Supplementary Table 2. List of the 373 KO genes with different prevalence among the clinical states and between T2DM and ND

KO gene ID	KO genes name	Microbial complex based on Socransky's designation
K01812	uxaC glucuronate isomerase	red complex
K01192	E3.2.1.25, MANBA, manB beta-mannosidase	red complex
K01815	kduI 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase	red complex
K10532	HGSNAT heparan-alpha-glucosaminide N-acetyltransferase	red complex
K05989	ramA alpha-L-rhamnosidase	red complex
K01194	TREH, treA, treF alpha,alpha-trehalase	red complex
K00041	uxaB tagaturonate reductase	red complex
K01051	E3.1.1.11 pectinesterase	red complex
K12500	tesC thioesterase III	red complex
K06139	pqqE pyrroloquinoline quinone biosynthesis protein E	red complex
K00096	araM, egsA glycerol-1-phosphate dehydrogenase [NAD(P)+]	red complex
K07115	rlmJ 23S rRNA (adenine2030-N6)-methyltransferase	red complex
K03568	tldD TldD protein	red complex
K01147	rnb exoribonuclease II	red complex
K03215	rumA 23S rRNA (uracil1939-C5)-methyltransferase	red complex
K03592	pmbA PmbA protein	red complex
K02427	rlmE, rrmJ, ftsJ 23S rRNA (uridine2552-2'-O)-methyltransferase	red complex
K02397	flgL flagellar hook-associated protein 3 FlgL	red complex
K01053	E3.1.1.17, gnl, RGN gluconolactonase	red complex
K03473	pdxB erythronate-4-phosphate dehydrogenase	red complex
K01850	E5.4.99.5 chorismate mutase	red complex
K11527	K11527 two-component system, sensor histidine kinase and response regulator	red complex
K10697	rpaA two-component system, OmpR family, response regulator RpaA	red complex
K02420	fliQ flagellar biosynthetic protein FliQ	red complex
K06968	rlmM 23S rRNA (cytidine2498-2'-O)-methyltransferase	red complex
K03214	yfiF, trmG RNA methyltransferase, TrmH family	red complex
K04770	lonH Lon-like ATP-dependent protease	red complex
K05979	comB 2-phosphosulfolactate phosphatase	red complex
K00803	AGPS, agpS alkyldihydroxyacetonephosphate synthase	red complex
K13403	MTHFD2 methylenetetrahydrofolate dehydrogenase(NAD+) / 5,10-methenyltetrahydrofolate cyclohydrolase	red complex
K02422	fliS flagellar protein FliS	red complex
K12343	SRD5A1 3-oxo-5-alpha-steroid 4-dehydrogenase 1	red complex
K01905	acdA acetate---CoA ligase (ADP-forming) subunit alpha	red complex
K09011	cimA (R)-citramalate synthase	red complex
K10976	ERO1LB ERO1-like protein beta	red complex
K00274	MAO, aofH monoamine oxidase	red complex
K06931	K06931 uncharacterized protein	red complex
K00179	iorA indolepyruvate ferredoxin oxidoreductase, alpha subunit	red complex
K01035	atoA acetate CoA/acetoacetate CoA-transferase beta subunit	red complex
K13043	argF N-succinyl-L-ornithine transcarbamylase	red complex
K03047	rpoD DNA-directed RNA polymerase subunit D	red complex
K13809	CMPK2 UMP-CMP kinase 2, mitochondrial	red complex
K09770	K09770 uncharacterized protein	red complex
K09768	K09768 uncharacterized protein	red complex
K01400	nprE bacillolysin	red complex
K08787	STE13 dipeptidyl aminopeptidase Ste13	red complex
K08138	xylE MFS transporter, SP family, xylose:H+ symportor	red complex
K00180	iorB indolepyruvate ferredoxin oxidoreductase, beta subunit	red complex
K07096	K07096 uncharacterized protein	red complex
K00729	ALG5 dolichyl-phosphate beta-glucosyltransferase	red complex
