geneID	**log2FoldChange**	**Annotation**
gene2460(KP1_RS12260)	-5.41926318	transcriptional regulator
gene4923(KP1_RS24550)	-4.973296302	Cold shock protein
gene228(KP1_RS01110)	-4.62740444	This protein binds directly to 23S ribosomal RNA (By similarity)
gene2446(KP1_RS12185)	-4.482884445	universal stress protein G
gene2424(KP1_RS12065)	-4.45234012	Catalyzes the excretion of spermidine (By
gene2439(KP1_RS12150)	-4.439544798	Protein of unknown function (DUF1161)
gene2442(KP1_RS12165)	-4.422919978	UPF0482 protein
gene4700(KP1_RS23435)	-4.420234068	Binds 16S rRNA, required for the assembly of 30S
gene4701(KP1_RS23440)	-4.401606682	This is 1 of the proteins that binds and probably mediates the attachment of the 5S RNA
gene2457(KP1_RS12250)	-4.398069452	Competence damage-inducible protein A
gene3625(KP1_RS18000)	-4.388425403	membrAne
gene1849(KP1_RS09230)	-4.356182692	outer membrane protein a
gene3755(KP1_RS18665)	-4.254259628	Phosphocarrier protein Hpr
gene81(cpxP)	-4.223362168	periplasmic
gene1193(KP1_RS05985)	-4.200704846	(ubiquinol oxidase) subunit II
gene4690(KP1_RS23390)	-4.169711846	Located on the platform of the 30S subunit, it
gene231(KP1_RS01120)	-4.161434116	50S ribosomal protein L10
gene2411(KP1_RS12005)	-4.159771563	Inherit from COG: Specifically catalyzes the
gene4345(KP1_RS21665)	-4.141026233	fructose-bisphosphate aldolase
gene4714(KP1_RS23505)	-4.136731146	Involved in the binding of tRNA to the ribosomes
gene2425(KP1_RS12070)	-4.089144093	Catalyzes the excretion of spermidine (By
gene2433(KP1_RS12120)	-4.085097891	Catalyzes a mechanistically unusual reaction, the ATP- dependent insertion of CO2 between the
gene4702(KP1_RS23445)	-4.075627889	One of the proteins that surrounds the
gene4121(KP1_RS20525)	-4.070066989	Catalyzes the reversible conversion of 2-
gene4699(KP1_RS23430)	-4.064043301	One of the primary rRNA binding proteins, it
gene4688(KP1_RS23380)	-4.056318832	DNA-dependent RNA polymerase catalyzes the
gene4697(KP1_RS23420)	-4.050657262	This is one of the proteins that binds and probably mediates the attachment of the 5S RNA
gene229(KP1_RS01115)	-4.010757357	Binds directly to 23S rRNA. The L1 stalk is
gene4720(KP1_RS23535)	-3.992020422	One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it nucleates
gene4028(KP1_RS20055)	-3.990112968	Can catalyze the hydrolysis of ATP in the presence of single-stranded DNA, the ATP-
gene1803(KP1_RS09005)	-3.952587227	thus facilitating recognition of the initiation
gene4582(KP1_RS22870)	-3.932200232	50S ribosomal protein L27
gene809(KP1_RS04045)	-3.91405047	Binds directly to 16S ribosomal RNA (By
gene4825(KP1_RS24055)	-3.856680132	Sigma factors are initiation factors that
gene1590(KP1_RS07945)	-3.853911503	dihydrolipoamide succinyltransferase
gene4698(KP1_RS23425)	-3.844802731	This protein binds to the 23S rRNA, and is important in its secondary structure. It is
gene2089(KP1_RS10410)	-3.831123915	Serine protein kinase
gene5006(KP1_RS24945)	-3.815472044	Promotes RNA polymerase assembly. Latches the N-
gene4719(KP1_RS23530)	-3.809883244	Catalyzes the GTP-dependent ribosomal translocation step during translation elongation. During this step, the ribosome
gene465(KP1_RS02325)	-3.806274003	Binds together with S18 to 16S ribosomal RNA (By
gene2243(KP1_RS27670)	-3.801359368	cold-shock protein
gene4691(KP1_RS23395)	-3.786692304	Located at the top of the head of the 30S subunit, it contacts several helices of the 16S
gene2093(KP1_RS10430)	-3.771569334	Catalyzes the NAD-dependent conversion of D-

gene2447(KP1_RS12190)	-3.768517076	transcriptional regulator
gene4859(KP1_RS24225)	-3.764024363	universal stress protein A
gene3617(KP1_RS17960)	-3.757498117	General inhibitor of pancreatic serine proteases
gene4721(KP1_RS23540)	-3.757377803	Interacts with and stabilizes bases of the 16S rRNA that are involved in tRNA selection in the A site and with the mRNA backbone. Located at
gene4689(KP1_RS23385)	-3.732728156	One of the primary rRNA binding proteins, it
gene3072(KP1_RS15315)	-3.730883928	Binds directly to 23S ribosomal RNA and is necessary for the in vitro assembly process of
gene4618(KP1_RS23050)	-3.700502288	This protein is one of the early assembly proteins of the 50S ribosomal subunit, although
gene4687(KP1_RS23375)	-3.698793822	50S ribosomal protein L17
gene5153(KP1_RS25700)	-3.67947122	F(1)F(0) ATP synthase produces ATP from ADP in the presence of a proton or sodium gradient. F-type ATPases consist of two structural domains,
gene1779(KP1_RS08885)	-3.673749069	however, it seems to stimulate more or less all
gene1594(KP1_RS07965)	-3.67093733	(Ubiquinol oxidase) subunit I
gene1921(KP1_RS09590)	-3.664939161	phosphate starvation-inducible protein
gene4739(KP1_RS23625)	-3.657727207	CAMP-regulatory protein
gene1191(KP1_RS05975)	-3.655052524	oxidase subunit III
gene1591(KP1_RS07950)	-3.643361426	succinyl-CoA synthetase subunit beta
gene1963(KP1_RS09780)	-3.637355787	metal-binding, possibly nucleic acid-binding
gene5020(KP1_RS25015)	-3.636506062	Key enzyme in the regulation of glycerol uptake
gene403(KP1_RS02010)	-3.631706378	Prevents misfolding and promotes the refolding
gene1589(KP1_RS07940)	-3.630833765	2-oxoglutarate dehydrogenase e1 component
gene3923(KP1_RS19525)	-3.624480354	Specifically methylates guanosine-37 in various
gene2456(KP1_RS12245)	-3.62427173	Heat shock protein
gene3075(KP1_RS15330)	-3.604245911	threonyl-tRNA synthetase
gene3924(rimM)	-3.585265684	An accessory protein needed during the final step in the assembly of 30S ribosomal subunit, possibly for assembly of the head region.
gene466(KP1_RS02330)	-3.573254376	Binds single-stranded DNA at the primosome
gene4709(KP1_RS23480)	-3.570333623	Protein S19 forms a complex with S13 that binds
gene3097(KP1_RS15455)	-3.561477723	DNA-binding protein H-ns
gene4346(KP1_RS21670)	-3.54381553	phosphoglycerate kinase
gene2448(KP1_RS12195)	-3.540128754	Dehydrogenase
gene3074(KP1_RS15325)	-3.539961412	IF-3 binds to the 30S ribosomal subunit and shifts the equilibrum between 70S ribosomes and
gene4583(KP1_RS22875)	-3.53314957	This protein binds to 23S rRNA in the presence
gene3912(KP1_RS19465)	-3.528381206	sigma 54 modulation protein ribosomal protein
gene1850(KP1_RS09235)	-3.527755991	Component of the SOS system and an inhibitor of cell division. Accumulation of SulA causes rapid cessation of cell division and the appearance of
gene4692(KP1_RS28220)	-3.522343116	50S ribosomal protein L36
gene4986(KP1_RS24840)	-3.514804157	50S ribosomal protein L28
gene5005(KP1_RS24940)	-3.510035506	Essential for recycling GMP and indirectly, cGMP
gene1728(bssR)	-3.509968184	Represses biofilm formation in M9C glu and LB glu media but not in M9C and LB media. Seems to
gene4718(KP1_RS23525)	-3.496614444	This protein promotes the GTP-dependent binding
gene3925(KP1_RS19535)	-3.486449877	30s ribosomal protein s16
gene975(KP1_RS04890)	-3.484782493	30S ribosomal protein S2
gene4572(KP1_RS22820)	-3.484134584	Preprotein translocase subunit SecG
gene4985(KP1_RS24835)	-3.4778117	50S ribosomal protein L33

gene4693(KP1_RS23400)	-3.471268282	The central subunit of the protein translocation channel SecYEG. Consists of two halves formed by TMs 1-5 and 6-10. These two domains form a lateral gate at the front which open onto the
gene452(KP1_RS02260)	-3.459091276	UPF0379 protein yjfN
gene4558(KP1_RS22745)	-3.458377479	Involved in mRNA degradation. Hydrolyzes single-
gene2385(KP1_RS11885)	-3.453898863	Fumarate nitrate reduction transcriptional
gene3636(KP1_RS18045)	-3.447552156	glycerophosphoryl diester phosphodiesterase
gene5152(KP1_RS25695)	-3.445007568	F(1)F(0) ATP synthase produces ATP from ADP in the presence of a proton or sodium gradient. F-type ATPases consist of two structural domains,
gene3669(KP1_RS18215)	-3.435354015	NDH-1 shuttles electrons from NADH, via FMN and
gene47(KP1_RS00225)	-3.421972477	Formate dehydrogenase
gene4556(KP1_RS22735)	-3.416577642	ATP-dependent RNA helicase
gene888(KP1_RS04430)	-3.414240433	Involved in the biosynthesis of lipid A, a
gene1595(KP1_RS07970)	-3.400314842	Cytochrome D ubiquinol oxidase, subunit II
gene1506(KP1_RS07535)	-3.394975389	Cold shock protein
gene232(KP1_RS01125)	-3.393514814	Seems to be the binding site for several of the
gene1586(KP1_RS07925)	-3.392269798	Succinate dehydrogenase hydrophobic membrane
gene1702(ompX)	-3.387507606	outer membrane protein x
gene4454(KP1_RS22215)	-3.380053909	30S ribosomal protein S21
gene4617(KP1_RS23045)	-3.366071203	30S ribosomal protein S9
gene3678(KP1_RS18260)	-3.361948723	Catalyzes the formation of acetyl phosphate from
gene1197(KP1_RS06005)	-3.355514932	Involved in protein export. Acts as a chaperone
gene1592(KP1_RS07955)	-3.355404037	Succinyl-CoA ligase ADP-forming subunit alpha
gene1778(KP1_RS08880)	-3.35502348	Atp-dependent clp protease atp-binding subunit
gene4510(KP1_RS22490)	-3.351750212	exported protein
gene2458(KP1_RS12255)	-3.34950273	Diguanylate phosphodiesterase
gene1588(sdhB)	-3.348600263	succinate dehydrogenase
gene3139(KP1_RS15650)	-3.348508709	Phosphoribosyl pyrophosphate synthase
gene5413(KP1_RS26925)	-3.345840645	Lysozyme inhibitor
gene4710(KP1_RS23485)	-3.3449768	One of the primary rRNA binding proteins. Required for association of the 30S and 50S
gene1964(KP1_RS09785)	-3.343875891	50s ribosomal protein l32
gene1020(KP1_RS05110)	-3.340257569	Lytic Murein transglycosylase
gene4101(KP1_RS20415)	-3.338130122	Sigma factors are initiation factors that
gene5151(KP1_RS25690)	-3.329421904	Produces ATP from ADP in the presence of a
gene4695(KP1_RS23410)	-3.328122963	50S ribosomal protein L30
gene45(KP1_RS00215)	-3.326587244	formate dehydrogenase, beta subunit
gene5150(KP1_RS25685)	-3.317651489	Produces ATP from ADP in the presence of a proton gradient across the membrane. The gamma
gene4790(KP1_RS23875)	-3.315527451	Glycerol-3-phosphate dehydrogenase
gene402(groES)	-3.312509384	Binds to cpn60 in the presence of Mg-ATP and
gene148(KP1_RS00705)	-3.310377162	Facilitates transcription termination by a mechanism that involves Rho binding to the
gene91(KP1_RS00440)	-3.304633942	Binds the 23S rRNA (By similarity)
gene2441(KP1_RS12160)	-3.304403236	spermidine N(1)-acetyltransferase
gene2088(KP1_RS10405)	-3.296732367	UPF0229 protein
gene799(KP1_RS03990)	-3.291079313	Transaldolase is important for the balance of
gene3637(KP1_RS18050)	-3.285089404	transporter
gene1796(KP1_RS08970)	-3.279098513	Formate acetyltransferase
gene1618(gpmA)	-3.278109536	Catalyzes the interconversion of 2-
gene985(KP1_RS04935)	-3.269637551	Molecular chaperone that interacts specifically with outer membrane proteins, thus maintaining

gene3319(KP1_RS16545)	-3.26877957	response regulator
gene4922(KP1_RS24545)	-3.267834514	transcriptional regulator
gene3756(KP1_RS18670)	-3.252598748	General (non sugar-specific) component of the phosphoenolpyruvate-dependent sugar phosphotransferase system (sugar PTS). This
gene1192(KP1_RS05980)	-3.24921759	oxidase) subunit I
gene4560(KP1_RS22755)	-3.248538225	One of the primary rRNA binding proteins, it binds directly to 16S rRNA where it helps
gene1982(KP1_RS09875)	-3.244443551	UPF0227 protein
gene3495(KP1_RS17360)	-3.238383282	utp--glucose-1-phosphate uridylyltransferase
gene1948(bssS)	-3.234363303	Biofilm formation regulatory protein BssS
gene2204(KP1_RS11000)	-3.23408101	phage shock protein B
gene2035(KP1_RS10135)	-3.224958316	Uncharacterized conserved protein (DUF2303)
gene1587(KP1_RS07930)	-3.217836075	succinate dehydrogenase, flavoprotein subunit
gene4696(KP1_RS23415)	-3.213938781	Located at the back of the 30S subunit body
gene2203(KP1_RS10995)	-3.213533953	Phage shock protein A
gene1189(KP1_RS05965)	-3.197286206	Converts heme B (protoheme IX) to heme O by
gene3922(KP1_RS19520)	-3.194899437	This protein is located at the 30S-50S ribosomal
gene224(KP1_RS01095)	-3.183338814	This protein promotes the GTP-dependent binding
gene4680(KP1_RS23345)	-3.18192826	Modifies the free amino group of the aminoacyl moiety of methionyl-tRNA(fMet). The formyl group
gene46(KP1_RS00220)	-3.178831594	formate dehydrogenase, alpha subunit
gene2555(KP1_RS12725)	-3.176755584	IIa component
gene5161(KP1_RS28325)	-3.172926298	Phosphoribosyl-amp cyclohydrolase
gene4557(KP1_RS22740)	-3.168307409	May be involved in cell division (By similarity)
gene2177(KP1_RS10855)	-3.154448296	aconitate hydratase
gene4435(KP1_RS22110)	-3.152374883	Involved in glycogen synthesis. May be involved
gene3667(KP1_RS18205)	-3.149832745	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron
gene789(KP1_RS03945)	-3.146191466	two-component response regulator
gene4024(KP1_RS20040)	-3.145610273	regulation of carbohydrate metabolic process
gene1789(KP1_RS08935)	-3.145136692	Catalyzes the attachment of serine to tRNA(Ser). Is also able to aminoacylate tRNA(Sec) with
gene887(KP1_RS04425)	-3.142287988	Essential cell division protein that forms a contractile ring structure (Z ring) at the future cell division site. The regulation of the
gene1585(sdhC)	-3.136361695	Succinate dehydrogenase, cytochrome b556 subunit
gene4676(KP1_RS23325)	-3.134940116	Dna topoisomerase
gene978(KP1_RS04905)	-3.133131818	Responsible for the release of ribosomes from messenger RNA at the termination of protein
gene4102(nlpD)	-3.130271726	lipoprotein NlpD
gene1526(KP1_RS07630)	-3.122620027	alpha helical protein
gene1559(KP1_RS07790)	-3.122422839	Ferric uptake
gene5412(KP1_RS26920)	-3.120650848	Removes the formyl group from the N-terminal Met of newly synthesized proteins. Requires at least
gene4712(KP1_RS23495)	-3.120225613	One of the primary rRNA binding proteins, this protein initially binds near the 5’-end of the
gene23(KP1_RS00110)	-3.119700898	serine (threonine) protein kinase
gene1583(KP1_RS07915)	-3.112743621	citrate synthase
gene4793(KP1_RS23890)	-3.10931608	Catalyzes the synthesis of ADP-glucose, a sugar
gene398(KP1_RS01980)	-3.108645207	Aspartate ammonia-lyase
gene3757(KP1_RS18675)	-3.103486603	pts system
gene453(KP1_RS02265)	-3.102430951	biofilm stress and motility protein A

