0736	I
YPO2234	0.011267721	0.0334077	1.645098	*cstA*	Putative carbon starvation protein A	Adaptions and atypical conditions	COG1966	T
YPO2073	0.00149697	0.019849387	1.642797		Putative lipoprotein	Membranes, lipoproteins and porins	COG3065	M
YPO2806	0.013720521	0.034748073	1.632153		Putative aldo,keto reductase	Unknown	COG0667	C
YPO3128	0.035207117	0.044591162	1.629381		Conserved hypothetical protein	Unknown		
YPO0917	0.016630562	0.035480778	1.622876	*yggE*	Putative exported protein	Membranes, lipoproteins and porins	COG2968	S
YPO2364	0.015559284	0.034956394	1.621092		Insertion sequence IS1, ATP-binding protein		COG1484	L
YPO3690	0.002341355	0.021602417	1.620768		Putative ribonuclease inhibitor	Unknown	COG2732	K
YPCD1.02	0.017992273	0.036375515	1.61931				COG1484	L
YPMT1.6	0.022422884	0.038972215	1.616559	*parA*			COG1192	D
YPO2325	0.002752214	0.022752142	1.61559	*dalD*	Putative mannitol dehydrogenase	Degradation of carbon compounds	COG0246	G
YPO0372	0.032716898	0.043409665	1.601915	*miaA, t*	tRNA delta(2)-isopentenylpyrophosphate transferase	Aminoacyl tRNA synthetases and their modification	COG0324	J
YPO2502	0.036003881	0.044927135	1.600474	*gutB*	Putative zinc-binding dehydrogenase	Unknown	COG1063	ER
YPO0563	0.00286935	0.022898051	1.595201		Putative exported protein	Membranes, lipoproteins and porins		
YPO1573	0.00221568	0.021479969	1.587404		Putative polysaccharide deacetylase	Unknown	COG0726	G
YPO2362	0.022217513	0.038728348	1.585025		Putative membrane protein	Membranes, lipoproteins and porins		
YPO0089	0.001611379	0.02045638	1.581383	*glpX*	GlpX protein (pseudogene)	Central intermediary metabolism		
YPO0700	0.04635886	0.048690731	1.572552		Fimbrial protein	Surface structures	COG3539	NU
terA	0.023803894	0.039017462	1.570981	*terA*	Putative tellurite resistance protein	Drug/analogue sensitivity		
YPO1149	0.002149533	0.021479969	1.565022		Conserved hypothetical protein	Unknown	COG2706	G
YPO3787	0.011317509	0.033480584	1.565022		Putative carboxymethylenebutenolidase	Degradation of small molecule	COG0412	Q
YPO3912	0.000913238	0.019104257	1.561739	*yijD*	Putative membrane protein	Membranes, lipoproteins and porins	COG0477	GEPR
YPO0157	0.021479683	0.038632787	1.561739	*trpS*	Tryptophanyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification	COG0180	J
YPO2745	0.000899758	0.019104257	1.560802		Conserved hypothetical protein	Unknown	COG3691	S
YPO3454	0.042313792	0.047230602	1.559398	*nrdD*	Anaerobic ribonucleoside-triphosphate reductase	2 -deoxyribonucleotide biosynthesis	COG1328	F
YPO1118	0.013428991	0.034748073	1.556438	*cydB*	Cytochrome D ubiquinol oxidase subunit II	Electron transport	COG1294	C
YPO2930	0.009855552	0.032793063	1.552862	*pdxJ*	Pyridoxal phosphate biosynthetic protein PdxJ	Pyridoxine Biosynthesis	COG0854	H
YPO1501	0.002231641	0.021479969	1.552086		Putative esterase	Unknown	COG0627	R
YPO2299	0.049840199	0.049925767	1.551	*ogt*	Putative methylated-DNA--protein-cysteine methyltransf	DNA replication, restriction/modification, recombination and	COG0350	L
YPO2746	0.037423967	0.045350365	1.550225		Putative 3-ketoacyl-CoA thiolase	Degradation of small molecule	COG0183	I
YPO0158	0.034912718	0.044591162	1.549295	*cysG*	Siroheme synthase	Heme and porphyrin Biosynthesis	COG0007	H
YPO0752	0.037913317	0.045350365	1.548056	*pcpY, p*	Putative lipoprotein (pseudogene)	Membranes, lipoproteins and porins		
YPO0114	0.008955234	0.032589115	1.547592	*metJ*	Ranscriptional repressor protein	Broad regulatory functions	COG3060	KE
YPO2158	0.025194692	0.039190458	1.545118		Conserved hypothetical protein	Unknown	COG0229	O

ompW	0.04515344	0.048328972	1.540643	2.47	*ompW*	Putative exported protein	Membranes, lipoproteins and porins		
YPO0838	0.037046971	0.045242152	1.53818			Putative acetylglucosamine-6-phosphate deacetylase	Degradation of carbon compounds	COG1820	G
YPO1551	0.001985576	0.021336704	1.536028			Putative exported protein	Membranes, lipoproteins and porins	COG0451	MG
YPO1117	0.001495685	0.019849387	1.53526		*cydA*	Cytochrome D ubiquinol oxidase subunit I	Electron transport	COG1271	C
YPO3254	0.029652641	0.041613421	1.534493			Putative amino acid ABC transporter, ATP-binding protei	Transport/binding Amino acids and amines	COG1126	E
YPO1650	0.002408785	0.021618465	1.532959			Hypothetical protein	Unknown		
YPO1968	0.012202984	0.034340969	1.532806			Transposase for insertion sequence IS1		COG1425	L
YPO0841	0.008783857	0.032476773	1.530815			Putative regulatory protein	Broad regulatory functions	COG0641	R
YPO3528	0.048468966	0.048995578	1.530355			Putative exported protein	Membranes, lipoproteins and porins	COG3054	R
YPO3888	0.007180108	0.031529203	1.524856		*ilvC*	Ketol-acid reductoisomerase	Pyruvate family biosynthesis	COG0059	EH
YPO0589	0.01564546	0.034956394	1.521657		*fadH, fa*	2,4-dienoyl-CoA reductase	Degradation of small molecule	COG1902	C
YPO0590	0.005855431	0.030095594	1.519984		*hdeD*	Putative membrane protein	Membranes, lipoproteins and porins	COG3247	S
YPO3639	0.02467008	0.039115715	1.517251		*yghU*	Putative glutathione S-transferase	Unknown	COG0625	O
YPO0560	0.00330431	0.02457963	1.515734		*ftsZ, sfi*	Cell division protein FtsZ	Cell division	COG0206	D
YPO1511	0.00015233	0.0134891	1.514674		*sfcA, m*	NAD-dependent malic enzyme	Gluconeogenesis	COG0281	C
YPO1566	0.029858057	0.041791102	1.510892			Putative hydrolase	Degradation of small molecule	COG0179	Q
YPO1641	0.009010891	0.032612957	1.505011		*icdA, ic*	Isocitrate dehydrogenase [NADP]	Tricarboxylic acid cycle	COG0538	C
YPO2363	0.002510222	0.022045547	1.504409			Conserved hypothetical protein	Unknown		
YPO0295	0.008385312	0.032332443	1.504108		*terA*	Putative tellurite resistance protein	Drug/analogue sensitivity	COG2310	T