K02852	wecG, rffM UDP-N-acetyl-D-mannosaminouronate:lipid I N-acetyl-D-mannosaminouronosyltransferase	red complex
K07752	CPD carboxypeptidase D	red complex
K08586	tpr thiol protease	red complex
K01213	E3.2.1.67 galacturan 1,4-alpha-galacturonidase	red complex
K08737	MSH6 DNA mismatch repair protein MSH6	red complex
K01369	LGMN legumain	red complex
K07762	PAPPA pappalysin-1	red complex
K14128	mvhG, vhuG, vhcG F420-non-reducing hydrogenase small subunit	red complex
K09024	rutF flavin reductase	red complex
K12659	ARG56 N-acetyl-gamma-glutamyl-phosphate reductase / acetylglutamate kinase	red complex
K03089	rpoH RNA polymerase sigma-32 factor	red complex
K00993	EPT1 ethanolaminephosphotransferase	red complex
K00608	pyrBI aspartate carbamoyltransferase	red complex
K01039	gctA glutaconate CoA-transferase, subunit A	orange complex
K01040	gctB glutaconate CoA-transferase, subunit B	orange complex
K00437	hydB [NiFe] hydrogenase large subunit	orange complex

K02834	rbfA ribosome-binding factor A	orange complex
K04757	rsbW serine/threonine-protein kinase RsbW	orange complex
K07793	tctA putative tricarboxylic transport membrane protein	orange complex
K01452	E3.5.1.41 chitin deacetylase	orange complex
K13378	nuoCD NADH-quinone oxidoreductase subunit C/D	orange complex
K01477	alc, ALLC allantoicase	orange complex
K05591	dbpA ATP-independent RNA helicase DbpA	orange complex
K01299	E3.4.17.19 carboxypeptidase Taq	orange complex
K07050	AARSD1, ALAX misacylated tRNA(Ala) deacylase	orange complex
K00385	asrC anaerobic sulfite reductase subunit C	orange complex
K00929	buk butyrate kinase	orange complex
K01114	plc phospholipase C	orange complex
K07000	K07000 uncharacterized protein	orange complex
K03296	TC.HAE1 hydrophobic/amphiphilic exporter-1 (mainly G- bacteria), HAE1 family	orange complex
K01884	cysS1 cysteinyl-tRNA synthetase, unknown class	orange complex
K06669	SMC3, CSPG6 structural maintenance of chromosome 3 (chondroitin sulfate proteoglycan 6)	orange complex
K09826	irr Fur family transcriptional regulator, iron response regulator	orange complex
K01858	INO1, ISYNA1 myo-inositol-1-phosphate synthase	orange complex
K02850	waaY, rfaY heptose II phosphotransferase	orange complex
K01753	dsdA D-serine dehydratase	orange complex
K00551	PEMT phosphatidylethanolamine/phosphatidyl-N-methylethanolamine N-methyltransferase	orange complex
K00830	AGXT alanine-glyoxylate transaminase / serine-glyoxylate transaminase / serine-pyruvate transaminase	orange complex
K00078	DHDH dihydrodiol dehydrogenase / D-xylose 1-dehydrogenase (NADP)	orange complex
K01706	gudD glucarate dehydratase	orange complex
K08297	caiA crotonobetainyl-CoA dehydrogenase	orange complex
K00030	IDH3 isocitrate dehydrogenase (NAD+)	orange complex
K00685	ATE1 arginyl-tRNA---protein transferase	orange complex
K01580	E4.1.1.15, gadB, gadA, GAD glutamate decarboxylase	orange complex
K03716	splB spore photoproduct lyase	orange complex
K05834	rhtB homoserine/homoserine lactone efflux protein	orange complex
K05972	AXE1 acetylxylan esterase	orange complex
K00011	AKR1B aldehyde reductase	orange complex
K11931	pgaB poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase	orange complex
K02365	ESP1 separase	orange complex
K00441	frhB coenzyme F420 hydrogenase subunit beta	orange complex