gene1190(KP1_RS05970)	-3.10114647	Cytochrome o ubiquinol oxidase, subunit IV
gene1711(KP1_RS08550)	-3.099457588	abc transporter atp-binding protein
gene4713(KP1_RS23500)	-3.098729024	One of the primary rRNA binding proteins, it
gene4675(KP1_RS23320)	-3.092351147	Required for the formation of a
gene4707(KP1_RS23470)	-3.09039073	Binds the lower part of the 30S subunit head.
gene1603(KP1_RS08010)	-3.085186099	Peptidoglycan-associated lipoprotein
gene2492(KP1_RS12425)	-3.080887111	phenazine biosynthesis protein, PhzF family
gene44(KP1_RS00210)	-3.079094188	formate dehydrogenase
gene4694(KP1_RS23405)	-3.07745868	Binds to the 23S rRNA (By similarity)
gene2103(KP1_RS10475)	-3.073595843	acid phosphatase
gene908(KP1_RS04540)	-3.072337176	dihydrolipoyl dehydrogenase
gene441(KP1_RS02200)	-3.071264965	RNA chaperone that binds small regulatory RNA (sRNAs) and mRNAs to facilitate mRNA
gene4342(KP1_RS21645)	-3.069422042	oxidative stress defense protein
gene4757(KP1_RS23720)	-3.069049466	Catalyzes the specific phosphorylation of the 3-
gene3668(KP1_RS18210)	-3.054513783	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron
gene1819(KP1_RS09080)	-3.050507182	exported protein
gene770(KP1_RS03860)	-3.050077342	Phosphotransfer between the C1 and C5 carbon
gene4726(KP1_RS23565)	-3.044442435	Peptidyl-prolyl cis-trans isomerase
gene1969(KP1_RS09810)	-3.044293353	Inherit from proNOG: Acyl carrier protein
gene987(KP1_RS04945)	-3.041422306	Involved in unsaturated fatty acids biosynthesis. Catalyzes the dehydration of short
gene988(KP1_RS04950)	-3.040631103	Involved in the biosynthesis of lipid A, a
gene2550(KP1_RS12695)	-3.034115982	Protein of unknown function (DUF3423)
gene1196(KP1_RS06000)	-3.031349762	BolA protein
gene2145(KP1_RS10700)	-3.028696848	outer membrane protein W
gene981(KP1_RS04915)	-3.028010276	Catalyzes the sequential condensation of isopentenyl diphosphate (IPP) with (2E,6E)-farnesyl diphosphate (E,E-FPP) to yield
gene1199(KP1_RS06015)	-3.026594314	ATP-dependent specificity component of the Clp
gene1596(KP1_RS07975)	-3.025830083	Cyd operon protein YbgT
gene3054(KP1_RS15225)	-3.023592014	Catalyzes the phosphorylation of pyruvate to
gene4728(KP1_RS23575)	-3.017809527	Peptidyl-prolyl cis-trans isomerase
gene4122(pyrG)	-3.014837371	Catalyzes the ATP-dependent amination of UTP to
gene3253(KP1_RS16225)	-3.014807179	Protein of unknown function (DUF1480)
gene4565(KP1_RS22780)	-3.012520422	Required for maturation of 30S ribosomal
gene5154(KP1_RS25705)	-3.011555552	F(1)F(0) ATP synthase produces ATP from ADP in the presence of a proton or sodium gradient. F-type ATPases consist of two structural domains,
gene4634(KP1_RS23130)	-3.001383779	UPF0379 protein yhcN
gene4511(KP1_RS22495)	-3.000099839	conserved protein
gene35(KP1_RS00165)	-2.995699155	gtp-binding protein typa
gene4320(KP1_RS21535)	-2.993769948	hemolysin III
gene3890(KP1_RS19350)	-2.986314042	sigma-e factor negative regulatory protein
gene2985(KP1_RS14870)	-2.985003499	Protein of unknown function (DUF1062)
gene1256(KP1_RS06305)	-2.979531866	Catalyzes the reversible transfer of the terminal phosphate group between ATP and AMP.
gene3772(KP1_RS18755)	-2.978989555	N-acetylmuramoyl-L-alanine amidase
gene443(KP1_RS02210)	-2.96727416	HflK protein
gene4677(KP1_RS23330)	-2.966022979	Protein smg homolog
gene3024(KP1_RS15075)	-2.963897995	outer membrane lipoprotein

gene841(KP1_RS04195)	-2.960251059	Transfers 2-(5''-triphosphoribosyl)-3'-dephosphocoenzyme-A on a serine residue to the
gene4708(KP1_RS23475)	-2.956882852	The globular domain of the protein is located near the polypeptide exit tunnel on the outside
gene373(KP1_RS01840)	-2.952790829	proline glycine betaine transporter
gene1323(KP1_RS06640)	-2.947095291	Protein of unknown function (DUF1471)
gene2877(KP1_RS14330)	-2.947043471	Destroys radicals which are normally produced
gene4575(hflB)	-2.946294594	Acts as a processive, ATP-dependent zinc
gene3068(KP1_RS15300)	-2.944565845	This protein is one of the two subunits of integration host factor, a specific DNA-binding
gene299(KP1_RS01455)	-2.943118758	CsbD family
gene2026(KP1_RS10105)	-2.942838354	isocitrate dehydrogenase (NADP)
gene84(KP1_RS00400)	-2.94261712	Globally modulates RNA abundance by binding to RNase E (Rne) and regulating its endonucleolytic
gene146(KP1_RS00700)	-2.938728368	Thioredoxin
gene2732(KP1_RS13615)	-2.936585033	alcohol dehydrogenase
gene4433(KP1_RS22100)	-2.929657989	Catalyzes the conversion of D-ribulose 5-
gene4512(KP1_RS22500)	-2.9215628	Inner membrane protein YqjE
gene1239(KP1_RS06215)	-2.921177158	Inner membrane protein ylaC
gene4615(sspA)	-2.912396684	Stringent starvation protein a
gene1631(KP1_RS08155)	-2.909935149	Biofilm development protein YmgB/AriR
gene1201(KP1_RS06025)	-2.906593175	DNA-binding protein
gene1848(KP1_RS09225)	-2.905629687	Required for spatial organization of the terminus region of the chromosome (Ter
gene5014(KP1_RS24985)	-2.903249139	Triose-phosphate isomerase
gene3098(KP1_RS15460)	-2.899269181	Utp--glucose-1-phosphate uridylyltransferase
gene5364(KP1_RS26715)	-2.896063282	tellurium resistance protein
gene4679(KP1_RS23340)	-2.895260189	Removes the formyl group from the N-terminal Met of newly synthesized proteins. Requires at least
gene1700(KP1_RS08490)	-2.892878455	During stationary phase, binds the chromosome non- specifically, forming a highly ordered and stable dps-DNA co- crystal within which
gene3080(KP1_RS15355)	-2.886463746	Fructosamine kinase
gene467(KP1_RS02335)	-2.884782252	Binds as a heterodimer with protein S6 to the
gene24(KP1_RS00115)	-2.881605363	Thiol disulfide Interchange Protein
gene422(KP1_RS02105)	-2.880708087	fumarate reductase iron-sulfur
gene3597(KP1_RS17860)	-2.878764652	(Lipo)protein
gene4620(KP1_RS23060)	-2.869877811	Cytochrome d ubiquinol oxidase subunit III
gene976(KP1_RS04895)	-2.864304641	Associates with the EF-Tu.GDP complex and induces the exchange of GDP to GTP. It remains
gene4330(KP1_RS21585)	-2.86215586	The glycine cleavage system catalyzes the
gene984(KP1_RS04930)	-2.861722109	Part of the outer membrane protein assembly
gene1198(KP1_RS06010)	-2.858923261	Cleaves peptides in various proteins in a process that requires ATP hydrolysis. Has a
gene2874(KP1_RS14315)	-2.858608808	Glutaredoxin
gene4329(KP1_RS21580)	-2.858296441	The glycine cleavage system catalyzes the
gene1785(KP1_RS08915)	-2.858292006	Transcriptional regulator
gene2094(KP1_RS10435)	-2.85503633	peptide-methionine (R)-S-oxide reductase
gene974(KP1_RS04885)	-2.853351233	Removes the N-terminal methionine from nascent
gene934(KP1_RS04675)	-2.852433868	Transcription factor that acts by binding directly to the RNA polymerase (RNAP). Required
gene312(KP1_RS01525)	-2.852344327	single-stranded DNA-binding protein
gene1787(lolA)	-2.851346105	Participates in the translocation of lipoproteins from the inner membrane to the

gene2561(KP1_RS12760)	-2.849120064	transcriptional regulator
gene5019(KP1_RS25010)	-2.847364561	glycerol uptake facilitator protein
gene3237(KP1_RS16155)	-2.845942679	Cold shock protein
gene297(KP1_RS01440)	-2.841697008	Represses a number of genes involved in the response to DNA damage (SOS response), including
gene771(KP1_RS03865)	-2.830293089	purine nucleoside phosphorylase DeoD-type
gene4009(KP1_RS19955)	-2.828262211	Transcriptional repressor Mpra
gene2690(KP1_RS13405)	-2.820377678	Bifunctional enzyme with both catalase and
gene4563(KP1_RS22770)	-2.81963867	One of the essential components for the initiation of protein synthesis. Protects
gene3248(KP1_RS16200)	-2.817936943	may be a structural element that influences the
gene1633(KP1_RS08165)	-2.81431765	Probably a connector protein for RcsB C regulation of biofilm formation, providing
gene2302(KP1_RS11470)	-2.814107013	Universal stress protein
gene906(KP1_RS04530)	-2.81314049	Component of the pyruvate dehydrogenase (PDH)
gene3206(KP1_RS15995)	-2.81311163	SpoVR family
gene4791(KP1_RS23880)	-2.811933677	Phosphorylase is an important allosteric enzyme in carbohydrate metabolism. Enzymes from
gene3836(KP1_RS19075)	-2.8113263	UPF0070 protein
gene3895(KP1_RS19375)	-2.810917555	Acts as a radical domain for damaged PFL and
gene5247(KP1_RS26205)	-2.810194698	Transcriptional regulator
gene964(KP1_RS04835)	-2.806744054	Required for insertion of 4Fe-4S clusters for at
gene3297(KP1_RS16440)	-2.806021704	Trehalose-6-phosphate phosphatase
gene2440(KP1_RS12155)	-2.804518432	UPF0257 lipoprotein ynfC
gene2383(KP1_RS11875)	-2.804435481	uncharacterized protein ydiH
gene2506(KP1_RS12495)	-2.793714462	GGDEF
gene3854(KP1_RS19165)	-2.793307262	Catalyzes the removal of elemental sulfur from
gene3577(KP1_RS17770)	-2.787637194	GTP cyclohydrolase I
gene1970(KP1_RS09815)	-2.786329095	Catalyzes the condensation reaction of fatty
gene1777(KP1_RS08875)	-2.785382375	Involved in the modulation of the specificity of
gene3891(KP1_RS19355)	-2.780108794	RNA polymerase sigma factor
gene4597(KP1_RS22945)	-2.774679318	lipopolysaccharide transport periplasmic protein
gene2484(KP1_RS12380)	-2.774187978	helix-turn-helix domain protein
gene1648(KP1_RS08245)	-2.772231563	Imidazolonepropionate hydrolase
gene3607(KP1_RS17910)	-2.772031345	This is one of the proteins that binds to the 5S
gene4425(KP1_RS22060)	-2.771903852	Hydrolyzes cAMP to 5'-AMP. Plays an important
gene969(KP1_RS04860)	-2.770604959	protease
gene203(KP1_RS01000)	-2.770301062	reductase
gene874(KP1_RS04360)	-2.76998713	Specifically methylates the N4 position of
gene3933(KP1_RS19575)	-2.769302165	Part of the outer membrane protein assembly
gene5018(KP1_RS25005)	-2.769062742	Non-essential, abundant cell division factor that is required for proper Z-ring formation. It
gene4589(KP1_RS22905)	-2.768527818	toluene tolerance
gene2384(KP1_RS11880)	-2.767822296	Universal stress protein
gene4564(nusA)	-2.764935713	Transcription elongation factor NusA
gene1509(tatE)	-2.757573059	Part of the twin-arginine translocation (Tat) system that transports large folded proteins
gene2861(KP1_RS14250)	-2.757530538	Outer membrane lipoprotein
gene22(KP1_RS00105)	-2.757004438	conserved protein
gene194(KP1_RS00950)	-2.746339114	Methyltransferase required for the conversion of demethylmenaquinone (DMKH2) to menaquinone
gene1499(KP1_RS07500)	-2.745522175	alkyl hydroperoxide reductase
gene3448(KP1_RS17125)	-2.744583415	Inhibits the supercoiling activity of DNA gyrase. Acts by inhibiting DNA gyrase at an