YPO1127	0.010480782	0.033134827	-1.50005		*nadA, n*	Quinolinate synthetase A	Pyridine nucleotide Biosynthesis	COG0379	H
hslR	0.040430826	0.046843737	-1.5011		*hslR*	Heat shock protein 15	Adaptions and atypical conditions		
YPO3394	0.046012601	0.048690731	-1.50125		*hrpB*	ATP-dependent helicase	DNA replication, restriction/modification, recombination and r	COG1643	L
YPO3811	0.044869178	0.048168098	-1.50908		*rpoH, h*	RNA polymerase sigma-32 factor	RNA synthesis, RNA modification and DNA transcription	COG0568	K
YPO2443	0.030995783	0.042303438	-1.50923			Putative membrane protein	Membranes, lipoproteins and porins		
YPO1309	0.035822853	0.044839876	-1.50999		*lysP, ca*	Putative lysine-specific permease	Transport/binding Amino acids and amines	COG0833	E
YPO2731	0.025387935	0.039349123	-1.51089			Putative membrane protein	Membranes, lipoproteins and porins	COG1512	R
YPO4119	0.003891333	0.026026647	-1.5118		*glmU*	UDP-N-acetylglucosamine pyrophosphorylase	Sugar nucleotides metabolism	COG1207	M
YPO0862	0.003310716	0.02457963	-1.51483			Putative exported protein	Membranes, lipoproteins and porins		
YPO3137	0.021626306	0.038632787	-1.51725			Conserved hypothetical protein	Unknown		
YPO2449	6.52528E-05	0.009786994	-1.51801			Putative LuxR-family regulatory protein	Broad regulatory functions	COG2197	TK
YPO1049	0.024625869	0.039115715	-1.51922		*uppS, rt*	Undecaprenyl pyrophosphate synthetase	Sugar nucleotides metabolism	COG0020	I
YPO3768	0.020636504	0.03822026	-1.51938		*fadI, fre*	NAD(P)H-flavin reductase	Electron transport	COG0543	HC
YPO3976	0.041235119	0.046904392	-1.52029			Conserved hypothetical protein	Unknown	COG2961	R
YPO3428	0.010710412	0.033239226	-1.52151		*guaC*	GMP reductase	Purine ribonucleotide biosynthesis	COG0516	F
YPO0037	0.042709327	0.047359741	-1.52303		*trmH, s*	tRNA (guanosine-2'-O-)-methyltransferase	Aminoacyl tRNA synthetases and their modification	COG0566	J
YPO1326	0.016566586	0.035480778	-1.52318			TrkA, Potassium channel-family protein	Transport/binding Cations	COG2985	R
YPO3722	0.009205987	0.032645574	-1.52531		*metH*	5-Methyltetrahydrofolate--homocysteine methyltransferas	Aspartate family biosynthesis	COG1410	E
YPO2218	0.007926862	0.032332443	-1.52547		*topA, su*	DNA topoisomerase I	DNA replication, restriction/modification, recombination and r	COG0550	L
YPO3439	0.011568752	0.033624732	-1.52623			Putative membrane protein	Membranes, lipoproteins and porins	COG0795	R
YPO3376	0.04144326	0.046969377	-1.52684		*eno*	Enolase	Glycolysis	COG0148	G
YPO3052	0.032753053	0.043409665	-1.52898			Conserved hypothetical protein	Unknown	COG1393	P
YPMT1.6	0.022571571	0.039017462	-1.53005					COG3668	R
YPO1158	0.036942661	0.045238369	-1.53158			Conserved hypothetical protein	Unknown	COG0391	S
YPO3377	0.039512558	0.046404601	-1.53158		*pyrG*	CTP synthase	Salvage of nucleosides and nucleotides	COG0504	F
YPO0120	0.016763045	0.035522094	-1.53173		*glpR*	Glycerol-3-phosphate repressor protein	Broad regulatory functions	COG1349	KG
YPO0282	0.008499656	0.032332443	-1.53265		*hmuS*	Hemin transport protein	Transport/binding proteins		
YPO4127	0.032828107	0.04343108	-1.53465		*atpB, u*	ATP synthase subunit B protein	ATP-proton motive force	COG0356	C
YPO1212	0.009232165	0.032645574	-1.5348			Putative iron-sulphur binding protein	Unknown	COG0633	C
YPO2398	0.034845935	0.044591162	-1.53726			Putative exported protein (pseudogene)	Membranes, lipoproteins and porins		
YPPCP1.0	3.58257E-05	0.007931073	-1.5388					COG1396	K
YPO4107	0.038069892	0.045350365	-1.54034		*yieG*	Xanthine,uracil permeases family protein	Transport/binding Carbohydrates,organic acids and alcohols	COG2252	R

YPO1203	0.011910611	0.034071988	-1.54218		Putative membrane protein	Membranes, lipoproteins and porins	COG0697	GER
YPO3829	0.009254626	0.032645574	-1.54589		Putative haloacid dehalogenase-like hydrolase	Unknown	COG0561	R
YPO2075	0.001431357	0.019849387	-1.54868	*rnd*	Ribonuclease D	Degradation of RNA	COG0349	J
YPO0943	0.028286419	0.040733399	-1.5493	*yggT*	Putative membrane protein	Membranes, lipoproteins and porins	COG0762	S
YPO4086	0.020937675	0.038542477	-1.55302		Putative lipoprotein	Membranes, lipoproteins and porins		
YPO2370	0.014570688	0.034956394	-1.55582	*pdxH*	Pyridoxamine 5'-phosphate oxidase	Pyridoxine Biosynthesis	COG0259	H
YPO3154	0.014847729	0.034956394	-1.55613	*hupB, h*	DNA-binding protein HU-beta	Adaptions and atypical conditions	COG0776	L
YPO1030	0.02455124	0.039115715	-1.55659		Conserved hypothetical protein	Unknown	COG2363	S
YPO0671	0.033199305	0.043747874	-1.55722	*parC*	DNA topoisomerase IV subunit A	DNA replication, restriction/modification, recombination and r	COG0188	L
YPO4022	0.027232649	0.040285015	-1.55737	*fitA*	Putative iron transport protein	Transport/binding Cations	COG0614	P
YPO0660	0.026402929	0.039943498	-1.55877		Conserved hypothetical protein	Unknown	COG0754	E
yscS	0.012882006	0.034490359	-1.5594	*yscS*				
YPO4115	0.00929022	0.032645574	-1.56065	*pstA, ph*	Putative phosphate transport system permease	Transport/binding proteins	COG0581	P
YPO3302	0.022660437	0.039017462	-1.5619	*yqaA*	Putative membrane protein	Membranes, lipoproteins and porins	COG1238	S
YPO2056	0.021771298	0.038637961	-1.56393	*ruvC*	Crossover junction endodeoxyribonuclease	DNA replication, restriction/modification, recombination and r	COG0817	L
YPO3612	0.02434086	0.039115715	-1.56565		Putative transcriptional regulatory protein	Broad regulatory functions	COG1396	K
YPO3834	0.008626988	0.032332443	-1.56596	*pldA*	Phospholipase A	Pathogenicity	COG2829	M
YPO3432	0.011134501	0.033373987	-1.56643		Conserved hypothetical protein	Unknown	COG3024	S