K13040	ttrS two-component system, LuxR family, sensor histidine kinase TtrS	orange complex
K01026	pct propionate CoA-transferase	orange complex
K02478	K02478 two-component system, LytTR family, sensor kinase	orange complex
K00696	E2.4.1.14 sucrose-phosphate synthase	orange complex
K01920	gshB glutathione synthase	orange complex
K12368	dppA dipeptide transport system substrate-binding protein	orange complex
K01141	sbcB, exoI exodeoxyribonuclease I	orange complex
K12655	OTUD5, DUBA OTU domain-containing protein 5	orange complex
K06152	E1.1.99.3G gluconate 2-dehydrogenase gamma chain	orange complex
K13541	cbiGH-cobJ cobalt-precorrin 5A hydrolase / precorrin-3B C17-methyltransferase	> 1 microbial complex
K01082	cysQ, MET22, BPNT1 3'(2'), 5'-bisphosphate nucleotidase	> 1 microbial complex
K10556	lsrC AI-2 transport system permease protein	> 1 microbial complex
K09769	K09769 uncharacterized protein	> 1 microbial complex
K05966	citG triphosphoribosyl-dephospho-CoA synthase	> 1 microbial complex
K13006	wbqR UDP-perosamine 4-acetyltransferase	> 1 microbial complex
K09695	nodI lipooligosaccharide transport system ATP-binding protein	> 1 microbial complex
K11788	ADE5 phosphoribosylamine--glycine ligase / phosphoribosylformylglycinamidine cyclo-ligase	> 1 microbial complex
K06883	K06883 uncharacterized protein	> 1 microbial complex
K00590	E2.1.1.113 site-specific DNA-methyltransferase (cytosine-N4-specific)	> 1 microbial complex
K07319	yhdJ adenine-specific DNA-methyltransferase	> 1 microbial complex
K13819	K13819 NifU-like protein	> 1 microbial complex
K13993	HSP20 HSP20 family protein	> 1 microbial complex
K01218	gmuG mannan endo-1,4-beta-mannosidase	> 1 microbial complex
K01023	assT arylsulfate sulfotransferase	> 1 microbial complex
K09788	prpF 2-methylaconitate isomerase	> 1 microbial complex
K07133	K07133 uncharacterized protein	> 1 microbial complex
K00207	DPYD dihydropyrimidine dehydrogenase (NADP+)	> 1 microbial complex
K01277	DPP3 dipeptidyl-peptidase III	> 1 microbial complex
K08676	tri tricorn protease	> 1 microbial complex
K11126	TERT, EST2 telomerase reverse transcriptase	> 1 microbial complex
K07755	AS3MT arsenite methyltransferase	> 1 microbial complex
K07458	vsr DNA mismatch endonuclease, patch repair protein	> 1 microbial complex
K01715	crt enoyl-CoA hydratase	> 1 microbial complex
K07240	chrA chromate transporter	> 1 microbial complex
K11381	bkdA 2-oxoisovalerate dehydrogenase E1 component	> 1 microbial complex
K01860	E5.5.1.7 chloromuconate cycloisomerase	> 1 microbial complex
K00074	paaH, hbd, fadB, mmgB 3-hydroxybutyryl-CoA dehydrogenase	> 1 microbial complex

K01209	abfA alpha-N-arabinofuranosidase	> 1 microbial complex
K03649	mug double-stranded uracil-DNA glycosylase	> 1 microbial complex
K01201	GBA, srfJ glucosylceramidase	> 1 microbial complex
K00842	E2.6.1.-E, patB aminotransferase	> 1 microbial complex
K12452	ascC, ddhC, rfbH CDP-4-dehydro-6-deoxyglucose reductase, E1	> 1 microbial complex
K01083	E3.1.3.8 3-phytase	> 1 microbial complex
K00283	gcvPB glycine dehydrogenase subunit 2	> 1 microbial complex
K00282	gcvPA glycine dehydrogenase subunit 1	> 1 microbial complex
K04070	pflX putative pyruvate formate lyase activating enzyme	> 1 microbial complex