gene4706(KP1_RS23465)	-2.743365585	Binds 23S rRNA and is also seen to make contacts
gene3713(KP1_RS18445)	-2.742134179	phosphohistidine phosphatase
gene2452(KP1_RS12215)	-2.737843886	Uncharacterised ACR, COG2135
gene4705(KP1_RS23460)	-2.737487904	50S ribosomal protein L29
gene3629(KP1_RS18020)	-2.734235606	DNA gyrase negatively supercoils closed circular double- stranded DNA in an ATP-dependent manner
gene3177(KP1_RS15845)	-2.723115525	phosphoenolpyruvate carboxylase
gene442(KP1_RS02205)	-2.722773167	GTPase that associates with the 50S ribosomal
gene3144(KP1_RS15675)	-2.722679739	GTP-dependent nucleic acid-binding protein engD
gene2946(KP1_RS14690)	-2.722381914	Phage-related regulatory protein cII
gene227(nusG)	-2.721599862	Participates in transcription elongation,
gene3936(KP1_RS19590)	-2.721368011	Binds specifically to the SsrA RNA (tmRNA) and
gene5371(KP1_RS26745)	-2.720658875	DNA-invertase from lambdoid prophage
gene415(KP1_RS02070)	-2.718823778	Involved in peptide bond synthesis. Alleviates ribosome stalling that occurs when 3 or more
gene3704(KP1_RS18400)	-2.717706727	Catalyzes the condensation reaction of fatty
gene5155(KP1_RS25710)	-2.713633464	it plays a direct role in the translocation of
gene1634(KP1_RS08170)	-2.713396057	Diguanylate phosphodiesterase
gene3494(KP1_RS17355)	-2.712270704	phosphoesterase, PA-phosphatase related protein
gene5119(KP1_RS25520)	-2.711871678	DNA gyrase negatively supercoils closed circular double- stranded DNA in an ATP-dependent manner
gene2859(KP1_RS14240)	-2.709079979	(LipO)protein
gene251(KP1_RS01220)	-2.704757837	DNA-binding protein
gene488(KP1_RS02440)	-2.702982209	pyrophosphate phospho-hydrolase
gene5363(KP1_RS26710)	-2.69711078	tellurium resistance protein
gene3491(KP1_RS17335)	-2.694320682	protein tyrosine phosphatase
gene43(KP1_RS00205)	-2.693090479	Necessary for formate dehydrogenase activity (By
gene1(KP1_RS00005)	-2.690133715	Flavodoxin
gene839(KP1_RS04185)	-2.686155281	citrate carrier protein
gene1902(KP1_RS09490)	-2.684555348	NAD(P)H quinone oxidoreductase
gene5341(KP1_RS26610)	-2.684229949	Protein of unknown function (DUF1778)
gene3639(KP1_RS18060)	-2.683122969	Conversion of glycerol 3-phosphate to
gene1534(KP1_RS07675)	-2.683004043	Magnesium and cobalt efflux protein
gene4632(KP1_RS23120)	-2.68037053	Catalyzes the reversible oxidation of malate to
gene1968(fabG)	-2.676962131	reductase
gene440(KP1_RS02195)	-2.67219743	Catalyzes the transfer of a dimethylallyl group onto the adenine at position 37 in tRNAs that
gene3837(KP1_RS19080)	-2.671141689	histidyl-tRNA synthetase
gene5125(KP1_RS25540)	-2.670969241	50s ribosomal protein l34
gene763(KP1_RS03825)	-2.669380851	BON
gene5149(KP1_RS25680)	-2.668271059	Produces ATP from ADP in the presence of a
gene1560(KP1_RS07795)	-2.66689456	Low-potential electron donor to a number of
gene1649(KP1_RS08250)	-2.665620426	Histidine ammonia-lyase
gene3023(KP1_RS15070)	-2.664829448	Pyruvate kinase
gene2590(KP1_RS12895)	-2.664237822	LysM domain BON superfamily protein
gene3638(KP1_RS18055)	-2.661447632	dehydrogenase, subunit A
gene1242(KP1_RS06235)	-2.661059678	Biofilm formation regulator YbaJ
gene4970(KP1_RS24760)	-2.660320914	Catalyzes the interconversion between ADP-D-
gene805(KP1_RS04020)	-2.659864477	Acts as a chaperone (By similarity)
gene3479(KP1_RS17285)	-2.6593155	Catalyzes the oxidative decarboxylation of 6-
gene4792(KP1_RS23885)	-2.659262351	Synthesizes alpha-1,4-glucan chains using ADP-
gene2126(KP1_RS10600)	-2.658046476	DNA-binding transcriptional activator OsmE
gene3848(KP1_RS19135)	-2.657946582	Fe-S assembly protein IscX
gene423(KP1_RS02110)	-2.657835944	succinate dehydrogenase, flavoprotein subunit

gene1127(KP1_RS05645)	-2.647155047	starvation-inducible protein
gene3086(KP1_RS15390)	-2.645482019	UPF0263 protein
gene2461(KP1_RS12265)	-2.645052652	Regulatory protein
gene3485(KP1_RS28050)	-2.643882515	Bacterial transferase hexapeptide (six repeats)
gene1200(KP1_RS06020)	-2.64374803	ATP-dependent serine protease that mediates the selective degradation of mutant and abnormal proteins as well as certain short-lived
gene2863(KP1_RS14260)	-2.643425043	Transcription regulator that can specifically
gene3785(KP1_RS18820)	-2.643245258	May be involved in the formation of a specific
gene3884(KP1_RS19315)	-2.640633011	An essential GTPase that binds both GDP and GTP, with rapid nucleotide exchange. Plays a role in
gene986(lpxD)	-2.634992028	as the acyl donor. Is involved in the
gene2931(KP1_RS14610)	-2.633821753	Protein of unknown function (DUF535)
gene4331(KP1_RS21590)	-2.633488297	The glycine cleavage system catalyzes the
gene2509(KP1_RS12510)	-2.632413931	Acetyltransferase (GNAT) family
gene5156(KP1_RS25715)	-2.628802588	Produces ATP from ADP in the presence of a
gene236(KP1_RS01145)	-2.627013198	phosphotransferase system PTS, lactose
gene226(KP1_RS01100)	-2.624459053	preprotein translocase subunit SecE
gene447(KP1_RS02235)	-2.622514543	Plays an important role in the de novo pathway
gene3889(KP1_RS19345)	-2.617759022	regulatory protein
gene1178(KP1_RS05910)	-2.617673739	UPF0234 protein
gene4716(KP1_RS23515)	-2.617011449	Iron-storage protein
gene3483(KP1_RS17305)	-2.615464837	GDP-fucose synthetase
gene3829(KP1_RS19040)	-2.615253829	Catalyzes the synthesis of GMP from XMP (By
gene3492(KP1_RS17340)	-2.613250868	polysaccharide export protein
gene4347(KP1_RS21675)	-2.607223425	Catalyzes the NAD-dependent conversion of D-
gene1524(KP1_RS07620)	-2.604711365	Rare lipoprotein B
gene4836(KP1_RS24110)	-2.603201947	(Lipo)protein
gene4018(KP1_RS20005)	-2.600463519	Transport-associated protein
gene170(KP1_RS00825)	-2.598905844	Adenylate cyclase
gene1215(KP1_RS06095)	-2.598851842	Glycoprotein polysaccharide metabolism
gene3484(KP1_RS17310)	-2.597771967	GDPmannose 4,6-dehydratase
gene3135(KP1_RS15635)	-2.597558413	Catalyzes the NADPH-dependent reduction of
gene3025(KP1_RS15080)	-2.596573012	ErfK YbiS YcfS YnhG family protein
gene971(KP1_RS04870)	-2.594904369	UPF0325 protein
gene2882(KP1_RS14360)	-2.593207396	cyclopropane-fatty-acyl-phospholipid synthase
gene3807(KP1_RS18925)	-2.592385408	Catalyzes the condensation of (S)-aspartate-
gene1599(KP1_RS07990)	-2.588332041	tolQ protein
gene3627(KP1_RS18010)	-2.58690418	regulatoR
gene4507(KP1_RS22475)	-2.586051636	Transcriptional regulator
gene873(KP1_RS04355)	-2.582435856	cell division protein MraZ
gene234(KP1_RS01135)	-2.58115707	DNA-dependent RNA polymerase catalyzes the
gene2345(KP1_RS11670)	-2.575803681	Glutamate dehydrogenase
gene1635(KP1_RS08175)	-2.573694557	Transcriptional regulator
gene381(KP1_RS01880)	-2.573267144	displays overlapping activities with DnaJ, but functions under different conditions, probably
gene3697(KP1_RS18365)	-2.57296934	Component of the acetyl coenzyme A carboxylase (ACC) complex. Biotin carboxylase (BC) catalyzes
gene4317(KP1_RS21520)	-2.569580779	Toxic component of a toxin-antitoxin (TA) module. Overexpression leads to growth arrest
gene4704(KP1_RS23455)	-2.569469343	One of the primary rRNA binding proteins, it
gene92(KP1_RS00445)	-2.567581862	This regulatory protein, when combined with SAM
gene4119(KP1_RS20510)	-2.565175181	Catalyzes the conversion of 6-carboxy-5,6,7,8-
gene4439(KP1_RS22135)	-2.564970638	domain protein

gene3079(KP1_RS15350)	-2.563698553	Uncharacterized protein ydiZ
gene4614(KP1_RS23035)	-2.562663451	stringent starvation protein b
gene5370(KP1_RS26740)	-2.561278203	alpha beta fold family
gene3486(KP1_RS17315)	-2.556989904	glycosyl transferase group 1
gene3838(KP1_RS19085)	-2.552063775	Converts 2C-methyl-D-erythritol 2,4-
gene4576(KP1_RS22840)	-2.550586843	Specifically methylates the uridine in position
gene4355(KP1_RS21710)	-2.544074198	Catalyzes the formation of S-adenosylmethionine from methionine and ATP. The overall synthetic
gene1598(KP1_RS07985)	-2.544066187	Thioesterase
gene2857(KP1_RS14230)	-2.543801712	Catalyzes the attachment of tyrosine to tRNA(Tyr) in a two-step reaction tyrosine is
gene1253(KP1_RS06290)	-2.542311453	Binds to DNA and alters its conformation. May be
gene1858(KP1_RS09275)	-2.535221039	Involved in the degradation of certain
gene2449(KP1_RS12200)	-2.534338645	peptidyl-dipeptidase Dcp
gene2552(KP1_RS12705)	-2.532303657	Diguanylate cyclase phosphodiesterase
gene3482(KP1_RS17300)	-2.530934376	GDP-mannose mannosyl hydrolase
gene499(KP1_RS02505)	-2.53033983	Cytochrome b(562)
gene2095(KP1_RS10440)	-2.528154806	cytoplasmic protein
gene3476(KP1_RS17270)	-2.527969041	UDP-glucose 6-dehydrogenase
gene3446(KP1_RS17115)	-2.527690997	UPF0265 protein
gene3666(KP1_RS18200)	-2.527237357	NADH dehydrogenase subunit E
gene4562(KP1_RS22765)	-2.526851871	Associates with free 30S ribosomal subunits (but not with 30S subunits that are part of 70S
gene3247(KP1_RS16195)	-2.526534452	protease
gene112(KP1_RS00535)	-2.525981601	Transcriptional regulator
gene3265(KP1_RS16285)	-2.523349345	DNA damage-inducible protein
gene493(KP1_RS02470)	-2.522947459	D-fructose-1,6-bisphosphate 1-phosphohydrolase
gene300(KP1_RS01460)	-2.522769363	Zinc uptake regulation protein
gene2124(KP1_RS10590)	-2.522318832	Incises the DNA at the 3' side of a lesion during nucleotide excision repair. Incises the DNA farther away from the lesion than UvrC. Not
gene233(KP1_RS01130)	-2.521800637	DNA-dependent RNA polymerase catalyzes the
gene2413(KP1_RS12015)	-2.521779075	Transcriptional regulator
gene421(KP1_RS02100)	-2.521212329	Seems to be involved in the anchoring of the
gene3529(KP1_RS17535)	-2.518280486	fructose-bisphosphate aldolase
gene1646(KP1_RS08235)	-2.517241109	Formiminoglutamate hydrolase
gene173(KP1_RS00840)	-2.515717211	Catalyzes the stereoinversion of LL-2,6-diaminoheptanedioate (L,L-DAP) to meso-
gene886(KP1_RS04420)	-2.51510776	This protein may be involved in anomalous
gene4336(KP1_RS21615)	-2.511947054	Activator of cell division through the inhibition of FtsZ GTPase activity, therefore
gene3835(KP1_RS19070)	-2.510301493	Part of the outer membrane protein assembly
gene3841(KP1_RS19100)	-2.509342681	Major role in the synthesis of nucleoside triphosphates other than ATP. The ATP gamma
gene4108(KP1_RS20450)	-2.508453253	Essential cell division protein. May link together the upstream cell division proteins,
gene3127(KP1_RS15595)	-2.505841603	Cation transport protein
gene2626(KP1_RS13080)	-2.505467977	Cell envelope integrity inner membrane protein
gene3613(KP1_RS17940)	-2.504649803	UPF0352 protein
gene3853(KP1_RS19160)	-2.504015773	scaffold protein
gene697(KP1_RS03495)	-2.500162235	dehydrogenase
gene5396(KP1_RS26850)	-2.496628193	Phenylalanyl-tRNA synthetase beta subunit
gene983(KP1_RS04925)	-2.496261808	Membrane-associated zinc metalloprotease
gene1513(KP1_RS07570)	-2.495758006	UPF0250 protein