YPO0236	0.047725346	0.048838565	-1.56721	*zntR*	MerR-family transcriptional regulator	Broad regulatory functions	COG0789	K
YPO0312	0.043649627	0.047790066	-1.56737	*plsB, b4*	Glycerol-3-phosphate acyltransferase	Synthesis and modification of Phospholipids	COG2937	I
YPO1208	0.009761539	0.03271037	-1.56753		Putative exported protein	Membranes, lipoproteins and porins		
YPO0112	0.007339603	0.031553633	-1.56784		Conserved hypothetical protein	Unknown		
YPO2558	0.010356912	0.033069335	-1.56878	*aat*	Probable aminotransferase	Unknown	COG0436	E
YPO3400	0.034868773	0.044591162	-1.57177	*folK*	2-amino-4-hydroxy-6-hydroxymethyldihydropteridi ne py	Folic acid Biosynthesis	COG0801	H
YPO3094	0.032529553	0.043338256	-1.57413	*rosB, yb*	Putative potassium antiporter	Transport/binding Cations	COG0475	P
YPO2244	0.006310573	0.030434909	-1.57665		Putative iron-sulfur binding NADH dehydrogenase	Unknown	COG1726	C
YPO0445	0.006254808	0.030374593	-1.57886		Conserved hypothetical protein	Unknown	COG3177	S
YPO0177	0.013175797	0.034490359	-1.57933		Putative membrane protein	Membranes, lipoproteins and porins	COG0477	GEPR
YPO1855	0.013980796	0.034834517	-1.58075		Putative exported protein	Membranes, lipoproteins and porins	COG2822	P
YPO1218	0.008192484	0.032332443	-1.58265	*rcsB*	Probable two component response regulator component B	Broad regulatory functions	COG2197	TK
YPO2387	0.001394392	0.019849387	-1.59345	*purR*	Purine nucleotide synthesis repressor	Broad regulatory functions	COG1609	K
yscG	0.006588565	0.030706792	-1.59728	*yscG*				
YPO2448	0.028717961	0.040972496	-1.59776	*solA, so*	Putative sarcosine oxidase	Unknown	COG0665	E
YPO2753	0.042928657	0.047359741	-1.59839	*yfcA*	Putative membrane protein	Membranes, lipoproteins and porins	COG0730	R
YPO4124	0.035766838	0.044819105	-1.59903	*atpH, u*	ATP synthase delta subunit protein	ATP-proton motive force	COG0712	C
sufI	0.020680662	0.03822026	-1.60095	*sufI*	Putative cell division protein	Cell division		
YPO3057	0.005414168	0.029716995	-1.60192	*yeaL*	Putative membrane protein	Membranes, lipoproteins and porins	COG2707	S
YPO1023	0.024913408	0.039115715	-1.60256		N-acetylmuramoyl-L-alanine amidase AmiC precursor	Murein sacculus and peptidoglycan	COG0860	M
YPO1735	0.014285636	0.03488102	-1.60304		Putative ABC transporter (ATP-binding protein)	Transport/binding proteins	COG1132	V
YPO2607	0.047031026	0.048690731	-1.60304	*nadD*	Putative nicotinate-nucleotide adenylyltransferase	Unknown	COG1057	H
pheS	0.004699878	0.027745502	-1.6032	*pheS*	Phenylalanyl-tRNA synthetase alpha chain	Aminoacyl tRNA synthetases and their modification		
YPO1753	0.034249175	0.044527354	-1.60384	*fcuA*	Ferrichrome receptor protein	Cell envelop	COG1629	P
YPO2061	0.044451212	0.048011847	-1.6085	*znuA*	Exported high-affinity zinc uptake system protein	Transport/binding Cations	COG0803	P
YPO1702	0.033438363	0.043888728	-1.60914	*yebS*	Putative membrane protein	Membranes, lipoproteins and porins	COG2995	S
YPO2430	0.036522218	0.045055609	-1.60914	*rplT, pd*	5S ribosomal protein L2	Ribosomal protein synthesis and modification	COG0292	J
YPO3077	0.02102218	0.038543268	-1.61011	*purK*	Phosphoribosylaminoimidazole carboxylase ATPase subu	Purine ribonucleotide biosynthesis	COG0026	F
YPO0306	0.037795162	0.045350365	-1.61123		Hypothetical protein	Unknown		
YPO1404	0.037893745	0.045350365	-1.61188	*mukE, k*	Conserved hypothetical protein	Unknown	COG3095	D
YPO0651	0.001982245	0.021336704	-1.61704		Putative exported protein	Membranes, lipoproteins and porins	COG3103	T
YPO1688	0.012324542	0.034349747	-1.61704		Hypothetical protein	Unknown		
yscM	0.001305458	0.019849387	-1.61753	*yscM, lcrQ*				

YPO2878	0.04766345	0.048838565	-1.61753	*hisS*	Histidyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification	COG0124	J
YPO0881	0.018374605	0.036508093	-1.62174		Conserved hypothetical protein	Unknown	COG2944	K
YPO3390	0.04610718	0.048690731	-1.62596	*fhuB*	Ferrichrome transport system permease protein FhuB	Transport/binding Cations	COG0609	P
YPO3754	0.04458166	0.04802658	-1.62629	*tufA, tu*	Elongation factor Tu	Protein translation and modification	COG0050	J
YPO3513	0.003106483	0.023851261	-1.62743	*ispB, ce*	Octaprenyl-diphosphate synthase	Menaquinone and ubiquinine Biosynthesis	COG0142	H
YPO1405	0.02519988	0.039190458	-1.62938	*mukB*	Cell division protein	Cell division	COG3096	D
YPO3372	0.026208527	0.039943498	-1.62954	*cysJ*	Sulfite reductase [NADPH] flavoprotein alpha-componen	Sulphur metabolism	COG0369	P
YPO2174	0.041397569	0.046968538	-1.63068	*pmrE*	Putative nucleotide sugar dehydrogenase	Sugar nucleotides metabolism	COG1004	M
YPO2400	0.018593959	0.036508093	-1.63215	*sufS*	Putative selenocysteine lyase	Central intermediary metabolism	COG0520	E
YPO1068	0.018359817	0.036508093	-1.63248	*proS, dr*	Prolyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification	COG0442	J
YPO2047	0.000467258	0.01718606	-1.63362		Conserved hypothetical protein	Unknown	COG3102	S
YPO3779	0.036155298	0.044966511	-1.63542	*aarF*	Ubiquinone biosynthesis protein	Menaquinone and ubiquinine Biosynthesis	COG0661	R
YPO2780	0.009220768	0.032645574	-1.63575		Conserved hypothetical protein	Unknown	COG0622	R
YPO1525	0.016913649	0.035522094	-1.63575	*dcd, du*	Deoxycytidine triphosphate deaminase	2 -deoxyribonucleotide biosynthesis	COG0717	F
YPO1037	0.041004295	0.046904392	-1.63837		Conserved hypothetical protein	Unknown	COG3098	S
YPO1025	0.007638172	0.03220827	-1.63984		Membrane-bound lytic murein transglycosylase A precurs	Murein sacculus and peptidoglycan	COG2821	M
YPO2708	0.030591685	0.042151677	-1.64165	*srmB, r*	ATP-dependent RNA helicase	RNA synthesis, RNA modification and DNA transcription	COG0513	LKJ