K02588	nifH nitrogenase iron protein NifH	> 1 microbial complex
K05499	cytR LacI family transcriptional regulator, repressor for deo operon, udp, cdd, tsx, nupC, and nupG	> 1 microbial complex
K07316	mod adenine-specific DNA-methyltransferase	> 1 microbial complex
K03408	cheW purine-binding chemotaxis protein CheW	> 1 microbial complex
K11184	chr, crh catabolite repression HPr-like protein	> 1 microbial complex
K09883	cobT cobaltochelatase CobT	> 1 microbial complex
K02395	flgJ flagellar protein FlgJ	> 1 microbial complex
K02406	fliC flagellin	> 1 microbial complex
K01761	E4.4.1.11 methionine-gamma-lyase	> 1 microbial complex
K07315	rsbU_P phosphoserine phosphatase RsbU/P	> 1 microbial complex
K00042	garR, glxR 2-hydroxy-3-oxopropionate reductase	> 1 microbial complex
K02388	flgC flagellar basal-body rod protein FlgC	> 1 microbial complex
K02389	flgD flagellar basal-body rod modification protein FlgD	> 1 microbial complex
K02400	flhA flagellar biosynthesis protein FlhA	> 1 microbial complex
K06441	E1.12.7.2G ferredoxin hydrogenase gamma subunit	> 1 microbial complex
K01184	E3.2.1.15 polygalacturonase	> 1 microbial complex
K01709	rfbG CDP-glucose 4,6-dehydratase	> 1 microbial complex
K00087	ygeS, xdhA xanthine dehydrogenase molybdenum-binding subunit	> 1 microbial complex
K02419	fliP flagellar biosynthetic protein FliP	> 1 microbial complex
K08589	rgpA_B gingipain R	> 1 microbial complex
K00079	CBR1 carbonyl reductase 1	> 1 microbial complex
K02409	fliF flagellar M-ring protein FliF	> 1 microbial complex
K00318	PRODH proline dehydrogenase	> 1 microbial complex
K02556	motA chemotaxis protein MotA	> 1 microbial complex
K03412	cheB two-component system, chemotaxis family, protein-glutamate methylesterase/glutaminase	> 1 microbial complex
K09710	ybeB ribosome-associated protein	> 1 microbial complex
K03415	cheV two-component system, chemotaxis family, chemotaxis protein CheV	> 1 microbial complex
K00455	hpaD, hpcB 3,4-dihydroxyphenylacetate 2,3-dioxygenase	> 1 microbial complex
K07576	K07576 metallo-beta-lactamase family protein	> 1 microbial complex
K00294	E1.2.1.88 1-pyrroline-5-carboxylate dehydrogenase	> 1 microbial complex
K03409	cheX chemotaxis protein CheX	> 1 microbial complex
K08260	cbiZ adenosylcobinamide hydrolase	> 1 microbial complex
K00844	HK hexokinase	> 1 microbial complex
K02488	pleD two-component system, cell cycle response regulator	> 1 microbial complex
K09798	K09798 uncharacterized protein	> 1 microbial complex
K04562	flhG, fleN flagellar biosynthesis protein FlhG	> 1 microbial complex
K00483	hpaB 4-hydroxyphenylacetate 3-monooxygenase	> 1 microbial complex
K00899	mtnK 5-methylthioribose kinase	> 1 microbial complex
K00462	bphC biphenyl-2,3-diol 1,2-dioxygenase	> 1 microbial complex
K06208	aroH chorismate mutase	> 1 microbial complex
K05988	dexA dextranase	> 1 microbial complex
K10352	MYH myosin heavy chain	> 1 microbial complex
K02568	napB cytochrome c-type protein NapB	> 1 microbial complex
K04835	mal methylaspartate ammonia-lyase	> 1 microbial complex
K09459	E4.1.1.82 phosphonopyruvate decarboxylase	> 1 microbial complex
K01841	pepM phosphoenolpyruvate phosphomutase	> 1 microbial complex
K01376	UFSP2 UFM1-specific protease 2	> 1 microbial complex
K00109	L2HGDH 2-hydroxyglutarate dehydrogenase	> 1 microbial complex