gene871(KP1_RS04350)	-2.495445104	DNA-binding transcriptional regulator FruR
gene3885(KP1_RS19320)	-2.492943657	Digests double-stranded RNA. Involved in the processing of primary rRNA transcript to yield
gene168(KP1_RS00810)	-2.49210716	Uroporphyrinogen-III synthase
gene4756(KP1_RS23715)	-2.491297909	3-dehydroquinate synthase
gene3226(KP1_RS16100)	-2.490367438	L-serine dehydratase
gene1532(KP1_RS07665)	-2.490277646	(ABC) transporter
gene418(KP1_RS02085)	-2.487274894	Multidrug resistance protein
gene448(KP1_RS02240)	-2.481868717	Nitric oxide-sensitive repressor of genes
gene449(KP1_RS02245)	-2.480707966	3'-5' exoribonuclease that releases 5'-
gene1821(KP1_RS09090)	-2.480578938	Aromatic amino acid aminotransferase
gene4961(KP1_RS24715)	-2.478860257	One of the proteins required for the normal export of preproteins out of the cell cytoplasm.
gene4551(KP1_RS22710)	-2.475262892	lipid carrier protein
gene5183(KP1_RS25910)	-2.472862469	phosphoadenosine phosphosulfate reductase
gene4885(KP1_RS24360)	-2.471055474	cytoplasmic protein
gene3934(KP1_RS19580)	-2.470791108	UPF0125 protein
gene4661(KP1_RS23250)	-2.470039882	Catalyzes the synthesis of dihydrouridine, a
gene1795(pflA)	-2.468616504	Pyruvate formate lyase-activating enzyme 1
gene4901(KP1_RS24440)	-2.468615234	Extracellular solute-binding protein, family 5
gene3768(KP1_RS18735)	-2.464604963	dyp-type peroxidase family protein
gene3295(KP1_RS16430)	-2.463812685	Universal stress protein
gene1501(KP1_RS07510)	-2.458527267	Universal stress protein
gene3809(KP1_RS18935)	-2.458125606	Thioredoxin-dependent thiol peroxidase
gene3789(KP1_RS18840)	-2.456046826	ethanolamine utilization protein
gene2431(KP1_RS12110)	-2.455174014	LysR family transcriptional regulator
gene4954(KP1_RS24680)	-2.448691274	Protein of unknown function (DUF2810)
gene1837(KP1_RS09175)	-2.446011093	Contributes to the efficiency of the cell division process by stabilizing the polymeric
gene480(KP1_RS02400)	-2.445704075	Protein of unknown function (DUF1107)
gene5146(KP1_RS25650)	-2.443548649	Catalyzes the first step in hexosamine
gene1602(KP1_RS08005)	-2.443192471	Involved in the TonB-independent uptake of
gene4578(KP1_RS22850)	-2.442091018	Necessary for efficient RNA polymerase transcription elongation past template-encoded arresting sites. The arresting sites in DNA have
gene5326(KP1_RS26545)	-2.440338822	Replication protein
gene905(KP1_RS04525)	-2.440208895	Transcriptional regulator
gene3490(KP1_RS17330)	-2.439647037	tyrosine-protein kinase
gene4599(KP1_RS22955)	-2.439588051	Sigma factors are initiation factors that
gene834(KP1_RS04160)	-2.437520683	Chaperone involved in the correct folding and assembly of outer membrane proteins. Recognizes
gene309(KP1_RS01510)	-2.437010013	UPF0047 protein yjbQ
gene4516(KP1_RS22520)	-2.436981739	membrAne
gene3213(KP1_RS16030)	-2.436848142	YcgL domain-containing protein
gene3911(KP1_RS19460)	-2.43628019	Part of the outer membrane protein assembly
gene4017(KP1_RS20000)	-2.436206762	phosphatase
gene885(KP1_RS04415)	-2.434676384	Essential cell division protein. May link together the upstream cell division proteins,
gene2180(KP1_RS10870)	-2.434606594	inner membrane protein yciS
gene914(KP1_RS04570)	-2.431681069	UPF0231 protein
gene935(KP1_RS04680)	-2.429501308	Sugar fermentation stimulation protein homolog
gene3659(KP1_RS18165)	-2.428740856	subunit 1
gene1955(KP1_RS09740)	-2.426824802	UPF0502 protein
gene80(KP1_RS00380)	-2.425034152	Transcriptional regulator

gene4596(KP1_RS22940)	-2.424463398	Required for the translocation of
gene3855(KP1_RS19170)	-2.423527668	Regulates the transcription of several operons
gene4601(KP1_RS22965)	-2.422886248	PTS IIA-like nitrogen-regulatory protein PtsN
gene4674(KP1_RS23315)	-2.419174153	shikimate dehydrogenase
gene2490(KP1_RS12415)	-2.413281419	multiple drug resistance protein MarC
gene3665(KP1_RS18195)	-2.410001066	NADH dehydrogenase I, subunit F
gene1241(KP1_RS06230)	-2.401783401	hemolysin expression-modulating protein
gene3282(KP1_RS16365)	-2.400886195	transcriptional regulatory protein
gene3935(KP1_RS19585)	-2.400540591	Cyclase dehydrase
gene3752(KP1_RS18640)	-2.400008281	receptor for the septal ring structure, may
gene4229(KP1_RS21075)	-2.399048615	Bacterial protein of unknown function (DUF903)
gene1167(nusB)	-2.398736931	Involved in the transcription termination
gene3856(KP1_RS19175)	-2.393362772	RNA methyltransferase, TrmH family, group 1
gene172(KP1_RS00835)	-2.392847427	(Lipo)protein
gene2162(KP1_RS10785)	-2.391732363	SUA5 YciO YrdC YwlC family protein
gene1128(KP1_RS05650)	-2.390636214	pyrroline-5-carboxylate reductase
gene5196(KP1_RS25970)	-2.39002841	Protein of unknown function (DUF1173)
gene814(KP1_RS04060)	-2.389163808	This protein specifically catalyzes the removal
gene875(KP1_RS04365)	-2.383748544	Essential cell division protein. May link together the upstream cell division proteins,
gene1965(KP1_RS09790)	-2.382381258	Catalyzes the reversible formation of acyl-phosphate (acyl-PO(4)) from acyl- acyl-carrier-
gene4335(KP1_RS21610)	-2.381539444	UPF0149 protein
gene1846(KP1_RS09215)	-2.380126931	Necessary for the introduction of cis unsaturation into fatty acids. Catalyzes the
gene4430(KP1_RS22085)	-2.374031527	glutathionylspermidine synthase
gene5148(atpC)	-2.372712996	Produces ATP from ADP in the presence of a
gene2478(KP1_RS12350)	-2.37268815	methionine synthase
gene1938(mdoG)	-2.372471497	Involved in the biosynthesis of osmoregulated
gene3244(KP1_RS16180)	-2.37092848	transcriptional regulator
gene14(KP1_RS00070)	-2.370392872	transcriptional regulator
gene4635(KP1_RS23135)	-2.370303903	Protein of unknown function (DUF1471)
gene3134(KP1_RS15630)	-2.368349549	Peptide chain release factor 1 directs the
gene876(KP1_RS04370)	-2.366799865	peptidoglycan synthetase ftsI
gene3734(KP1_RS18555)	-2.363847712	conserved protein
gene883(KP1_RS04405)	-2.36272378	Cell wall formation (By similarity)
gene4334(KP1_RS21605)	-2.362580913	aminopeptidase p
gene1153(KP1_RS05780)	-2.362008687	alkyl hydroperoxide reductase
gene4770(KP1_RS23780)	-2.361292333	phosphoenolpyruvate carboxylase
gene1988(KP1_RS09910)	-2.360534353	Reduces the permeability of the outer membrane to copper. Seems to be involved in the
gene621(KP1_RS03115)	-2.358077447	cytosine-specific methyltransferase
gene486(KP1_RS02430)	-2.35504131	aig2 family
gene5246(KP1_RS26200)	-2.354563577	Uncharacterized protein conserved in bacteria
gene1433(KP1_RS07180)	-2.353305072	inhibitor of vertebrate lysozyme
gene3228(KP1_RS16115)	-2.352378172	membrane protein TerC
gene835(KP1_RS04165)	-2.348500673	involved in the assembly of LPS in the outer leaflet of the outer membrane. Determines N-
gene5248(KP1_RS26210)	-2.346673867	Transposase
gene1597(KP1_RS07980)	-2.344840524	cyd operon protein YbgE
gene996(KP1_RS04990)	-2.344650884	rho-binding antiterminator
gene2307(KP1_RS11490)	-2.34372594	cytoplasmic protein
gene5193(KP1_RS25950)	-2.342154511	Protein of unknown function (DUF2384)
gene3142(KP1_RS15665)	-2.341136958	transcription activated by CRP (cyclic AMP

gene1510(KP1_RS07555)	-2.337383365	Catalyzes the radical-mediated insertion of two sulfur atoms into the C-6 and C-8 positions of
gene1047(frsA)	-2.336642669	Fermentation respiration switch protein
gene4683(KP1_RS23360)	-2.334029916	Channel that opens in response to stretch forces
gene1157(KP1_RS05805)	-2.333366063	Preprotein translocase, subunit YajC
gene1699(KP1_RS08485)	-2.33153705	glutamine ABC transporter periplasmic protein
gene919(KP1_RS04595)	-2.331294579	uncharacterized protein yacC
gene3996(KP1_RS19885)	-2.330829698	Protein of unknown function (DUF2002)
gene2867(KP1_RS14280)	-2.327599855	Destroys radicals which are normally produced
gene3290(KP1_RS16405)	-2.325445758	Involved in copper homeostasis (By similarity)
gene3806(KP1_RS18920)	-2.325412868	Part of the outer membrane protein assembly
gene4428(KP1_RS22075)	-2.324715012	Outer membrane protein tolc
gene3664(KP1_RS18190)	-2.32449937	NADH dehydrogenase subunit G
gene1302(KP1_RS06535)	-2.322847637	PPIases accelerate the folding of proteins (By
gene5128(KP1_RS25555)	-2.320191794	Required for the insertion and or proper folding and or complex formation of integral membrane
gene4641(KP1_RS23165)	-2.317850245	peptidase U62, modulator of DNA gyrase
gene101(gldA)	-2.31642885	glycerol dehydrogenase
gene5147(KP1_RS25655)	-2.316356618	Catalyzes the last two sequential reactions in the de novo biosynthetic pathway for UDP-N-acetylglucosamine (UDP- GlcNAc). The C-terminal
gene2090(KP1_RS10415)	-2.315603326	MltA-interacting protein
gene992(KP1_RS04970)	-2.314259097	Component of the acetyl coenzyme A carboxylase (ACC) complex. First, biotin carboxylase
gene4794(KP1_RS23895)	-2.313931464	pullulanase
gene3488(KP1_RS17325)	-2.313703585	Polysaccharide pyruvyl transferase
gene3640(KP1_RS18065)	-2.307188121	dehydrogenase subunit C
gene3832(KP1_RS19055)	-2.307066593	cellular component movement
gene169(KP1_RS00815)	-2.306398743	Tetrapolymerization of the monopyrrole PBG into
gene3049(KP1_RS15205)	-2.306325976	Transglycosylase-associated protein
gene3830(KP1_RS19045)	-2.304443974	Catalyzes the conversion of inosine 5'-phosphate (IMP) to xanthosine 5'-phosphate (XMP), the
gene3318(KP1_RS16540)	-2.300721232	The UvrABC repair system catalyzes the recognition and processing of DNA lesions. UvrC
gene4422(KP1_RS22045)	-2.294141756	Antibiotic biosynthesis monooxygenase
gene1977(KP1_RS09850)	-2.292703424	Histidine triad (HIT) protein
gene3908(KP1_RS19445)	-2.289619746	Part of a stress-induced multi-chaperone system, it is involved in the recovery of the cell from
gene3481(KP1_RS17295)	-2.289617278	Glycosyl Transferase
gene4577(KP1_RS22845)	-2.28515135	RNA-binding protein
gene3788(KP1_RS18835)	-2.283634905	Ethanolamine utilization protein eutQ
gene2165(KP1_RS10800)	-2.281512017	Pseudouridine synthase
gene1525(KP1_RS07625)	-2.281291113	Leucyl-tRNA synthetase
gene1616(KP1_RS08075)	-2.281029903	homeobox protein
gene3467(KP1_RS17220)	-2.278631854	Glycosyl transferase
gene1166(KP1_RS05850)	-2.277879563	Catalyzes the formation of 6,7-dimethyl-8-ribityllumazine by condensation of 5-amino-6-(D-
gene1031(KP1_RS05160)	-2.276504816	Catalyzes the isomerization of sedoheptulose 7-
gene3740(KP1_RS18585)	-2.275509229	regulatoR
gene972(KP1_RS04875)	-2.275134811	Tetrahydrodipicolinate N-succinyltransferase
gene4940(KP1_RS24625)	-2.275039124	BAX protein
gene2356(KP1_RS11735)	-2.274239589	YqaE family transport protein
gene3100(KP1_RS15470)	-2.273595943	K07001 NTE family protein
gene2170(KP1_RS10825)	-2.272684233	Protein of unknown function (DUF2498)

gene953(KP1_RS04775)	-2.266987074	Transposase
gene4374(KP1_RS21810)	-2.265843132	Protein with unknown function (DUF469)
gene3471(KP1_RS17240)	-2.262648135	Glycosyl transferase family protein
gene2123(KP1_RS10585)	-2.260859824	Periplasmic protein
gene800(KP1_RS03995)	-2.260791758	molybdenum cofactor biosynthesis protein
gene1505(KP1_RS07530)	-2.257440909	PagP is required both for biosynthesis of hepta-acylated lipid A species containing palmitate and for resistance to cationic antimicrobial
gene1820(KP1_RS09085)	-2.256263619	beta-lactamase domain protein
gene417(KP1_RS02080)	-2.255847682	entericidin B
gene1467(KP1_RS07340)	-2.25564646	Plasmid stabilisation system protein
gene4014(KP1_RS19985)	-2.255520695	Involved in the synthesis of autoinducer 2 (AI-2) which is secreted by bacteria and is used to communicate both the cell density and the
gene4795(KP1_RS23900)	-2.253823073	Catalyzes the formation of the alpha-1,6-glucosidic linkages in glycogen by scission of a
gene2178(KP1_RS10860)	-2.252454954	Catalyzes the conversion of GTP to 2,5-diamino-
gene1604(KP1_RS08015)	-2.248437522	tol-pal system protein YbgF
gene444(KP1_RS02215)	-2.245951312	hflC protein
gene3325(KP1_RS16575)	-2.245187997	Cystine transporter subunit
gene1170(KP1_RS05870)	-2.244070548	aldo keto reductase
gene3128(chaB)	-2.240096057	Cation transport regulator
gene1303(KP1_RS06540)	-2.239511385	cysteinyl-tRNA synthetase
gene5181(KP1_RS28360)	-2.237472351	Transposase
gene741(KP1_RS03710)	-2.235407429	dna replication protein
gene3898(KP1_RS19390)	-2.233834584	Thioredoxin 2
gene1677(KP1_RS08370)	-2.232644905	inner membrane protein ybhQ
gene4789(KP1_RS23870)	-2.225475315	Catalyzes, although with low efficiency, the
gene1784(KP1_RS27540)	-2.225045773	Transcriptional regulator
gene3944(KP1_RS19625)	-2.224754508	Transcriptional regulator
gene4026(KP1_RS20045)	-2.224441894	Catalyzes the attachment of alanine to tRNA(Ala) in a two-step reaction alanine is first
gene1008(KP1_RS05050)	-2.222052026	d,d-heptose 1,7-bisphosphate phosphatase
gene154(KP1_RS00735)	-2.219230084	Catalyzes the formation of dTDP-glucose, from
gene3455(KP1_RS17160)	-2.217718565	Nad-dependent epimerase dehydratase
gene1978(KP1_RS09855)	-2.216593359	(Lipo)protein
gene4962(KP1_RS24720)	-2.211918009	glutaredoxin 3
gene4292(KP1_RS21395)	-2.210330602	Uncharacterized protein yoac
gene1857(KP1_RS09270)	-2.210018203	domain protein
gene3790(KP1_RS18845)	-2.209706097	May be involved in the formation of a specific
gene4093(KP1_RS20375)	-2.207035356	Hok Gef family protein
gene2023(KP1_RS10090)	-2.206661124	Catalyzes the 2-thiolation of uridine at the
gene5381(KP1_RS26795)	-2.204694504	Predicted nucleotide-binding protein containing
gene2542(KP1_RS12660)	-2.203232117	Lipoprotein
gene3137(KP1_RS15645)	-2.20305635	Catalyzes the phosphorylation of the position 2
gene890(KP1_RS04440)	-2.198219684	Part of the Sec protein translocase complex. Interacts with the SecYEG preprotein conducting channel. Has a central role in coupling the
gene3550(KP1_RS17635)	-2.196497365	UPF0387 membrane protein YohO
gene1952(KP1_RS09725)	-2.194532294	Lipoprotein
gene523(KP1_RS02635)	-2.19385074	endoribonuclease L-PSP
gene4953(KP1_RS24675)	-2.191468155	LF82 chromosome, complete sequence
gene1466(KP1_RS07335)	-2.190282021	Xre family transcriptional regulator
gene1202(KP1_RS06030)	-2.188994608	Peptidyl-prolyl cis-trans isomerase