YPO4130	0.033281496	0.043812715	-1.6474	*gidA*	Glucose inhibited division protein A	Cell division	COG0445	D
YPO3393	0.025801732	0.039776249	-1.64856	*mrcB, p*	Penicillin-binding protein 1B	Murein sacculus and peptidoglycan	COG0744	M
YPO4113	0.008844602	0.032476773	-1.64905	*phoU, n*	Putative phosphate transport system protein	Central intermediary metabolism	COG0704	P
YPO3397	0.006784286	0.031073821	-1.64955	*dksA*	DnaK suppressor protein homologue	Broad regulatory functions	COG1734	T
YPO3448	0.017159173	0.035559502	-1.65235		Putative extracellular solute-binding protein (pseudogene)	Transport/binding proteins		
yscH	0.000708948	0.017718588	-1.65334	*yscH, yopR, lcrP*				
YPO2315	0.002330805	0.021602417	-1.65533		Putative exported protein	Membranes, lipoproteins and porins	COG2353	S
YPO1260	0.015078865	0.034956394	-1.65533		Putative membrane protein	Membranes, lipoproteins and porins	COG3083	R
YPO2369	0.011778525	0.033997735	-1.65616	*tyrS*	Tyrosyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification	COG0162	J
YPO1444	0.034562482	0.044541346	-1.65881		Conserved hypothetical protein	Unknown		
YPO0240	0.043898345	0.047957484	-1.65881		Conserved hypothetical protein	Unknown	COG0144	J
YPO1755	0.027991414	0.040733399	-1.65964	*yobD*	Putative membrane protein	Membranes, lipoproteins and porins		
YPO4025	0.019432208	0.037273669	-1.66263	*fitD*	Putative iron ABC transporter, ATP-binding protein	Transport/binding Cations	COG1120	PH
YPO3170	0.019061157	0.036907416	-1.6628		Conserved hypothetical protein	Unknown	COG1666	S
YPO1773	0.041135628	0.046904392	-1.66779	*pabB*	Para-aminobenzoate synthase component I	Folic acid Biosynthesis	COG0147	EH
YPO1351	0.011000943	0.03336898	-1.66796	*artI*	Arginine-binding periplasmic protein 1 precursor	Transport/binding Amino acids and amines	COG0834	ET
YPO2335	0.01402257	0.034834517	-1.66796		Conserved hypothetical protein	Unknown	COG0037	D
YPO4128	0.041999582	0.047157278	-1.66812	*atpI, un*	ATP synthase protein I	ATP-proton motive force	COG3312	C
YPO1594	0.037228106	0.045242152	-1.66863		Conserved hypothetical protein	Unknown	COG1399	R
YPO1505	0.006771853	0.031073821	-1.66879	*folE*	GTP cyclohydrolase I	Folic acid Biosynthesis	COG0302	H
YPO2235	0.044774058	0.048155733	-1.67096	*rnb*	Exoribonuclease II	Degradation of RNA	COG0557	K
YPO2704	0.010134288	0.03304557	-1.67464	*ung*	Putative uracil-DNA glycosylase	DNA replication, restriction/modification, recombination and r	COG0692	L
YPO4048	0.048176835	0.04891816	-1.6785	*mdfA, c*	Multidrug translocase	Drug/analogue sensitivity	COG0477	GEPR
YPO4125	0.015642036	0.034956394	-1.68759	*atpF, un*	ATP synthase subunit B protein	ATP-proton motive force	COG0711	C
YPO3866	0.012440496	0.034349747	-1.69503	*rfe, b37*	Putative undecaprenyl-phosphate alpha-N-acetylglucosam	Surface polysaccharides, lipopolysaccharides and antigens	COG0472	M
YPO0950	0.02364663	0.039017462	-1.69503		Conserved hypothetical protein	Unknown	COG3171	S
YPO3505	0.010302516	0.03304557	-1.69706	*greA*	Transcription elongation factor	RNA synthesis, RNA modification and DNA transcription	COG0782	K
YPO3321	0.000312735	0.016712285	-1.69757	*cybB*	Probable cytochrome B561	Electron transport	COG3038	C
YPO2245	0.015584443	0.034956394	-1.69757		Putative iron-sulfur protein	Unknown	COG2878	C
YPO3010	0.015145456	0.034956394	-1.70199		Hypothetical protein	Unknown		
YPO0309	0.012653882	0.034426687	-1.71189		Putative exported protein	Membranes, lipoproteins and porins	COG3468	MU
YPO2403	0.005042714	0.028262688	-1.71927	*sufB*	Conserved hypothetical protein	Unknown	COG0719	O
yscL	0.002947855	0.022898051	-1.72013	*yscL*				
YPO3769	0.018518715	0.036508093	-1.72168		Conserved hypothetical protein	Unknown	COG0043	H

YPO0239	0.005879066	0.030095594	-1.72444	*trkA*	Trk system potassium uptake protein	Transport/binding proteins	COG0569	P
ipk	0.003826612	0.026026647	-1.72547	*ipk*	Putative 4-diphosphocytidyl-2-C-methyl-D-erythritol kina	Menaquinone and ubiquinine Biosynthesis		
YPO0338	0.027616123	0.040505664	-1.72668		Hypothetical protein	Unknown		
YPO2404	0.001484006	0.019849387	-1.72806	*sufA*	Conserved hypothetical protein	Unknown	COG0316	S
YPO1031	0.006425958	0.030434909	-1.72962		Conserved hypothetical protein	Unknown	COG2933	R
YPO3079	0.01990415	0.037684198	-1.73204	*ybbA*	Putative ABC transporter ATP-binding protein	AI-2	COG1136	V
YPO2368	0.017850569	0.036199225	-1.73429	*pdxY*	Pyridoxamine kinase	Central intermediary metabolism	COG2240	H
YPO2993	0.000545663	0.01725695	-1.7362	*ptsH, hp*	PTS system, phosphocarrier protein	Transport/binding Carbohydrates,organic acids and alcohols	COG1925	G
YPO1098	0.008630675	0.032332443	-1.73794		Putative prophage integrase		COG0582	L
intA	0.009715433	0.032670333	-1.73846	*intA*	Phage integrase (partial)			
YPO3443	0.004140032	0.026694697	-1.74124	*valS*	Valyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification	COG0525	J
YPO0672	0.01890982	0.036721447	-1.74351	*plsC, pa*	Putative acyltransferase	Unknown	COG0204	I
YPO1597	0.047994936	0.048914567	-1.74386	*fabH*	3-oxoacyl-[acyl-carrier-protein] synthase III	Fatty acid biosynthesis	COG0332	I
YPO1420	0.031236949	0.042327267	-1.75155	*pqiA*	Putative paraquat-inducible protein A	Membranes, lipoproteins and porins	COG2995	S
ptsI	0.007552935	0.032015477	-1.75242	*ptsI*	PTS sytem, enzyme I component	Transport/binding Carbohydrates,organic acids and alcohols		
YPO1086a	0.007314177	0.031553633	-1.75313		Phage integrase (partial)		COG0582	L
YPO2273	0.01541687	0.034956394	-1.75523		Phage hypothetical protein	Unknown	COG2932	K
yscI	0.000708852	0.017718588	-1.75558	*yscI, lcrO*				
YPO3410	0.024639469	0.039115715	-1.75558	*yacC*	Putative exported protein	Membranes, lipoproteins and porins		