K07257	spsF spore coat polysaccharide biosynthesis protein SpsF	> 1 microbial complex
K01453	nylB 6-aminohexanoate-oligomer exohydrolase	> 1 microbial complex
K13832	aroDE, DHQ-SDH 3-dehydroquinate dehydratase / shikimate dehydrogenase	> 1 microbial complex
K13503	trpEG anthranilate synthase	> 1 microbial complex
K00819	rocD, OAT ornithine--oxo-acid transaminase	> 1 microbial complex
K03170	topG, rgy reverse gyrase	> 1 microbial complex
K02396	flgK flagellar hook-associated protein 1 FlgK	> 1 microbial complex
K07662	cpxR two-component system, OmpR family, response regulator CpxR	> 1 microbial complex
K01813	rhaA L-rhamnose isomerase	> 1 microbial complex
K07443	ybaZ methylated-DNA-protein-cysteine methyltransferase related protein	> 1 microbial complex
K11333	bchX 3,8-divinyl chlorophyllide a/chlorophyllide a reductase subunit X	> 1 microbial complex
K04566	lysK lysyl-tRNA synthetase, class I	> 1 microbial complex
K00043	gbd 4-hydroxybutyrate dehydrogenase	> 1 microbial complex
K11444	wspR two-component system, chemotaxis family, response regulator WspR	> 1 microbial complex
K07318	K07318 adenine-specific DNA-methyltransferase	> 1 microbial complex

K01034	atoD acetate CoA/acetoacetate CoA-transferase alpha subunit	> 1 microbial complex
K02407	fliD flagellar hook-associated protein 2	> 1 microbial complex
K02482	K02482 two-component system, NtrC family, sensor kinase	> 1 microbial complex
K01682	acnB aconitate hydratase 2 / 2-methylisocitrate dehydratase	> 1 microbial complex
K01442	E3.5.1.24 choloylglycine hydrolase	> 1 microbial complex
K01127	E3.1.4.50 glycosylphosphatidylinositol phospholipase D	> 1 microbial complex
K07317	K07317 adenine-specific DNA-methyltransferase	> 1 microbial complex
K13016	wbpB UDP-N-acetyl-2-amino-2-deoxyglucuronate dehydrogenase	> 1 microbial complex
K12820	DHX15, PRP43 pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15/PRP43	> 1 microbial complex
K13830	ARO1 pentafunctional AROM polypeptide	> 1 microbial complex
K06917	selU tRNA 2-selenouridine synthase	> 1 microbial complex
K01047	PLA2G, SPLA2 secretory phospholipase A2	> 1 microbial complex
K13941	folKP 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase / dihydropteroate synthase	> 1 microbial complex
K02394	flgI flagellar P-ring protein precursor FlgI	> 1 microbial complex
K11541	URA2 carbamoyl-phosphate synthase / aspartate carbamoyltransferase	> 1 microbial complex
K02481	K02481 two-component system, NtrC family, response regulator	> 1 microbial complex
K01062	PLA2G7, PAFAH platelet-activating factor acetylhydrolase	> 1 microbial complex
K03646	tolA colicin import membrane protein	> 1 microbial complex
K07452	mcrB 5-methylcytosine-specific restriction enzyme B	> 1 microbial complex
K03955	NDUFAB1 NADH dehydrogenase (ubiquinone) 1 alpha/beta subcomplex 1	> 1 microbial complex
K00476	ASPH aspartate beta-hydroxylase	> 1 microbial complex
K08077	NUDT14 UDP-sugar diphosphatase	> 1 microbial complex
K09835	crtISO, crtH prolycopene isomerase	> 1 microbial complex
K13960	UBE2T, HSPC150 ubiquitin-conjugating enzyme E2 T	> 1 microbial complex
K07310	ynfF Tat-targeted selenate reductase subunit YnfF	> 1 microbial complex
K12357	NEU2_3_4 sialidase-2/3/4	> 1 microbial complex