gene4405(KP1_RS21960)	-2.182330677	Biopolymer transport protein exbB
gene5348(KP1_RS26640)	-2.181360791	von willebrand factor, type a
gene153(KP1_RS00730)	-2.180612644	dtdp-glucose 4,6-dehydratase
gene479(KP1_RS02395)	-2.177582865	transcriptional regulator
gene1811(KP1_RS09045)	-2.177236445	transferase activity, transferring phosphorus-
gene195(KP1_RS00955)	-2.176733413	sterol-binding domain protein
gene1630(KP1_RS08150)	-2.176159508	Catalyzes the hydrolysis of 6-
gene3096(KP1_RS15445)	-2.175203744	thymidine kinase
gene4132(KP1_RS20575)	-2.175038122	Flavodoxin
gene3321(KP1_RS16555)	-2.174879352	transcriptional regulator
gene5123(dnaA)	-2.174710416	it binds specifically double-stranded DNA at a 9
gene3742(KP1_RS18595)	-2.173505383	Catalyzes the attachment of glutamate to tRNA(Glu) in a two-step reaction glutamate is
gene1267(KP1_RS06370)	-2.172580646	SPFH domain, Band 7 family protein
gene4343(KP1_RS21650)	-2.170983225	Involved in the export of arginine. Important to
gene1673(KP1_RS08350)	-2.170005898	membrAne
gene1797(KP1_RS08975)	-2.168010744	transporter
gene4352(KP1_RS21700)	-2.16783357	Catalyzes the biosynthesis of agmatine from
gene3559(KP1_RS17680)	-2.166565164	inner membrane protein yohC
gene404(KP1_RS02015)	-2.165844147	(LipO)protein
gene4226(KP1_RS21055)	-2.165775799	Accelerates the degradation of transcripts by removing pyrophosphate from the 5’-end of
gene4314(KP1_RS21505)	-2.163512091	Thiol disulfide interchange protein (DsbC)
gene3634(KP1_RS18040)	-2.162008781	Ferredoxin
gene3095(KP1_RS15440)	-2.160125187	alcohol dehydrogenase
gene196(ubiB)	-2.159402085	Required, probably indirectly, for the
gene1173(KP1_RS05885)	-2.159041216	Bidirectionally degrades single-stranded DNA
gene3676(KP1_RS18250)	-2.159023231	UPF0304 protein
gene3997(KP1_RS19890)	-2.15844789	uncharacterized protein ygaM
gene1133(KP1_RS05675)	-2.158393431	Protein of aro operon, regulated by aroR
gene1997(KP1_RS09960)	-2.15627408	transcriptional regulator
gene2726(KP1_RS13575)	-2.155563123	30S ribosomal subunit S22
gene3793(KP1_RS18860)	-2.155163865	transketolase (EC 2.2.1.1)
gene87(KP1_RS00415)	-2.155039916	Protease subunit of a proteasome-like
gene237(KP1_RS01150)	-2.154639762	PTS system lactose cellobiose-specific
gene884(ddl)	-2.151544106	Cell wall formation (By similarity)
gene1647(KP1_RS08240)	-2.151168927	histidine utilization repressor
gene4456(KP1_RS22225)	-2.145856498	Sigma factors are initiation factors that
gene4161(KP1_RS20725)	-2.144714581	transcriptional
gene4318(KP1_RS21525)	-2.144387178	TPR repeat protein
gene1691(KP1_RS08445)	-2.141042401	UPF0379 protein ybiJ
gene3716(KP1_RS18460)	-2.140740117	UPF0381 protein
gene5105(KP1_RS25450)	-2.138791078	transport protein
gene1564(KP1_RS07820)	-2.13735363	phosphoglucomutase EC 5.4.2.2
gene83(KP1_RS00395)	-2.135145795	ec 2.7.1.11
gene998(KP1_RS05000)	-2.134734694	YaeQ family
gene922(KP1_RS04615)	-2.132889355	Hypoxanthine phosphoribosyltransferase
gene3231(KP1_RS16130)	-2.128714236	PTS system mannose-specific transporter subunit
gene4857(KP1_RS24215)	-2.128394835	phosphate transporter
gene4999(KP1_RS24905)	-2.127916656	YicC domain protein
gene4124(KP1_RS20540)	-2.127371529	In eubacteria ppGpp (guanosine 3’-diphosphate 5-’ diphosphate) is a mediator of the stringent
gene1056(KP1_RS05280)	-2.125712544	UPF0386 protein
gene1979(KP1_RS09860)	-2.12278482	Regulator of peptidoglycan synthesis that is

gene2189(KP1_RS10925)	-2.122246067	Enoyl- acyl-carrier-protein reductase NADH
gene1941(KP1_RS09675)	-2.121227142	Acidic protein msyB
gene2379(KP1_RS11845)	-2.116888532	Exported protein
gene439(KP1_RS02190)	-2.111849338	This protein is involved in the repair of mismatches in DNA. It is required for dam-
gene2181(KP1_RS10875)	-2.110748446	Tetratricopeptide repeat protein
gene1804(KP1_RS09010)	-2.110043556	This protein is one of the two subunits of integration host factor, a specific DNA-binding
gene881(KP1_RS04395)	-2.107349537	Essential cell division protein. Transports
gene4600(KP1_RS22960)	-2.105481734	modulation protein
gene2205(KP1_RS11005)	-2.105257547	phage shock protein C
gene1243(KP1_RS06240)	-2.103374805	Resistance protein
gene5171(KP1_RS25865)	-2.09474784	sam-dependent methyltransferase
gene1809(KP1_RS09035)	-2.094230593	UPF0434 protein
gene278(KP1_RS01350)	-2.091318799	Phosphohexose isomerase
gene3215(KP1_RS16045)	-2.085644191	site-determining protein
gene1817(KP1_RS09075)	-2.082403466	ErfK YbiS YcfS YnhG family protein
gene3808(KP1_RS18930)	-2.081808184	Glycine cleavage system transcriptional
gene1561(KP1_RS07800)	-2.0815868	LexA regulated protein
gene3792(KP1_RS18855)	-2.078957242	Transaldolase is important for the balance of
gene248(KP1_RS01205)	-2.070993946	Catalyzes the decarboxylation of four acetate
gene3663(KP1_RS18185)	-2.070957952	NDH-1 shuttles electrons from NADH, via FMN and iron- sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron
gene4858(KP1_RS24220)	-2.069592361	universal stress protein B
gene785(KP1_RS03925)	-2.067273759	Catabolite regulation protein A
gene1244(KP1_RS06245)	-2.06558227	RND Family Efflux Transporter MFP Subunit
gene813(KP1_RS04055)	-2.065467537	amino acids such as valine, to avoid such errors it has two additional distinct tRNA(Ile)-
gene4865(KP1_RS24255)	-2.064800675	Glutathione reductase
gene2173(KP1_RS10835)	-2.063655022	Releases the supercoiling and torsional tension of DNA, which is introduced during the DNA replication and transcription, by transiently cleaving and rejoining one strand of the DNA duplex. Introduces a single-strand break via
gene4828(KP1_RS24070)	-2.059610687	Involved in targeting and insertion of nascent membrane proteins into the cytoplasmic membrane. Acts as a receptor for the complex formed by the
gene4787(KP1_RS23860)	-2.059515721	Glycerol-3-phosphate regulon repressor
gene4662(fis)	-2.058792261	Activates ribosomal RNA transcription. Plays a
gene3545(KP1_RS17610)	-2.057177575	Atp-binding protein
gene3078(KP1_RS15345)	-2.056431583	6-phosphofructokinase
gene1823(KP1_RS09100)	-2.055887908	asparaginyl-tRNA synthetase
gene4398(KP1_RS21925)	-2.055755752	Glutathione S-transferase
gene3031(KP1_RS15110)	-2.055725598	Is able to transfer iron-sulfur clusters to apo-ferredoxin. Multiple cycles of 2Fe2S cluster formation and transfer are observed, suggesting
gene4344(KP1_RS21660)	-2.055612672	Mechanosensitive ion channel
gene4423(KP1_RS22050)	-2.054156488	DNA topoisomerase IV, subunit B
gene1645(KP1_RS08230)	-2.053562878	imidazolone-5-propionate hydrolase
gene3281(KP1_RS16360)	-2.051983077	Nuclease that resolves Holliday junction intermediates in genetic recombination. Cleaves
gene3718(KP1_RS18470)	-2.051794326	(LipO)protein
gene2710(KP1_RS13500)	-2.050628273	Osmotically inducible protein

gene5280(KP1_RS26365)	-2.050621298	Transposase
gene3926(KP1_RS19540)	-2.050096018	Involved in targeting and insertion of nascent membrane proteins into the cytoplasmic membrane. Binds to the hydrophobic signal sequence of the ribosome-nascent chain (RNC) as it emerges from
gene197(KP1_RS00965)	-2.049159034	Part of the twin-arginine translocation (Tat) system that transports large folded proteins
gene997(KP1_RS04995)	-2.047606125	UPF0253 protein
gene5108(KP1_RS25465)	-2.042660019	Heat shock protein
gene41(KP1_RS00195)	-2.040106293	Ribbon-helix-helix protein, copG family
gene1500(KP1_RS07505)	-2.039800621	alkyl hydroperoxide reductase
gene3886(KP1_RS19330)	-2.037871554	Signal peptidase I
gene1329(KP1_RS06665)	-2.03733553	lysyl-tRNA synthetase
gene4653(KP1_RS23220)	-2.036480766	Catalyzes a trans-dehydration via an enolate
gene3099(KP1_RS15465)	-2.035782147	response regulator
gene1802(KP1_RS09000)	-2.035255385	cytidine monophosphate kinase
gene3871(KP1_RS19245)	-2.033685477	nitrogen regulatory protein PII
gene1814(KP1_RS09060)	-2.033549824	Involved in chromosome condensation, segregation and cell cycle progression. May participate in facilitating chromosome segregation by
gene926(KP1_RS04635)	-2.032984094	IIa component
gene4411(KP1_RS21990)	-2.026006528	reductase
gene3130(KP1_RS15610)	-2.025945568	Phospho-2-dehydro-3-deoxyoctonate aldolase
gene5349(KP1_RS26645)	-2.025551956	Pfam:Tellurium_res
gene4377(KP1_RS21825)	-2.025079158	Could be a mediator in iron transactions between
gene3472(KP1_RS17245)	-2.022811611	ABC transporter
gene482(KP1_RS02410)	-2.022068076	inner membrane protein YtfL
gene4598(KP1_RS22950)	-2.021690541	abc transporter atp-binding protein
gene3061(KP1_RS15265)	-2.021538136	Glutathione peroxidase
gene3714(KP1_RS18450)	-2.021312602	Catalyzes the formation of a hydroxyacyl-CoA by
gene1757(KP1_RS08785)	-2.020100144	(ABC) transporter
gene1000(KP1_RS05010)	-2.015369244	Lipoprotein involved with copper homeostasis and
gene3993(KP1_RS19870)	-2.013434392	dna binding protein
gene3732(KP1_RS18545)	-2.012420077	decarboxylase
gene907(aceF)	-2.009935051	Dihydrolipoamide acetyltransferase
gene1172(KP1_RS05880)	-2.009417522	geranyltranstransferase
gene3030(KP1_RS15105)	-2.008598502	cysteine desulfurase activator complex subunit
gene3658(KP1_RS18160)	-2.008449885	subunit m
gene3264(KP1_RS16280)	-2.005033386	Inner membrane protein YebE
gene4778(KP1_RS23820)	-2.003935534	Protein of unknown function (DUF1471)
gene2271(KP1_RS11325)	2.002603808	Type VI secretion
gene1095(KP1_RS05470)	2.003569462	cell wall organization
gene5067(KP1_RS25265)	2.004838839	transporter
gene385(KP1_RS01905)	2.005715971	in Yersinia this gene is involved in biofilm
gene2920(KP1_RS14550)	2.006190418	Transcriptional regulator, LysR family
gene2808(KP1_RS13995)	2.006193657	oxidase) subunit II
gene2829(KP1_RS14095)	2.006198445	protocatechuate 3,4-dioxygenase, alpha
gene592(KP1_RS02975)	2.006817723	F pilus assembly Type-IV secretion system for
gene851(thiP)	2.00697573	thiamine transporter membrane protein
gene1712(KP1_RS08555)	2.008351221	hydrolase, family 31
gene5116(KP1_RS25505)	2.009693504	membrAne
gene3366(KP1_RS16785)	2.011415643	synthase
gene1101(livG)	2.01145458	leucine isoleucine valine transporter, ATP-
gene3404(KP1_RS16925)	2.013649001	Conjugal transfer protein