YPO3206	0.044653338	0.048064815	-1.75804	*sbcD*	Exonuclease SbcD	Degradation of DNA	COG0420	L
YPO3013	0.016574259	0.035480778	-1.75874	*cysW*	Sulfate transport system permease protein CysW	Transport/binding Anions	COG0555	O
YPO3118	0.005613108	0.029919034	-1.76191	*adk, pls*	Adenylate kinase	Purine ribonucleotide biosynthesis	COG0563	F
YPO1636	0.048382957	0.048983191	-1.76191	*purB*	Adenylosuccinate lyase	Purine ribonucleotide biosynthesis	COG0015	F
YPO2755	0.008223997	0.032332443	-1.76456		Conserved hypothetical protein	Unknown		
YPO0165	0.021539123	0.038632787	-1.77252		LacI-family transcriptional regulator	Broad regulatory functions	COG1609	K
YPO0944	0.044084683	0.048011847	-1.77731		Conserved hypothetical protein	Unknown	COG1872	S
YPO0280	0.00788662	0.032332443	-1.78229	*hmuU*	Hemin transport system permease protein HmuU	Transport/binding proteins	COG0609	P
YPO4064	0.005728151	0.029973848	-1.78407		Hypothetical protein	Unknown		
YPO3120	0.001994208	0.021336704	-1.79123	*recR*	Recombination protein RecR	DNA replication, restriction/modification, recombination and r	COG0353	L
YPO1854	0.001205195	0.019298639	-1.7932		Putative membrane protein	Membranes, lipoproteins and porins	COG0672	P
YPO3320	0.000344471	0.016712285	-1.80273	*cybC*	Putative cytochrome B562	Electron transport		
YPO0952	0.019614971	0.037434059	-1.80399	*mutY, m*	A,G-specific adenine glycosylase	DNA replication, restriction/modification, recombination and r	COG1194	L
YPO3360	0.011482174	0.03357332	-1.80543	*ispF, me*	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	Central intermediary metabolism	COG0245	I
YPO3364	0.000276943	0.016712285	-1.80868	*cysC*	Adenylylsulfate kinase	Sulphur metabolism	COG0529	P
YPO1522	0.030855576	0.04228564	-1.81013	*metG*	Methionyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification	COG0143	J
YPO4093	0.030229015	0.041957104	-1.81321		Putative haloacid dehalogenase-like hydrolase	Unknown	COG0561	R
YPO2402	0.014699348	0.034956394	-1.81503	*sufC*	Putative ATP-dependent transporter	Transport/binding proteins	COG0396	O
YPO1628	0.044894345	0.048168098	-1.81993	*lolE*	Lipoprotein releasing system, transmembrane protein	Membranes, lipoproteins and porins	COG0577	V
YPO1575	0.021641702	0.038632787	-1.82412		225 conserved hypothetical protein	Unknown	COG3122	S
msbA	0.032390125	0.043282739	-1.8254	*msbA*	Probable transport ATP-binding protein	Transport/binding proteins		
YPO1524	0.031436808	0.042392665	-1.83345	*udk, b2*	Uridine kinase	Miscellaneous nucleoside/nucleotide reactions	COG0572	F
YPO2429	0.012360623	0.034349747	-1.83584	*pheS*	Phenylalanyl-tRNA synthetase alpha chain	Aminoacyl tRNA synthetases and their modification	COG0016	J
YPO3911	0.008830168	0.032476773	-1.83933	*trmA*	tRNA (uracil-5)-methyltransferase	Aminoacyl tRNA synthetases and their modification	COG2265	J
YPO3391	0.04809422	0.048914567	-1.84154	*fhuD*	Ferrichrome-binding periplasmic protein precursor	Transport/binding Cations	COG0614	P
yopM	0.040325904	0.046843737	-1.84264	*yopM*	Probable targeted effector protein	YOP		
caf1A	0.000495847	0.01725695	-1.84744	*caf1A*	Putative F1 capsule anchoring protein, caf1A			
YPO4084	0.010190711	0.03304557	-1.84966	*ibpB, hs*	Heat shock protein	Adaptions and atypical conditions	COG0071	O
YPO3570	0.024622294	0.039115715	-1.85466		BolA-like protein	Unknown	COG0271	T
YPO3123	0.00686101	0.031317247	-1.86209	*apt*	Adenine phosphoribosyltransferase	Salvage of nucleosides and nucleotides	COG0503	F
YPO2994	0.015432568	0.034956394	-1.86433	*ptsI*	PTS sytem, enzyme I component	Transport/binding Carbohydrates,organic acids and alcohols	COG1080	G
YPO1856	0.000683077	0.017718588	-1.86713		Conserved hypothetical protein	Unknown	COG2837	P

YPO3026	0.030287092	0.041957104	-1.86881	*yfeY*	Putative lipoprotein	Membranes, lipoproteins and porins		
YPO0954	0.013754732	0.034748073	-1.87142	*mltC*	Membrane-bound lytic murein transglycosylase C	Murein sacculus and peptidoglycan	COG0741	M
YPO3153	0.009234023	0.032645574	-1.87611	*ppiD*	Peptidyl-prolyl cis-trans isomerase D	Protein translation and modification	COG0760	O
YPO0644	0.046380077	0.048690731	-1.88401	*dnaG, d*	DNA primase	DNA replication, restriction/modification, recombination and r	COG0358	L
YPO2559	0.002406245	0.021618465	-1.89118		Conserved hypothetical protein	Unknown	COG1896	R
nusG	0.012491547	0.034349747	-1.89534	*nusG*	Transcription antitermination protein	RNA synthesis, RNA modification and DNA transcription		
YPO1284	0.009054919	0.032645574	-1.89629		Putative elongation factor P	Protein translation and modification	COG0231	J
metG	0.016412748	0.035390695	-1.90104	*metG*	Methionyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification		
YPO1531	0.021443827	0.038632787	-1.90465	*alcB*	Putative siderophore biosynthetic enzyme	Iron uptake	COG1670	J
YPO4085	0.029682623	0.041613421	-1.90465	*ibpA, hs*	Heat shock protein	Adaptions and atypical conditions	COG0071	O
YPO2908	0.04177422	0.047103324	-1.90503	*hmp, hn*	Flavohemoprotein	Aerobic respiration	COG1018	C
YPO1350	0.043026873	0.047428702	-1.90599	*artQ*	Arginine transport system permease protein	Transport/binding Amino acids and amines	COG0765	E
YPO2565	0.046299294	0.048690731	-1.91152		Hypothetical protein	Unknown		
YPO1107	0.003519477	0.025248501	-1.91229	*grpE*	Heat shock protein GrpE	Adaptions and atypical conditions	COG0576	O
YPO3138	0.001714867	0.020788226	-1.91612	*ymoA*	Modulating protein YmoA (histone-like protein)	Broad regulatory functions	COG0326	O
YPO2246	0.034477864	0.044527354	-1.91861		Putative membrane protein	Membranes, lipoproteins and porins	COG2209	C
YPO2399	0.023958377	0.039017462	-1.92283	*sufE*	Conserved hypothetical protein	Unknown	COG2166	R