K00273	DAO, aao D-amino-acid oxidase	> 1 microbial complex
K04086	clpL ATP-dependent Clp protease ATP-binding subunit ClpL	> 1 microbial complex
K00364	E1.7.1.7, guaC GMP reductase	> 1 microbial complex
K00076	hdhA 7-alpha-hydroxysteroid dehydrogenase	> 1 microbial complex
K14261	alaC alanine-synthesizing transaminase	> 1 microbial complex
K10906	recE exodeoxyribonuclease VIII	> 1 microbial complex
K01390	iga IgA-specific metalloendopeptidase	> 1 microbial complex
K06674	SMC2 structural maintenance of chromosome 2	> 1 microbial complex
K11994	DNASE1 deoxyribonuclease-1	> 1 microbial complex
K12140	hyfE hydrogenase-4 component E	> 1 microbial complex
K07151	STT3 dolichyl-diphosphooligosaccharide---protein glycosyltransferase	> 1 microbial complex
K12141	hyfF hydrogenase-4 component F	> 1 microbial complex
K03832	tonB periplasmic protein TonB	> 1 microbial complex
K03782	katG catalase-peroxidase	> 1 microbial complex
K05352	tarJ ribitol-5-phosphate 2-dehydrogenase (NADP+)	> 1 microbial complex
K11401	SAS2 histone acetyltransferase SAS2	> 1 microbial complex
K03483	mtlR mannitol operon transcriptional antiterminator	> 1 microbial complex
K13678	cpoA 1,2-diacylglycerol-3-alpha-glucose alpha-1,2-galactosyltransferase	> 1 microbial complex
K01464	DPYS, dht, hydA dihydropyrimidinase	purple complex
K02566	nagD NagD protein	purple complex
K01804	araA L-arabinose isomerase	purple complex
K13498	trpCF indole-3-glycerol phosphate synthase / phosphoribosylanthranilate isomerase	purple complex
K10546	ABC.GGU.S, chvE putative multiple sugar transport system substrate-binding protein	purple complex
K10548	ABC.GGU.A, gguA putative multiple sugar transport system ATP-binding protein	purple complex
K10547	ABC.GGU.P, gguB putative multiple sugar transport system permease protein	purple complex
K06182	rluF 23S rRNA pseudouridine2604 synthase	purple complex
K01720	prpD 2-methylcitrate dehydratase	purple complex
K00086	dhaT 1,3-propanediol dehydrogenase	purple complex
K12984	waaE, kdtX (heptosyl)LPS beta-1,4-glucosyltransferase	purple complex
K08100	E1.3.3.5 bilirubin oxidase	purple complex
K10038	glnQ glutamine transport system ATP-binding protein	purple complex
K09162	cld chlorite dismutase	purple complex
K03638	moaB molybdopterin adenylyltransferase	purple complex
K01474	hyuB N-methylhydantoinase B	purple complex
K02068	ABC.X2.A putative ABC transport system ATP-binding protein	purple complex
K01470	E3.5.2.10 creatinine amidohydrolase	green complex
K07753	PECR peroxisomal trans-2-enoyl-CoA reductase	green complex
K13713	purCD fusion protein PurCD	green complex
K13059	nahK, lnpB N-acetylhexosamine 1-kinase	green complex
K02636	petC cytochrome b6-f complex iron-sulfur subunit	green complex
K07664	baeR, smeR two-component system, OmpR family, response regulator BaeR	green complex
K07704	lytS two-component system, LytTR family, sensor histidine kinase LytS	green complex
K00809	DHPS, dys deoxyhypusine synthase	green complex
K13800	CMPK1, UMPK UMP-CMP kinase	green complex
K00285	dadA D-amino-acid dehydrogenase	green complex
K02558	mpl UDP-N-acetylmuramate: L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase	green complex

K12137	hyfB hydrogenase-4 component B	green complex
K11358	yhdR aspartate aminotransferase	outlier