gene141(KP1_RS00680)	2.014180026	amidohydrolase 2
gene5130(KP1_RS25565)	2.014474126	Gcn5-related n-acetyltransferase
gene241(KP1_RS01170)	2.014810848	Catalyzes the rearrangement of 1-deoxy-D-xylulose 5- phosphate (DXP) to produce the
gene3541(KP1_RS17590)	2.016234144	Xanthine uracil vitamin C permease
gene4389(KP1_RS21875)	2.017487364	cysteine synthase
gene2633(KP1_RS13115)	2.018812339	amino acid AbC transporter
gene5085(KP1_RS25350)	2.019770872	sugar phosphate antiporter
gene3266(KP1_RS16290)	2.023371676	Catalyzes two reactions the first one is the
gene2245(KP1_RS11200)	2.026072064	Short-chain dehydrogenase reductase Sdr
gene856(KP1_RS04280)	2.02636702	Sugar (and other) transporter
gene845(KP1_RS04215)	2.026610458	L-ribulose-5-phosphate 4-epimerase
gene1958(KP1_RS09755)	2.029063088	Major Facilitator
gene4470(pduC)	2.029109823	Dehydratase large subunit
gene4930(KP1_RS24580)	2.030726874	Inner membrane protein yiaH
gene587(KP1_RS02950)	2.031125114	PTS system
gene4585(KP1_RS22885)	2.036077284	Transcriptional regulator
gene5081(nepI)	2.036355964	Major Facilitator
gene3019(KP1_RS15045)	2.036448713	4-hydroxyphenylpyruvate dioxygenase
gene1103(KP1_RS05515)	2.038993993	branched-chain amino acid
gene4113(KP1_RS20475)	2.042572702	Multifunctional enzyme that catalyzes the SAM-dependent methylation of uroporphyrinogen III at position C-2 and C-7 to form precorrin-2 and
gene5075(KP1_RS25305)	2.042777161	Part of the ABC transporter complex PotABCD
gene1346(KP1_RS06760)	2.045961845	Protein of unknown function (DUF3302)
gene3961(KP1_RS19710)	2.046395699	Prolyl oligopeptidase family
gene3960(KP1_RS19705)	2.047114155	Glyoxalase/Bleomycin resistance
gene505(KP1_RS02540)	2.049519789	dihydro-orotase (EC 3.5.2.3)
gene3151(KP1_RS15710)	2.049560649	type VI secretion protein
gene3036(KP1_RS15140)	2.050644307	acriflavin resistance protein
gene4153(KP1_RS20680)	2.051069911	l-fuculose phosphate aldolase
gene2285(KP1_RS11395)	2.051901014	Aminotransferase class I and II
gene4096(KP1_RS20390)	2.052000726	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
gene3986(KP1_RS19835)	2.052624095	Transcriptional regulator
gene2746(KP1_RS13680)	2.053267623	formate dehydrogenase, alpha subunit
gene5332(KP1_RS26570)	2.057883126	nitrilase cyanide hydratase and apolipoprotein
gene3017(KP1_RS15035)	2.057983181	shikimate dehydrogenase substrate binding
gene4090(KP1_RS20360)	2.060145723	Permease protein
gene1295(KP1_RS06505)	2.060723797	carboxylase
gene2939(KP1_RS14655)	2.061396908	LysR family transcriptional regulator
gene2975(KP1_RS14820)	2.061752661	#NAME?
gene2352(KP1_RS11710)	2.063994112	transporter
gene3174(KP1_RS15830)	2.066088548	Major Facilitator Superfamily
gene1376(KP1_RS06910)	2.068398957	Oxidoreductase
gene586(KP1_RS02945)	2.06910393	PTS system glucitol sorbitol-specific IIA
gene707(KP1_RS03545)	2.069929231	Major Facilitator
gene1478(KP1_RS07395)	2.070359249	Inositol monophosphatase
gene2908(KP1_RS14490)	2.072997629	transporter
gene3170(KP1_RS15810)	2.075251889	Pseudouridine synthase
gene4043(KP1_RS20130)	2.076011434	uses NADH to detoxify nitric oxide (NO), protecting several 4Fe-4S NO-sensitive enzymes.
gene1398(KP1_RS07015)	2.0774168	ATPase, P-type (transporting), HAD superfamily,
gene4302(KP1_RS21445)	2.078894943	NAD(P)H dehydrogenase (quinone)
gene695(KP1_RS27300)	2.079863746	AraC family transcriptional regulator

gene5063(KP1_RS25245)	2.081635834	4-carboxy-4-hydroxy-2-oxoadipate aldolase
gene2003(KP1_RS09990)	2.0821687	isomerase B
gene4855(KP1_RS24205)	2.084996709	transporter
gene343(KP1_RS01680)	2.085182004	Fimbrial
gene1443(KP1_RS07230)	2.085941813	Glycerol kinase
gene3365(KP1_RS16780)	2.086361475	isochorismatase
gene3942(KP1_RS19615)	2.090254122	RND Family Efflux Transporter MFP Subunit
gene3181(KP1_RS15865)	2.090572817	(ABC) transporter
gene2753(KP1_RS13715)	2.090927359	catechol 1,2-dioxygenase
gene5055(KP1_RS25205)	2.091559293	RND efflux system, outer membrane lipoprotein
gene4111(KP1_RS20465)	2.091816301	may be the GTPase, regulating ATP sulfurylase
gene1805(KP1_RS09015)	2.098030473	DNA internalization-related competence protein
gene2197(KP1_RS10965)	2.104521094	NmrA-like family
gene3519(KP1_RS17485)	2.104525631	mandelate racemase muconate lactonizing
gene1890(KP1_RS09430)	2.104854881	Oxidoreductase
gene2774(KP1_RS13820)	2.104930336	Gcn5-related n-acetyltransferase
gene4145(KP1_RS20635)	2.105269277	transport system
gene5022(KP1_RS25030)	2.111045057	permease
gene3920(KP1_RS19505)	2.114919812	Iron-regulated membrane protein
gene4445(KP1_RS22175)	2.115896494	Urea amidohydrolase subunit gamma
gene2940(KP1_RS14660)	2.1161613	Alpha-acetolactate decarboxylase
gene4271(KP1_RS21290)	2.116889142	EamA-like transporter family
gene2346(KP1_RS11680)	2.118643612	Acetylornithine aminotransferase
gene1623(KP1_RS08115)	2.122810974	ATP-binding protein
gene1832(ssuC)	2.124254093	transporter, permease
gene4207(KP1_RS20955)	2.125003287	propanediol utilization protein
gene1484(KP1_RS07425)	2.125236064	xylulokinase (EC 2.7.1.17)
gene2919(KP1_RS14545)	2.125714341	ABC transporter Periplasmic
gene2706(KP1_RS13480)	2.126229539	cation diffusion facilitator family transporter
gene1111(tauB)	2.127895739	Part of the ABC transporter complex TauABC
gene5076(KP1_RS25310)	2.128374491	(ABC) transporter
gene5094(KP1_RS25390)	2.128741077	membrAne
gene5334(KP1_RS26580)	2.12897336	Gcn5-related n-acetyltransferase
gene1477(KP1_RS07390)	2.132012396	Regulatory protein UhpC
gene607(KP1_RS03050)	2.133331113	Inherit from proNOG: pilL protein
gene1100(KP1_RS05500)	2.135185826	(ABC) transporter
gene66(KP1_RS00315)	2.136913698	(ABC) transporter
gene2871(KP1_RS14300)	2.13828182	Nadh flavin oxidoreductase nadh oxidase
gene3609(KP1_RS17920)	2.139052593	6-aminohexanoate-dimer hydrolase
gene2349(KP1_RS11695)	2.139212435	Catalyzes the hydrolysis of N(2)-
gene292(KP1_RS01415)	2.142583922	maltose operon periplasmic protein
gene475(KP1_RS02375)	2.14276696	NmrA Family
gene3457(KP1_RS17170)	2.142976745	Catalyzes the sequential NAD-dependent
gene656(KP1_RS03295)	2.145467871	Efflux transporter, RND family, MFP subunit
gene4091(KP1_RS20365)	2.148372201	Part of the ABC transporter complex HmuTUV
gene2404(KP1_RS11970)	2.148570104	transporter
gene4664(KP1_RS23265)	2.149728098	RND Family Efflux Transporter MFP Subunit
gene651(KP1_RS03270)	2.150135317	Transcriptional regulator
gene4938(KP1_RS24615)	2.15080586	ABC transporter (Permease)
gene4419(KP1_RS22030)	2.152742767	regulatoR
gene3999(KP1_RS19900)	2.154499184	Antioxidant protein with alkyl hydroperoxidase activity. Required for the reduction of the AhpC
gene2819(KP1_RS27830)	2.156568406	tellurite resistance protein tehB
gene598(KP1_RS03005)	2.158657175	Protein of unknown function (DUF2976)

gene2955(KP1_RS14730)	2.159753341	heme exporter protein
gene4853(KP1_RS24195)	2.1606754	Transcriptional regulator
gene1348(KP1_RS06770)	2.162913748	(ABC) transporter
gene4295(KP1_RS21410)	2.164264529	Arsenical pump membrane protein
gene3182(KP1_RS15870)	2.164822338	(ABC) transporter
gene2952(KP1_RS14715)	2.164879806	Cytochrome c-type biogenesis protein ccmF
gene3508(KP1_RS17430)	2.16492901	Resistance protein
gene3164(KP1_RS15785)	2.166337375	Type IV VI secretion system protein, DotU family
gene725(KP1_RS03630)	2.167421297	Symporter
gene5086(KP1_RS25355)	2.167481267	transporter
gene2322(KP1_RS11555)	2.168903309	Phenylacetate-CoA oxygenase, PaaG subunit
gene4448(KP1_RS22190)	2.169856754	Involved in urease metallocenter assembly. Binds
gene617(KP1_RS03095)	2.170208922	Inherit from proNOG: ParB-like nuclease domain
gene4467(KP1_RS22280)	2.170389679	diol glycerol dehydratase reactivating factor
gene1403(KP1_RS07040)	2.173949282	Extracellular solute-binding protein, family 5
gene1414(KP1_RS07095)	2.176243074	amino acid AbC transporter
gene2310(KP1_RS11505)	2.177878606	DedA family
gene846(KP1_RS04220)	2.180626625	Catalyzes the conversion of L-arabinose to L-
gene3197(KP1_RS15950)	2.181279813	Pfam:DUF407
gene3432(KP1_RS17040)	2.181289613	Transcriptional regulator
gene3368(KP1_RS16795)	2.184415791	Thioesterase
gene5027(KP1_RS25055)	2.184535101	the transfer of alpha-xylosyl residue from
gene2906(KP1_RS14480)	2.18517314	chloramphenicol
gene503(KP1_RS02530)	2.186418458	membrAne
gene1362(KP1_RS06845)	2.187913486	Transcriptional regulator
gene2647(KP1_RS13185)	2.188135884	Protein of unknown function, DUF606
gene338(KP1_RS01650)	2.188779309	LrgA family
gene2005(KP1_RS10000)	2.188890491	transketolase (EC 2.2.1.1)
gene3956(KP1_RS19685)	2.188948429	Major Facilitator
gene1878(KP1_RS09375)	2.190155267	pyruvate formate lyase II activase
gene365(KP1_RS01800)	2.191947831	Phosphonate metabolism
gene555(KP1_RS02795)	2.194470205	binding-protein-dependent transport systems
gene2326(KP1_RS11575)	2.194953334	Phenylacetate-CoA oxygenase reductase, PaaK
gene2694(KP1_RS13420)	2.197218842	transporter
gene3042(KP1_RS15170)	2.197570025	transport system permease protein
gene2278(KP1_RS11360)	2.199313844	NmrA-like family
gene4279(KP1_RS21330)	2.199409156	Fimbrial protein
gene4447(KP1_RS22185)	2.200154442	Urea amidohydrolase subunit alpha
gene5061(KP1_RS25235)	2.201285978	Dehydrogenase
gene1408(KP1_RS07065)	2.202367252	allantoate amidohydrolase
gene1898(KP1_RS09470)	2.204186359	Short-chain dehydrogenase reductase sdr
gene3966(KP1_RS19735)	2.205791283	Catalyzes the formation of putrescine from
gene3943(KP1_RS19620)	2.206754279	Resistance protein
gene3523(KP1_RS17505)	2.210504389	Mannitol dehydrogenase
gene1496(KP1_RS07485)	2.210586202	Domain of unknown function (DUF3440)
gene5337(KP1_RS26595)	2.211794264	oxidoreductase
gene4194(pduD)	2.212941625	dehydratase, medium subunit
gene4079(KP1_RS20305)	2.214082818	abc transporter atp-binding protein
gene5043(KP1_RS25140)	2.215620237	Transcriptional regulator
gene613(KP1_RS03075)	2.216344953	Protein of unknown function (DUF3158)
gene726(KP1_RS03635)	2.218834217	2-oxo-3-deoxygalactonate kinase
gene243(KP1_RS01180)	2.221756729	Molybdopterin biosynthesis protein (MoeB)
gene4325(KP1_RS21560)	2.221903761	biogenesis protein
gene2775(KP1_RS13825)	2.226595409	extracellular solute-binding protein

gene1068(KP1_RS05335)	2.230250885	Dihydrolipoamide acetyltransferase
gene68(KP1_RS00325)	2.233439088	(ABC) transporter
gene2348(KP1_RS11690)	2.236718752	Catalyzes the NAD-dependent reduction of
gene1469(KP1_RS07350)	2.239078166	Iron-containing alcohol dehydrogenase
gene713(KP1_RS03575)	2.239968738	4-hydroxyphenylacetate degradation bifunctional
gene2771(KP1_RS13805)	2.240810934	extracellular solute-binding protein, family 3
gene4076(KP1_RS20290)	2.241717989	(ROK) family
gene4474(KP1_RS22315)	2.242139643	ATP cob(I)alamin adenosyltransferase
gene1451(KP1_RS07260)	2.245651737	esterase
gene1098(KP1_RS05485)	2.247750297	ABC transporter, (ATP-binding protein)
gene2942(KP1_RS14670)	2.250675204	reductase
gene5406(KP1_RS26895)	2.250986814	Siderophore biosynthesis protein
gene5335(KP1_RS26585)	2.252264986	AIR synthase related protein
gene1528(KP1_RS07640)	2.252437838	Hemolysin activator protein
gene4155(KP1_RS20695)	2.252553603	Converts the aldose L-fucose into the
gene2160(KP1_RS10775)	2.255122498	anthranilate synthase component I
gene4537(KP1_RS22640)	2.256663517	Galactitol-1-phosphate dehydrogenase
gene2394(KP1_RS11930)	2.258200281	CoA-transferase subunit A
gene2148(KP1_RS10715)	2.258492528	Short-chain dehydrogenase reductase sdr
gene649(KP1_RS03260)	2.261125451	amine oxidase
gene1344(KP1_RS06745)	2.2626762	Aminoimidazole riboside kinase
gene2658(KP1_RS13245)	2.267219691	GntR Family Transcriptional Regulator
gene2773(KP1_RS13815)	2.270745128	ABC transporter (permease)
gene1909(KP1_RS09530)	2.276465309	May reduce aminoacrylate peracid to
gene3507(KP1_RS17425)	2.277559416	Resistance protein
gene1438(KP1_RS07205)	2.279965719	reductase
gene3043(KP1_RS15175)	2.283244635	(ABC) transporter
gene655(KP1_RS03290)	2.284075342	Heavy metal efflux pump, CzcA
gene3954(KP1_RS19675)	2.28424019	Glycoside hydrolase family 3 domain protein
gene1456(KP1_RS07285)	2.284904684	transport system permease protein
gene1907(KP1_RS09520)	2.285032896	May reduce toxic product malonic semialdehyde to
gene5187(KP1_RS28365)	2.28541424	Anti-FecI sigma factor, FecR
gene3950(KP1_RS19655)	2.285620461	Major Facilitator
gene1908(KP1_RS09525)	2.286232883	May increase the rate of spontaneous hydrolysis of aminoacrylate to malonic semialdehyde.
gene4533(KP1_RS22620)	2.286860091	that is required for full activity and stability
gene1371(KP1_RS06885)	2.287750256	40-residue yvtn family beta-propeller repeat
gene2956(KP1_RS14735)	2.288026084	Required for the export of heme to the periplasm
gene4149(KP1_RS20655)	2.289919168	Catalyzes the desulfonation of aliphatic
gene4146(KP1_RS20640)	2.2965097	ABC transporter
gene1183(KP1_RS05935)	2.297409263	Fumarate reductase succinate dehydrogenase
gene2328(KP1_RS11585)	2.298885883	Enoyl-CoA hydratase
gene3982(KP1_RS19815)	2.300272661	Outer membrane usher protein
gene681(KP1_RS03420)	2.300595849	Glutathione transferase
gene712(KP1_RS03570)	2.302947817	dehydrogenase
gene4451(KP1_RS22205)	2.303121932	Inherit from proNOG: Histidine kinase
gene1834(KP1_RS09160)	2.310507698	(ABC) transporter
gene1713(KP1_RS08560)	2.310711436	hexuronate transporter
gene898(KP1_RS04485)	2.310767747	Major pilin subunit
gene2687(KP1_RS13390)	2.311836193	Protein of unknown function, DUF606
gene3367(KP1_RS16790)	2.314714897	Yersiniabactin biosynthetic protein YbtU
gene4358(KP1_RS21725)	2.314994849	endonuclease I
gene1470(KP1_RS07355)	2.316411508	(ABC) transporter
gene4063(KP1_RS20230)	2.317338489	hydrogenase nickel incorporation protein HypB