YPO3760	0.013572046	0.034748073	-1.92553	*murB*	UDP-N-acetylenolpyruvoylglucosamine reductase	Murein sacculus and peptidoglycan	COG0812	M
YPO2991	0.000919192	0.019104257	-1.92572	*cysZ*	Putative membrane protein	Membranes, lipoproteins and porins	COG2981	E
yscJ	0.000137016	0.012999653	-1.9346	*yscJ, ylpB*				
YPO1627	0.010553374	0.033139004	-1.93944	*lolD*	Lipoprotein releasing system, ATP-binding protein	Membranes, lipoproteins and porins	COG1136	V
YPO2659	0.010429114	0.033134827	-1.93964	*cspB*	Cold shock protein	Adaptions and atypical conditions	COG1278	K
YPO1431	0.010039596	0.03304557	-1.94897		Putative Lon protease	Unknown	COG1067	O
YPO0050	0.046901647	0.048690731	-1.95033	*rpmB*	5S ribosomal protein L28	Ribosomal protein synthesis and modification	COG0227	J
YPO2401	0.006571501	0.030706792	-1.95228	*sufD*	Conserved hypothetical protein	Unknown	COG0719	O
YPO3386	0.017407561	0.035748992	-1.95874	*yadS*	Putative membrane protein	Membranes, lipoproteins and porins	COG2860	S
YPO3569	0.015127421	0.034956394	-1.95932	*murA, n*	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	Murein sacculus and peptidoglycan	COG0766	M
YPO1418	0.041523086	0.046997203	-1.96089		Conserved hypothetical protein	Unknown	COG0116	L
YPO0643	0.014096462	0.034834517	-1.96129	*rpoD, a*	RNA polymerase sigma factor RpoD	RNA synthesis, RNA modification and DNA transcription	COG0568	K
YPO2635	0.008106512	0.032332443	-1.96187	*fldA*	Flavodoxin 1	Electron transport	COG0716	C
YPO1385	0.024028343	0.039017462	-1.96227		Conserved hypothetical protein	Unknown	COG1944	S
YPO1262	0.042123375	0.047216448	-1.96384		Putative nucleoid-associated protein	Unknown	COG3081	R
YPO0042	0.01598209	0.035233071	-1.9658		Putative membrane protein	Membranes, lipoproteins and porins	COG2860	S
YPO0442	0.016450202	0.035413965	-1.97348	*serB, b4*	Phosphoserine phosphatase	Serine family biosynthesis	COG0560	E
YPO3753	0.022175262	0.038728348	-1.97724	*secE, pr*	Preprotein translocase SecE subunit	Transport/binding proteins	COG0690	U
YPO2428	0.024520069	0.039115715	-1.9802	*pheT*	Phenylalanyl-tRNA synthetase beta chain	Aminoacyl tRNA synthetases and their modification	COG0072	J
YPO1595	0.021787506	0.038637961	-1.98179	*rpmF*	Ribosomal protein L32	Ribosomal protein synthesis and modification	COG0333	J
YPO1601	0.025534247	0.039437839	-1.98377	*fabF, fa*	3-oxoacyl-[acyl-carrier-protein] synthase II	Fatty acid biosynthesis	COG0304	IQ
YPO3189	0.028462808	0.04087187	-1.99372	*secD*	Protein-export membrane protein SecD	Transport/binding proteins	COG0342	U
YPO3873	0.006438576	0.030434909	-1.99731	*ppiC*	Peptidyl-prolyl cis-trans isomerase C	Protein translation and modification	COG0760	O
YPO3746	0.046825899	0.048690731	-2.01013	*rpoC, ta*	DNA-directed RNA polymerase beta, chain	RNA synthesis, RNA modification and DNA transcription	COG0086	K
YPO3361	0.015430824	0.034956394	-2.03236	*ispD, b2*	4-diphosphocytidyl-2C-methyl-D-erythritol synthase	Central intermediary metabolism	COG1211	I
YPO1626	0.040994579	0.046904392	-2.03481	*lolC*	Lipoprotein releasing system, transmembrane protein	Membranes, lipoproteins and porins	COG0577	V
YPO3362	0.002703397	0.022752142	-2.04316		Conserved hypothetical protein	Unknown	COG2919	D
yopP	0.000642748	0.017718588	-2.0448	*yopP, yo*	Putative targeted effector protein	YOP		
YPO0281	0.014237705	0.034834517	-2.04541	*hmuT*	Hemin-binding periplasmic protein	Transport/binding proteins	COG0614	P
YPO0228	0.047164835	0.048709161	-2.04746	*rplO*	5S ribosomal protein L15	Ribosomal protein synthesis and modification	COG0200	J
YPO3752	0.023929875	0.039017462	-2.04807	*nusG*	Transcription antitermination protein	RNA synthesis, RNA modification and DNA transcription	COG0250	K
YPO2011	0.017327453	0.035683176	-2.04971	*pth*	Peptidyl-tRNA hydrolase	Aminoacyl tRNA synthetases and their modification	COG0193	J
YPO2452	0.025198862	0.039190458	-2.05012		Hypothetical protein	Unknown	COG1063	ER
YPO0955	0.027397586	0.040345421	-2.06618		Hypothetical protein	Unknown	COG0614	P

YPO1398	0.000989579	0.019298639	-2.07321	*cspB*	Cold shock-like protein	Adaptions and atypical conditions	COG1278	K
YPO1630	0.023468148	0.039017462	-2.08819	*cobB*	Putative Sir2 family protein	Unknown	COG0846	K
yscF	0.000351924	0.016712285	-2.08966	*yscF*				
YPO2010	0.006994328	0.031365063	-2.09049	*ychF*	Conserved hypothetical protein	Unknown	COG0012	J
YPO1186	0.022168828	0.038728348	-2.09154		Conserved hypothetical protein	Unknown		
YPO0951	0.004756416	0.027776406	-2.09887		Putative methyltransferase	RNA synthesis, RNA modification and DNA transcription	COG0220	R
YPO2772	0.01933607	0.037222679	-2.10876	*purF*	Amidophosphoribosyltransferase	Purine ribonucleotide biosynthesis	COG0034	F
YPO1301	0.004790602	0.027776406	-2.11066	*psaE*	Putative regulatory protein	Broad regulatory functions	COG0745	TK
YPO3190	0.031771005	0.04267005	-2.11129	*yajC*	Putative membrane protein	Membranes, lipoproteins and porins	COG1862	U
YPO3903	0.002353529	0.021602417	-2.13038		Conserved hypothetical protein	Unknown	COG3085	S
YPO3365	0.0006694	0.017718588	-2.15588	*cysN*	Sulfate adenylyltransferase subunit 1	Sulphur metabolism	COG2895	P
YPO2648	0.009262801	0.032645574	-2.1561	*nrdF*	Ribonucleoside-diphosphate reductase 2 beta chain	Sugar nucleotides metabolism	COG0208	F
YPO2295	0.035515509	0.044715087	-2.16517		Haloacid dehalogenase-like hydrolase family protein	Unknown	COG1011	R
YPO3563	0.036022167	0.044927135	-2.18497	*rplM*	5S ribosomal protein L13	Ribosomal protein synthesis and modification	COG0102	J
YPO0934	0.035066603	0.044591162	-2.18737		Conserved hypothetical protein	Unknown	COG1385	S
YPO3373	0.027081609	0.040256329	-2.19241	*ygcM*	Putative 6-pyruvoyl tetrahydrobiopterin synthase family p	Unknown	COG0720	H
YPO1412	0.001150328	0.019298639	-2.19482	*asnS, ts*	Asparaginyl-tRNA synthetase	Aminoacyl tRNA synthetases and their modification	COG0017	J
YPO1430	0.014981598	0.034956394	-2.20296	*fabA*	3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase	Fatty acid biosynthesis	COG0764	I
YPO1744	0.006047137	0.030310453	-2.20406	*pagP*	Putative exported protein	Membranes, lipoproteins and porins		
YPO2922	0.048678252	0.049169718	-2.20869		Putative membrane protein	Membranes, lipoproteins and porins	COG0741	M
YPO1370	0.009368907	0.032645574	-2.2098	*infA*	Translation initiation factor IF-1	Protein translation and modification	COG0361	J
YPO1445	0.043432821	0.047599667	-2.21068		Conserved hypothetical protein	Unknown	COG1092	R
YPO1264	0.00834474	0.032332443	-2.21112	*rplY*	5S ribosomal protein L25	Ribosomal protein synthesis and modification	COG1825	J
YPO2637	0.000906778	0.019104257	-2.24207		Conserved hypothetical protein	Unknown		
fruA	0.015648502	0.034956394	-2.24364	*fruA, pt*	PTS system, fructose-specific IIBC component	Transport/binding Carbohydrates,organic acids and alcohols		
YPO3499	0.013794029	0.034757824	-2.25173	*secG*	Protein-export membrane protein	Transport/binding proteins	COG1314	U
YPO1261	0.035131222	0.044591162	-2.25624		Conserved hypothetical protein	Unknown	COG3082	S
YPO1312	0.000972781	0.019298639	-2.25963	*yiuC*	Putative siderophore ABC transporter, ATP-binding subun	Transport/binding proteins	COG1120	PH
YPO0472	0.043903735	0.047957484	-2.27254	*rpsT, b2*	3S ribosomal protein S2	Ribosomal protein synthesis and modification	COG0268	J
YPO0936	0.016953863	0.035522094	-2.2947		Conserved hypothetical protein	Unknown	COG1678	K
YPO3366	0.000366854	0.016802858	-2.29745	*cysD*	Sulfate adenylyltransferase subunit 2	Sulphur metabolism	COG0175	EH
YPO0220	0.038158626	0.045350365	-2.29768	*rplN*	5S ribosomal protein L14	Ribosomal protein synthesis and modification	COG0093	J
yscE	7.36819E-05	0.009786994	-2.3032	*yscE*				
YPO0155	0.014865093	0.034956394	-2.30689	*rpe*	Ribulose-phosphate 3-epimerase	Degradation of Polysaccharides	COG0036	G
YPO3212	0.01311299	0.034490359	-2.31081	*rdgC*	Recombination associated protein RdgC	DNA replication, restriction/modification, recombination and r	COG2974	L
YPO2649	0.011435503	0.03357332	-2.32914	*nrdE*	Ribonucleoside-diphosphate reductase 2 alpha chain	Sugar nucleotides metabolism	COG0209	F
YPO3294	0.046304518	0.048690731	-2.32914	*rimM*	16S rRNA processing protein	Ribosome maturation and modification	COG0806	J
YPO4102	0.035266951	0.044591162	-2.33101	*yidC*	Probable membrane protein	Membranes, lipoproteins and porins	COG0706	U
YPO2416	0.035275458	0.044591162	-2.33451		Putative membrane protein	Membranes, lipoproteins and porins	COG2076	P
YPO0417	0.013134322	0.034490359	-2.34762	*waaL*	Putative O-antigen biosynthesis protein	Membranes, lipoproteins and porins	COG3307	M
YPO1435	0.012286264	0.034349747	-2.3509	*ompA, t*	Putative outer membrane porin A protein	Cell envelop	COG2885	M
YPO3159	0.048912162	0.049286019	-2.35891		Hypothetical protein	Unknown		
YPO4101	0.046453383	0.048690731	-2.39408	*rnpA*	Ribonuclease P protein	Degradation of RNA	COG0594	J
YPO3295	0.034393484	0.044527354	-2.41959	*rpsP*	3S ribosomal protein S16	Ribosomal protein synthesis and modification	COG0228	J
YPO3367	0.000170902	0.013938223	-2.42614	*cysG*	Siroheme synthase	Heme and porphyrin Biosynthesis	COG0007	H
YPO0416	0.013145784	0.034490359	-2.42808	*rfaQ, wa*	Putative lipopolysaccharide core biosynthesis protein	Surface polysaccharides, lipopolysaccharides and antigens	COG0859	M
YPO2013	0.039662875	0.046539987	-2.43075	*prsA, pr*	Ribose-phosphate pyrophosphokinase	Sugar nucleotides metabolism	COG0462	FE
yscK	0.002722711	0.022752142	-2.43635	*yscK*				
YPO4082	0.015311202	0.034956394	-2.44929	*avtA*	Valine--pyruvate aminotransferase	Pyruvate family biosynthesis	COG0436	E
YPO1298	0.048245066	0.04891816	-2.45199	*fruB, fr*	Bifunctional fructose-specific PTS IIA/HPr protein	Transport/binding Carbohydrates,organic acids and alcohols	COG1762	GT
YPO3748	0.030104955	0.041948654	-2.45543	*rplL*	5S ribosomal protein L7,L12	Ribosomal protein synthesis and modification	COG0222	J

YPO3644	0.023963461	0.039017462	-2.46231		*cspa1*	Major cold shock protein Cspa1	Adaptions and atypical conditions	COG1278	K
yscD	5.31127E-07	0.000705483	-2.46502	-1.95	*yscD*				
YPO0234	0.046638807	0.048690731	-2.47218		*rpoA*	DNA-directed RNA polymerase alpha chain	RNA synthesis, RNA modification and DNA transcription	COG0202	K
YPO1715	0.017757074	0.036119915	-2.55027		*ybjR, b8*	Probable N-acetylmuramoyl-L-alanine amidase	Degradation of Proteins, peptides and glycopeptides	COG3023	V
YPO1313	0.000245788	0.016712285	-2.55921		*yiuR*	Putative outer membrane protein	Cell envelop	COG1629	P
YPO1395	0.024877899	0.039115715	-2.56434		*msbA*	Probable transport ATP-binding protein	Transport/binding proteins	COG1132	V
YPO1537	0.000544383	0.01725695	-2.56819		*ysuR*	Putative iron-siderophore receptor	Iron uptake	COG1629	P
yscB	0.014785636	0.034956394	-2.56844		*yscB*				
YPO3173	0.035653121	0.044730947	-2.58261		*thiI*	Thiamine biosynthesis protein	Thiamine Biosynthesis	COG0301	H
YPO0467	0.012356363	0.034349747	-2.58778		*yaaH*	Putative membrane protein	Membranes, lipoproteins and porins	COG1584	S
YPO3158	0.027900444	0.04071882	-2.59218		*tig*	Trigger factor	Cell division	COG0544	O
YPO0956	0.030900134	0.04228564	-2.61876			Putative hydroxamate-type ferrisiderophore receptor	Iron uptake	COG1629	P
YPO3751	0.029189161	0.041422305	-2.62505		*rplK, re*	5S ribosomal protein L11	Ribosomal protein synthesis and modification	COG0080	J