gene2643(KP1_RS13165)	2.31735391	transcriptional regulator
gene4304(KP1_RS21455)	2.318569302	carboxymuconolactone decarboxylase
gene4811(KP1_RS23975)	2.318646707	transporter permease
gene2783(KP1_RS13865)	2.320234239	receptor
gene4058(KP1_RS20210)	2.321067561	formate hydrogenlyase subunit 3
gene2752(KP1_RS13710)	2.324638393	alpha subunit
gene356(KP1_RS01755)	2.325021746	transport system, permease
gene1491(KP1_RS07460)	2.327435393	reductase
gene643(KP1_RS03230)	2.327585616	Conserved protein
gene3018(KP1_RS15040)	2.327676805	Major Facilitator
gene2733(KP1_RS13620)	2.332196013	Extracellular solute-binding protein, family 5
gene5087(KP1_RS25360)	2.332624791	sensory histidine kinase UhpB
gene1926(KP1_RS09610)	2.333251715	pirin domain protein
gene847(KP1_RS04225)	2.333806603	ribulokinase
gene5079(KP1_RS25320)	2.336147289	Involved in phosphonate degradation (By
gene4446(KP1_RS22180)	2.344699089	Urea amidohydrolase subunit beta
gene4156(KP1_RS20700)	2.345168546	L-fuculokinase
gene4206(KP1_RS20950)	2.345533713	respiratory-chain NADH dehydrogenase domain, 51
gene4046(KP1_RS20145)	2.346300244	hydrogenase maturation protein HypF
gene3196(KP1_RS15945)	2.347766141	Pfam:DUF403
gene4060(KP1_RS28115)	2.349399862	small subunit of hydrogenase-3, iron-sulfur
gene950(KP1_RS04755)	2.349976994	General secretion pathway protein C
gene3120(KP1_RS15555)	2.350268476	Nitrite reductase (NAD(P)H) large subunit
gene2898(KP1_RS14430)	2.353463665	beta-lactamase domain protein
gene2911(KP1_RS14505)	2.353971747	(ABC) transporter
gene5080(KP1_RS25325)	2.355998524	Involved in phosphonate degradation (By
gene72(KP1_RS00345)	2.356642703	Rhamnulose kinase
gene2645(KP1_RS13175)	2.35700382	drug resistance transporter, EmrB QacA subfamily
gene2815(KP1_RS14030)	2.357190568	benzoate
gene1489(KP1_RS07450)	2.360974047	(ABC) transporter
gene4780(KP1_RS23830)	2.364215979	Competence protein
gene1411(KP1_RS07080)	2.364803458	GntR family transcriptional regulator
gene2729(KP1_RS13595)	2.36517612	(ABC) transporter
gene960(KP1_RS04815)	2.368922668	periplasmic
gene939(KP1_RS04700)	2.369065581	general secretion pathway protein N
gene3015(KP1_RS15025)	2.370200138	ABC transporter
gene647(KP1_RS03250)	2.370811296	cyclopropane-fatty-acyl-phospholipid synthase
gene897(KP1_RS04480)	2.372800508	pathway protein e
gene2917(KP1_RS14535)	2.376528532	2OG-Fe(II) oxygenase
gene1457(KP1_RS07290)	2.377077166	Enterobactin exporter entS
gene804(KP1_RS04015)	2.378128636	UPF0412 protein YaaI
gene3502(KP1_RS17395)	2.378416443	signal transduction histidine kinase
gene3522(KP1_RS17500)	2.380333413	xylulokinase (EC 2.7.1.17)
gene3971(KP1_RS19760)	2.380430866	Class II aldolase
gene4142(KP1_RS20625)	2.382345204	Major Facilitator Superfamily
gene1086(KP1_RS05425)	2.383806738	transporter
gene2350(KP1_RS11700)	2.38488615	Transforms N(2)-succinylglutamate into succinate
gene4624(KP1_RS23080)	2.38860142	decarboxylase, beta
gene2669(KP1_RS13300)	2.390486886	ABC transporter (Permease)
gene3121(KP1_RS15560)	2.39084196	(ABC) transporter
gene1449(KP1_RS07255)	2.392108832	Outer membrane receptor FepA
gene1185(KP1_RS05945)	2.394190647	Fumarate reductase succinate dehydrogenase
gene2200(KP1_RS10980)	2.399864092	amidohydrolase
gene4203(KP1_RS20935)	2.400687368	ATP cob(I)alamin adenosyltransferase

gene2668(KP1_RS13295)	2.401001583	(ABC) transporter
gene2929(KP1_RS14595)	2.402157064	FAD linked oxidase
gene1374(KP1_RS06900)	2.40319099	Nucleoside
gene4055(KP1_RS20195)	2.404732729	formate hydrogenlyase complex iron-sulfur
gene1208(KP1_RS06060)	2.405325214	Cysteine synthase
gene3163(KP1_RS15780)	2.408139496	OmpA family
gene706(KP1_RS03540)	2.408465987	4-hydroxyphenylacetate catabolism regulatory
gene65(KP1_RS00310)	2.409321393	alcohol dehydrogenase
gene558(KP1_RS02810)	2.409878854	carbonic anhydrase
gene4863(KP1_RS24245)	2.40995142	Phosphoesterase, PA-phosphatase related
gene1454(KP1_RS07275)	2.410782445	Atp-binding protein
gene4141(KP1_RS20620)	2.413724176	acyl-CoA dehydrogenase
gene3190(KP1_RS15915)	2.414018021	monooxygenase
gene1410(KP1_RS07075)	2.416399287	Transcriptional regulator GntR family
gene4283(KP1_RS21350)	2.416997667	Fimbrial
gene1105(KP1_RS05530)	2.418582241	ethanolamine ammonia-lyase small subunit
gene650(KP1_RS03265)	2.418954817	short-chain dehydrogenase reductase
gene1094(KP1_RS05465)	2.420695897	Receptor
gene1881(KP1_RS09390)	2.421429756	pts system
gene4191(KP1_RS20875)	2.423739289	Microcompartments protein
gene1407(dppD)	2.424449072	(ABC) transporter
gene2725(KP1_RS13570)	2.425494567	Beta-lactamase domain-containing protein
gene708(KP1_RS03550)	2.425648998	Catalyzes the reversible retro-aldol cleavage of
gene4468(KP1_RS22285)	2.426024178	Dehydratase small subunit
gene2778(KP1_RS13840)	2.43041159	Luciferase family
gene714(KP1_RS03580)	2.431292921	4-hydroxyphenylacetate degradation
gene2644(KP1_RS13170)	2.433429201	Multidrug resistance protein
gene4012(KP1_RS19975)	2.435675139	Catalyzes the condensation of the acetyl group of acetyl-CoA with 3-methyl-2-oxobutanoate (2-
gene5405(KP1_RS26890)	2.435842977	Siderophore biosynthesis protein
gene2924(KP1_RS14570)	2.439266878	endoribonuclease
gene2776(KP1_RS13830)	2.439803823	monooxygenase
gene3191(KP1_RS15920)	2.441843538	ABC phosphate phosphonate transporter,
gene1409(KP1_RS07070)	2.442321285	EamA-like transporter family
gene581(KP1_RS02920)	2.443595576	outer membrane usher protein
gene657(KP1_RS03300)	2.444231037	Periplasmic copper-binding protein
gene4195(pduE)	2.444591786	Dehydratase small subunit
gene3981(KP1_RS19810)	2.447234881	Fimbrial protein
gene2188(KP1_RS10915)	2.448108238	oxidoreductase
gene2330(KP1_RS11595)	2.449166518	phenylacetic acid degradation protein
gene1144(KP1_RS05730)	2.451292031	Transcriptional regulator
gene1406(KP1_RS07055)	2.453485974	oligopeptide dipeptide ABC transporter
gene1093(KP1_RS05460)	2.455363635	putative enzyme
gene1462(KP1_RS07315)	2.456800937	23-dihydro-2,3-dihydroxybenzoate dehydrogenase
gene1186(KP1_RS05950)	2.457101469	shikimate dehydrogenase substrate binding
gene1099(KP1_RS05490)	2.458005523	extracellular solute-binding protein, family 3
gene4088(KP1_RS20350)	2.462877417	transport protein
gene4056(hycE)	2.463177367	Hydrogenase 3, large subunit
gene3968(KP1_RS19745)	2.472026601	2OG-Fe(II) oxygenase
gene1480(KP1_RS07405)	2.473531214	cytosine deaminase
gene4449(KP1_RS22195)	2.476641685	Required for maturation of urease via the
gene346(KP1_RS01695)	2.477070193	Inner membrane protein yjcH
gene705(KP1_RS03535)	2.477728516	4-hydroxyphenylacetate 3-monooxygenase oxygenase
gene2767(KP1_RS13785)	2.47799698	(ABC) transporter

gene557(KP1_RS02805)	2.478653427	Sulfate transporter
gene612(KP1_RS03070)	2.480272239	dNA topoisomerase
gene2288(KP1_RS11410)	2.481538393	ABC transporter (permease)
gene3501(KP1_RS17390)	2.484168088	Heat shock protein
gene3972(KP1_RS19765)	2.485330168	D-isomer specific 2-hydroxyacid dehydrogenase
gene4031(KP1_RS20070)	2.486182461	(ABC) transporter
gene1114(KP1_RS05580)	2.486493508	Phospholipid Glycerol Acyltransferase
gene3002(KP1_RS14960)	2.489221634	Cysteine dioxygenase type I
gene3057(KP1_RS15245)	2.492652026	Hemin uptake protein
gene942(KP1_RS04715)	2.495792004	type II secretion system protein K
gene4848(KP1_RS24170)	2.49960727	Extracellular solute-binding protein, family 5
gene614(KP1_RS03080)	2.500098105	Domain of unknown function (DUF1845)
gene2910(KP1_RS14500)	2.501432217	(ABC) transporter
gene616(KP1_RS03090)	2.502493033	Protein of unknown function (DUF2857)
gene2250(KP1_RS11230)	2.507010699	type VI secretion protein, VC_A0114 family
gene1054(KP1_RS05275)	2.50942735	May be involved in the control of utilization of
gene3033(KP1_RS15125)	2.510092855	DoxX Family
gene4202(KP1_RS20930)	2.510691249	utilization protein
gene1910(KP1_RS09535)	2.512525086	In vivo, quickly hydrolyzes the ureidoacrylate peracid to avoid toxicity, but can also
gene3963(KP1_RS19720)	2.512612953	monooxygenase
gene2987(KP1_RS14880)	2.514205812	amino acid AbC transporter
gene1453(entF)	2.515205967	Peptide synthetase
gene2999(KP1_RS14945)	2.516021256	acyl-Coa dehydrogenase
gene363(KP1_RS01790)	2.518548056	phosphonate C-P lyase system protein PhnL
gene5046(KP1_RS25155)	2.520389826	pyridoxamine 5-phosphate
gene3957(KP1_RS19690)	2.522005785	cyclase family
gene2323(KP1_RS11560)	2.522286928	Phenylacetate-CoA oxygenase subunit PaaB
gene3148(KP1_RS15695)	2.522635705	Type VI secretion system
gene5333(KP1_RS26575)	2.525867107	radical SAM domain protein
gene896(KP1_RS04475)	2.526728706	type IV pilin biogenesis protein
gene2933(KP1_RS14625)	2.530781442	CoA-transferase subunit A
gene2351(KP1_RS11705)	2.533181907	Amino acid permease
gene4057(hycD)	2.539510066	Formate hydrogenlyase subunit 4
gene1349(KP1_RS06775)	2.543395584	transport system permease protein
gene2251(KP1_RS11235)	2.54522046	Type IV VI secretion system protein, DotU family
gene4284(KP1_RS21355)	2.546588173	FIMH SUBUNIT MANNOSE-sensitive type 1 fimbrial
gene2923(KP1_RS14565)	2.546650114	cytosine deaminase
gene2915(KP1_RS14525)	2.546839218	Major Facilitator
gene2296(KP1_RS11450)	2.550563506	DeoR family transcriptional regulator
gene1471(KP1_RS07360)	2.554204827	inner-membrane translocator
gene368(KP1_RS01815)	2.563529909	Phosphonate C-P lyase system protein PhnG
gene2252(KP1_RS11240)	2.563786923	Ompa motb domain protein
gene1835(KP1_RS09165)	2.564876578	fmn reductase
gene946(KP1_RS04735)	2.565081509	general secretion pathway protein G
gene1096(KP1_RS05475)	2.567198163	amino acid ABC transporter
gene1089(KP1_RS05440)	2.570420205	Phosphonate ABC transporter
gene2329(KP1_RS11590)	2.5714947	3-hydroxyacyl-coa dehydrogenase
gene2115(KP1_RS10540)	2.573045751	SNARE associated Golgi protein
gene576(KP1_RS02895)	2.580342629	exported protein
gene3952(KP1_RS19665)	2.581419466	monooxygenase
gene3200(KP1_RS15960)	2.582494434	receptor
gene2083(KP1_RS10375)	2.582498795	Major facilitator transporter
gene2925(KP1_RS14575)	2.585045618	K01470 creatinine amidohydrolase EC 3.5.2.10