YPO0481	0.032779239	0.043409665	-2.63399		*carA, py*	Carbamoyl-phosphate synthase small chain	Glutamate family biosynthesis	COG0505	EF
YPO2441	0.013637551	0.034748073	-2.639		*yfeC*	Chelated iron transport system membrane protein	Transport/binding Cations	COG1108	P
YPO2650	0.009100456	0.032645574	-2.64587		*nrdI*	NrdI protein homologue	Unknown	COG1780	F
YPO3536	0.009670224	0.032670333	-2.66499		*rplI*	5S ribosomal protein L9	Ribosomal protein synthesis and modification	COG0359	J
YPO1045	0.047544892	0.048838565	-2.67139		*tsf*	Elongation factor Ts	Protein translation and modification	COG0264	J
YPO3225	0.003563966	0.025248501	-2.67888		*gpt, gpp*	Xanthine-guanine phosphoribosyltransferase	Salvage of nucleosides and nucleotides	COG0503	F
YPO3666	0.017200964	0.035559502	-2.68989		*mreC*	Rod shape-determining protein MreC	Murein sacculus and peptidoglycan	COG1792	M
YPO3749	0.020226374	0.037786523	-2.69689		*rplJ*	5S ribosomal protein L1	Ribosomal protein synthesis and modification	COG0244	J
YPO2439	0.029356949	0.041483135	-2.71502		*yfeA*	Periplasmic-binding protein	Transport/binding Cations	COG0803	P
YPO3562	0.039120768	0.046066665	-2.75027		*rpsI*	3S ribosomal protein S9	Ribosomal protein synthesis and modification	COG0103	J
yscC	0.008541071	0.032332443	-2.75385		*yscC*				
rpsC	0.03566281	0.044730947	-2.76047		*rpsC*	3S ribosomal protein S3	Ribosomal protein synthesis and modification		
YPO3643	0.015945856	0.035233071	-2.81032		*cspa2*	Major cold shock protein Cspa2	Adaptions and atypical conditions	COG1278	K
YPO3510	0.045054572	0.048300993	-2.82611			Putative membrane protein	Membranes, lipoproteins and porins	COG0697	GER
YPO3292	0.046963948	0.048690731	-2.83346		*rplS*	5S ribosomal protein L19	Ribosomal protein synthesis and modification	COG0335	J
YPO1655	0.033827732	0.044199211	-2.84482		*cspC, m*	Cold shock protein	Adaptions and atypical conditions	COG1278	K
rnpA	0.040388806	0.046843737	-2.8528		*rnpA*	Ribonuclease P protein	Degradation of RNA		
YPO1044	0.037291847	0.045277774	-2.85508		*rpsB*	3S ribosomal protein S2	Ribosomal protein synthesis and modification	COG0052	J
YPO2757	0.00546589	0.029730694	-2.91859		*fabB, fa*	3-oxoacyl-[acyl-carrier-protein] synthase I	Fatty acid biosynthesis	COG0304	IQ
YPO3750	0.031318079	0.042361578	-2.93909		*rplA*	5S ribosomal protein L1	Ribosomal protein synthesis and modification	COG0081	J
YPO2506	0.002005618	0.021336704	-2.9488		*ompX, c*	Putative outer membrane protein	Cell envelop	COG2885	M
YPO0003	0.001487025	0.019849387	-3.03436		*asnA*	Aspartate-ammonia ligase	Aspartate family biosynthesis	COG2502	E
rplK	0.030324122	0.041957104	-3.05048		*rplK, re*	5S ribosomal protein L11	Ribosomal protein synthesis and modification		
YPO2442	0.022445435	0.038972215	-3.05751		*yfeD*	Chelated iron transport system membrane protein	Transport/binding Cations	COG1108	P
YPO2440	0.013663002	0.034748073	-3.06179		*yfeB*	ATP-binding transport protein	Transport/binding Cations	COG1121	P
YPO3293	0.028699818	0.040972496	-3.06516		*trmD*	tRNA (guanine-N1)-methyltransferase	Aminoacyl tRNA synthetases and their modification	COG0336	J
YPO1743	0.004862446	0.027776406	-3.08176		*aroP*	Aromatic amino acid transport protein	Transport/binding Amino acids and amines	COG1113	E
sycE	0.000225955	0.016673944	-3.17053		*sycE*	Putative yopE chaperone			
YPO1300	0.01261581	0.034409208	-3.24852		*fruA, pt*	PTS system, fructose-specific IIBC component	Transport/binding Carbohydrates,organic acids and alcohols	COG1299	G
YPO0218	0.026169253	0.039943498	-3.26187		*rpmC*	5S ribosomal protein L29	Ribosomal protein synthesis and modification	COG0255	J
YPO1299	0.040907758	0.046904392	-3.27003		*fruK, fp*	1-phosphofructokinase	Glycolysis	COG1105	G
YPO3512	0.040130865	0.046773956	-3.36255		*rplU*	5S ribosomal protein L21	Ribosomal protein synthesis and modification	COG0261	J
YPO1310	0.013044161	0.034490359	-3.42945		*yiuA*	Putative periplasmic substrate-binding transport protein	Transport/binding proteins	COG0614	P
YPO1311	0.015994818	0.035233071	-3.44733		*yiuB*	Putative FecCD-family membrane transport protein	Transport/binding proteins	COG0609	P
YPO0216	0.04159594	0.047022052	-3.47155		*rpsC*	3S ribosomal protein S3	Ribosomal protein synthesis and modification	COG0092	J
YPO3511	0.034763938	0.044591162	-3.47676		*rpmA*	5S ribosomal protein L27	Ribosomal protein synthesis and modification	COG0211	J
YPO0645	0.02332367	0.039017462	-3.48407		*rpsU*	3S ribosomal protein S21	Ribosomal protein synthesis and modification	COG0828	J
YPO0219	0.010206434	0.03304557	-3.56762		*rpsQ, n*	3S ribosomal protein S17	Ribosomal protein synthesis and modification	COG0186	J

YPO3538	0.048210928	0.04891816	-3.56834	*priB*	Primosomal replication protein n	DNA replication, restriction/modification, recombination and r	COG2965	L
YPO1649	0.000178389	0.013938223	-3.68106		Conserved hypothetical protein	Unknown	COG1566	V
YPO3537	0.042912358	0.047359741	-3.71137	*rpsR*	3S ribosomal protein S18	Ribosomal protein synthesis and modification	COG0238	J
YPO1078	0.018743336	0.036558493	-3.73034	*mltD, d*	Membrane-bound lytic murein transglycosylase D precurs	Murein sacculus and peptidoglycan	COG0741	M
YPO3539	0.047923141	0.048914567	-3.74342	*rpsF*	3S ribosomal protein S6	Ribosomal protein synthesis and modification	COG0360	J
YPO0215	0.046500398	0.048690731	-4.09432	*rplV, er*	5S ribosomal protein L22	Ribosomal protein synthesis and modification	COG0091	J
YPO0217	0.026582151	0.040036778	-4.39998	*rplP*	5S ribosomal protein L16	Ribosomal protein synthesis and modification	COG0197	J
YPO0211	0.046395976	0.048690731	-4.81194	*rplD, er*	5S ribosomal protein L4	Ribosomal protein synthesis and modification	COG0088	J

* FC = Fold Change