gene1363(KP1_RS06850)	2.585439265	Major Facilitator
gene3826(KP1_RS19025)	2.585562605	Major Facilitator Superfamily
gene5054(KP1_RS25200)	2.58930002	Resistance protein
gene4147(KP1_RS20645)	2.592547944	monooxygenase
gene3005(KP1_RS14975)	2.594369702	transporter
gene2347(KP1_RS11685)	2.59466716	Arginine
gene4094(KP1_RS20380)	2.595003265	Inherit from bactNOG: cytoplasmic protein
gene940(KP1_RS04705)	2.595606592	General secretion pathway
gene1905(KP1_RS09510)	2.600575585	permease
gene1570(KP1_RS07850)	2.600982258	One of the components of the high-affinity ATP-driven potassium transport (or KDP) system,
gene387(pgaB)	2.609607158	Biofilm PGA synthesis lipoprotein PgaB
gene1097(KP1_RS05480)	2.616119429	amino acid abc transporter
gene4205(KP1_RS20945)	2.616638011	alcohol dehydrogenase
gene1110(KP1_RS05560)	2.617051411	taurine ABC transporter, periplasmic binding
gene3009(KP1_RS14995)	2.618164629	Alpha beta hydrolase
gene938(KP1_RS04695)	2.620812783	Cleaves type-4 fimbrial leader sequence and
gene2740(KP1_RS13655)	2.620912344	glyoxalase bleomycin resistance protein
gene67(KP1_RS00320)	2.626128789	(ABC) transporter
gene4148(KP1_RS20650)	2.626796683	Pyridine nucleotide-disulphide oxidoreductase
gene5062(KP1_RS25240)	2.637325197	AcnD-accessory protein PrpF
gene605(KP1_RS03040)	2.640981272	Lytic transglycosylase catalytic
gene3044(KP1_RS15180)	2.643787368	Major Facilitator Superfamily protein
gene1361(KP1_RS06840)	2.64523281	Involved in 'Ser-type' sulfatase maturation under anaerobic conditions. Catalyzes the post-
gene3969(KP1_RS19750)	2.646960667	ABC transporter substrate-binding protein
gene3006(KP1_RS14980)	2.648864618	Catalyzes the retro-aldol cleavage of 4-hydroxy-2- oxopentanoate to pyruvate and acetaldehyde.
gene658(KP1_RS03305)	2.64903439	RND efflux system, outer membrane lipoprotein
gene3007(KP1_RS14985)	2.650830563	Catalyzes the conversion of acetaldehyde to acetyl-CoA, using NAD( ) and coenzyme A. Is the
gene507(KP1_RS02550)	2.653235731	4-hydroxy-2-oxoglutarate aldolase
gene2254(KP1_RS11250)	2.653625648	Type VI secretion ATPase, ClpV1 family
gene1358(KP1_RS06825)	2.65428911	Molybdenum cofactor biosynthesis protein F
gene3959(KP1_RS19700)	2.654656865	Rieske [2Fe-2S] domain
gene1569(KP1_RS07845)	2.659276414	One of the components of the high-affinity ATP-driven potassium transport (or KDP) system,
gene945(KP1_RS04730)	2.659894528	General secretion pathway protein H
gene4849(KP1_RS24175)	2.660267025	Nickel transporter permease NikB
gene2765(KP1_RS13775)	2.666264393	binding-protein-dependent transport systems
gene1460(entE)	2.667042169	2,3-dihydroxybenzoate-AMP ligase
gene4089(KP1_RS20355)	2.669389191	periplasmic
gene2979(KP1_RS14840)	2.669703775	Catalytic subunit of the periplasmic nitrate reductase (NAP). Only expressed at high levels
gene1871(KP1_RS09340)	2.670918471	abc transporter permease protein
gene2114(KP1_RS10535)	2.673233489	Antioxidant protein with alkyl hydroperoxidase activity. Required for the reduction of the AhpC
gene2928(KP1_RS14590)	2.67355205	binding-protein-dependent transport systems
gene5056(KP1_RS25210)	2.673739635	drug resistance transporter, Bcr CflA
gene2750(KP1_RS13700)	2.673887683	Benzoate 12-dioxygenase
gene1435(KP1_RS07190)	2.674902064	Transcriptional regulator
gene648(KP1_RS03255)	2.676482606	plasmid partition ParA protein
gene362(KP1_RS01785)	2.679819759	phosphonate metabolism protein PhnM
gene2992(KP1_RS14910)	2.687263549	transport system permease protein

gene2663(KP1_RS13270)	2.69461979	Catalyzes the dehydration of inosose (2-keto-myo- inositol, 2KMI or 2,4,6 3,5-
gene5073(KP1_RS25295)	2.7020521	#NAME?
gene604(KP1_RS03035)	2.704452912	Inherit from proNOG: TRANSFER protein
gene1334(KP1_RS06690)	2.704482767	2-dehydrogenase
gene364(KP1_RS01795)	2.704759647	phosphonate C-P lyase system protein PhnK
gene553(KP1_RS02785)	2.705626545	Hydrolyzes cAMP to 5'-AMP. Plays an important
gene322(KP1_RS01580)	2.707370523	Transcriptional regulator
gene3516(KP1_RS17470)	2.711286389	binding-protein-dependent transport systems
gene3725(KP1_RS18505)	2.712560518	transporter
gene2270(KP1_RS11320)	2.712689877	type VI secretion protein, VC_A0111 family
gene2628(KP1_RS13090)	2.714999141	2-nitropropane dioxygenase
gene4444(KP1_RS22170)	2.717840295	Required for maturation of urease via the
gene2918(KP1_RS14540)	2.718703895	K03382 hydroxyatrazine ethylaminohydrolase EC
gene1911(KP1_RS09540)	2.720628206	Catalyzes the pyrimidine ring opening between N-3 and C- 4 by an unusual flavin hydroperoxide-
gene71(KP1_RS00340)	2.724458674	L-rhamnose isomerase
gene2922(KP1_RS14560)	2.727039671	vanillate o-demethylase oxidoreductase
gene2684(KP1_RS13375)	2.729724109	coenzyme PQQ biosynthesis protein PqqF
gene1405(KP1_RS07050)	2.733307267	inner membrane component
gene2660(KP1_RS13255)	2.734516952	Guanine deaminase
gene2995(KP1_RS14925)	2.736239007	(ABC) transporter
gene594(KP1_RS02985)	2.740866056	exported protein
gene2937(KP1_RS14645)	2.742723974	Citrate transporter
gene3003(KP1_RS14965)	2.745272142	Rhodanese domain protein
gene718(KP1_RS27305)	2.747886095	Oxidoreductase
gene4001(nrdI)	2.749631413	Probably involved in ribonucleotide reductase
gene2327(KP1_RS11580)	2.752091165	Enoyl-CoA hydratase
gene2682(KP1_RS13365)	2.755621743	Pyrroloquinoline quinone biosynthesis protein D
gene366(KP1_RS01805)	2.757893584	Phosphonate metabolism
gene2934(KP1_RS14630)	2.759093564	transferase, beta subunit
gene2755(KP1_RS13725)	2.760890757	Muconate
gene3948(KP1_RS19645)	2.763301223	major facilitator superfamily protein
gene2989(KP1_RS14895)	2.767292611	Transcriptional regulator
gene2994(KP1_RS14920)	2.769419345	receptor
gene606(KP1_RS03045)	2.771426076	exported protein
gene4047(KP1_RS20150)	2.771879294	electron transport protein hydN
gene1416(KP1_RS07105)	2.773370127	Dehydrogenase
gene242(KP1_RS01175)	2.77422419	thiamine biosynthesis protein ThiS
gene2289(KP1_RS11415)	2.775689251	Aromatic amino acid aminotransferase
gene2325(KP1_RS11570)	2.78066097	Phenylacetate-CoA oxygenase PaaJ subunit
gene1425(KP1_RS07145)	2.789267234	binding-protein-dependent transport systems
gene3165(KP1_RS15790)	2.790737277	type VI secretion protein, VC_A0114 family
gene3953(KP1_RS19670)	2.794436236	NAD(P)H-dependent FMN reductase
gene2991(KP1_RS14905)	2.801850634	ABC transporter (Permease)
gene3458(KP1_RS17175)	2.804768169	imidazole acetol-phosphate transaminase
gene1181(KP1_RS05925)	2.80623712	transporter
gene4282(KP1_RS21345)	2.80634091	Fimbrial
gene1833(KP1_RS09155)	2.806495211	Catalyzes the desulfonation of aliphatic
gene2909(KP1_RS14495)	2.813292317	Permease protein
gene1404(KP1_RS07045)	2.813692752	binding-protein-dependent transport systems
gene4466(KP1_RS22275)	2.814452422	glycerol uptake facilitator protein
gene1488(KP1_RS07445)	2.817616415	Permease protein
gene2073(KP1_RS10325)	2.829734007	transporter

gene4281(KP1_RS21340)	2.829767212	outer membrane usher protein
gene552(KP1_RS02780)	2.834179145	(ABC) transporter
gene2777(KP1_RS13835)	2.842572142	amidohydrolase
gene2324(KP1_RS11565)	2.844713438	Phenylacetate-CoA oxygenase, PaaI subunit
gene1482(KP1_RS07415)	2.845650183	Cytosine permease
gene3967(KP1_RS19740)	2.84724616	Xylose Isomerase Domain-Containing protein
gene2766(KP1_RS13780)	2.85007567	extracellular solute-binding protein, family 1
gene2749(benD)	2.85053	1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate
gene4150(KP1_RS20665)	2.858309434	transcriptional regulator
gene1417(KP1_RS07110)	2.862653665	Aminotransferase
gene1439(KP1_RS07210)	2.869142216	ABC transporter (Permease)
gene2990(KP1_RS14900)	2.871232712	iron compound-binding protein of ABC transporter
gene947(KP1_RS04740)	2.875735644	General secretion pathway protein F
gene1481(KP1_RS07410)	2.876630251	PucR family transcriptional regulator
gene3123(KP1_RS15570)	2.887829608	ABC-type nitrate sulfonate bicarbonate transport
gene2738(KP1_RS13645)	2.890793838	Antioxidant protein with alkyl hydroperoxidase activity. Required for the reduction of the AhpC
gene1359(KP1_RS06830)	2.898474134	short-chain dehydrogenase reductase
gene3147(KP1_RS15690)	2.903844784	type VI secretion-associated protein
gene944(KP1_RS04725)	2.906390909	General secretion pathway protein I
gene3008(KP1_RS14990)	2.915815636	hydratase
gene3149(KP1_RS15700)	2.918785697	Inherit from COG: Type VI secretion
gene2639(KP1_RS13145)	2.930665472	Protein of unknown function (DUF3225)
gene3150(KP1_RS15705)	2.934585693	type VI secretion protein, VC_A0111 family
gene2998(KP1_RS14940)	2.936750537	(ABC) transporter
gene388(KP1_RS01920)	2.937660711	outer membrane protein PgaA
gene1455(KP1_RS07280)	2.938837739	transporter, permease
gene2736(KP1_RS13635)	2.949696531	(ABC) transporter
gene2936(KP1_RS14640)	2.958389762	3-hydroxyacyl-coa dehydrogenase
gene2737(KP1_RS13640)	2.964502515	monooxygenase
gene1459(KP1_RS07300)	2.970008087	Isochorismate synthase
gene1486(KP1_RS07435)	2.971914657	pfkB family carbohydrate kinase
gene709(KP1_RS03555)	2.975177409	hydratase
gene572(KP1_RS02875)	2.980616951	DNA primase
gene4625(KP1_RS23085)	2.981484307	Oxaloacetate decarboxylase
gene2941(KP1_RS14665)	2.98675059	acetolactate synthase
gene593(KP1_RS02980)	3.023394053	(Lipo)protein
gene4062(KP1_RS20225)	3.027123291	Probably plays a role in a hydrogenase nickel
gene2735(KP1_RS13630)	3.044922266	binding-protein-dependent transport systems
gene323(KP1_RS01585)	3.050320892	Metallo-beta-lactamase superfamily
gene1380(KP1_RS06930)	3.050862957	Major Facilitator Superfamily
gene2395(KP1_RS11935)	3.059109832	CoA-transferase subunit B
gene585(KP1_RS02940)	3.060116162	Pts system, glucitol sorbitol-specific
gene2997(KP1_RS14935)	3.06448922	Substrate-binding protein
gene3011(mhpA)	3.07275453	Catalyzes the insertion of one atom of molecular
gene1891(KP1_RS09435)	3.085061942	dehydrogenase
gene2670(KP1_RS13305)	3.087518085	ABC transporter substrate-binding protein
gene595(KP1_RS02990)	3.088474027	exported protein
gene2638(KP1_RS13140)	3.090266009	Allows the formation of correctly charged Gln-tRNA(Gln) through the transamidation of
gene948(KP1_RS04745)	3.094409358	pathway protein e
gene2583(KP1_RS12865)	3.098849103	Aldo/keto reductase family
gene2926(KP1_RS14580)	3.106654927	(ABC) transporter
gene609(KP1_RS03060)	3.139644493	Protein of unknown function (DUF3577)

gene3122(KP1_RS15565)	3.141950995	nitrate ABC transporter
gene2996(KP1_RS14930)	3.144932134	Binding-protein-dependent transport systems,
gene4201(KP1_RS20925)	3.147887854	Propanediol utilization
gene1087(KP1_RS05430)	3.155096191	Phosphonate ABC transporter
gene943(KP1_RS04720)	3.181197046	General secretion pathway protein J
gene941(KP1_RS04710)	3.182744938	Involved in a type II secretion system (T2SS,
gene2935(KP1_RS14635)	3.194353564	Catalyzes the final step of fatty acid oxidation
gene4038(KP1_RS20105)	3.213916971	DNA-binding transcriptional activator GutM
gene3958(KP1_RS19695)	3.223586005	fumarylacetoacetate (FAA) hydrolase
gene693(KP1_RS03480)	3.224154864	lysine exporter protein LysE YggA
gene1182(KP1_RS05930)	3.235771863	Xylose Isomerase Domain-Containing protein
gene2636(KP1_RS13130)	3.240693405	gamma-glutamyltranspeptidase EC 2.3.2.2
gene1487(KP1_RS07440)	3.27684689	ABC transporter (Permease)
gene1184(KP1_RS05940)	3.285970325	NIPSNAP family containing protein
gene2927(KP1_RS14585)	3.317322977	(ABC) transporter
gene5053(KP1_RS25195)	3.356610409	RND Family Efflux Transporter MFP Subunit
gene1102(KP1_RS05510)	3.382701554	leucine isoleucine valine transporter permease
gene1906(KP1_RS09515)	3.440439334	Catalyzes the reduction of FMN to FMNH2 which is
gene282(KP1_RS01370)	3.457999519	Branched-chain amino acid transport protein
gene3010(mhpB)	3.47806858	Catalyzes the non-heme iron(II)-dependent oxidative cleavage of 2,3-
gene1458(KP1_RS07295)	3.520423205	Iron-enterobactin transporter periplasmic
gene4000(KP1_RS19905)	3.537082659	Glutaredoxin-like protein
gene2734(KP1_RS13625)	3.537798247	binding-protein-dependent transport systems
gene369(KP1_RS01820)	3.609180416	Transcriptional regulator
gene367(KP1_RS01810)	3.869971054	Carbon-phosphorus lyase complex subunit
gene4064(KP1_RS20235)	4.052735038	hydrogenase assembly chaperone
gene4059(KP1_RS20215)	4.085266839	small subunit of hydrogenase-3, iron-sulfur