K02299	cyoC cytochrome o ubiquinol oxidase subunit III	outlier
K02586	nifD nitrogenase molybdenum-iron protein alpha chain	outlier
K03187	ureE urease accessory protein	outlier
K03188	ureF urease accessory protein	outlier
K08253	E2.7.10.2 non-specific protein-tyrosine kinase	outlier
K01429	ureB urease subunit beta	outlier
K01721	nthA nitrile hydratase subunit alpha	outlier
K00299	ssuE FMN reductase	outlier
K11422	SETD1, SET1 histone-lysine N-methyltransferase SETD1	outlier
K02193	ccmA heme exporter protein A	outlier
K03411	cheD chemotaxis protein CheD	outlier
K03410	cheC chemotaxis protein CheC	outlier
K11782	mqnA chorismate dehydratase	outlier
K03006	RPB1, POLR2A DNA-directed RNA polymerase II subunit RPB1	outlier
K00137	prr aminobutyraldehyde dehydrogenase	outlier
K10615	HERC4 E3 ubiquitin-protein ligase HERC4	outlier
K01403	MMP9 matrix metalloproteinase-9 (gelatinase B)	outlier
K02408	fliE flagellar hook-basal body complex protein FliE	outlier
K00317	dmd-tmd dimethylamine/trimethylamine dehydrogenase	outlier
K00841	patA aminotransferase	yellow complex
K01919	gshA glutamate--cysteine ligase	yellow complex
K01641	E2.3.3.10 hydroxymethylglutaryl-CoA synthase	yellow complex
K02819	PTS-Tre-EIIC, treB PTS system, trehalose-specific IIC component	yellow complex
K07015	K07015 uncharacterized protein	yellow complex
K08484	PTS-EI.PTSP, ptsP phosphotransferase system, enzyme I, PtsP	yellow complex
K02911	RP-L32, MRPL32, rpmF large subunit ribosomal protein L32	yellow complex
K03366	butA, budC meso-butanediol dehydrogenase / (S,S)-butanediol dehydrogenase / diacetyl reductase	yellow complex
K02744	PTS-Aga-EIIA, agaF PTS system, N-acetylgalactosamine-specific IIA component	yellow complex
K02240	comFA competence protein ComFA	yellow complex
K03476	ulaG L-ascorbate 6-phosphate lactonase	yellow complex
K12997	rgpB rhamnosyltransferase	yellow complex
K03700	recU recombination protein U	yellow complex
K04045	hscC molecular chaperone HscC	yellow complex
K01635	lacD tagatose 1,6-diphosphate aldolase	yellow complex
K02082	agaS tagatose-6-phosphate ketose/aldose isomerase	yellow complex
K08310	nudB, ntpA dihydroneopterin triphosphate diphosphatase	yellow complex
K07078	K07078 uncharacterized protein	yellow complex
K03693	pbp1b penicillin-binding protein 1B	yellow complex
K05362	murE UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-L-lysine ligase	yellow complex
K07104	catE catechol 2,3-dioxygenase	yellow complex
K03342	pabBC para-aminobenzoate synthetase / 4-amino-4-deoxychorismate lyase	yellow complex
K01281	pepX X-Pro dipeptidyl-peptidase	yellow complex
K03471	rnhC ribonuclease HIII	yellow complex
K02771	PTS-Fru1-EIID, levG PTS system, fructose-specific IID component	yellow complex
K00712	tagE poly(glycerol-phosphate) alpha-glucosyltransferase	yellow complex
K05363	murM serine/alanine adding enzyme	yellow complex
K12556	pbp2X penicillin-binding protein 2X	yellow complex
K03346	dnaB replication initiation and membrane attachment protein	yellow complex
K08234	yaeR glyoxylase I family protein	yellow complex
K01220	E3.2.1.85, lacG 6-phospho-beta-galactosidase	yellow complex
K08643	zmpB zinc metalloprotease ZmpB	yellow complex
K02786	PTS-Lac-EIIA, lacF PTS system, lactose-specific IIA component	yellow complex
K13549	btrN 2-deoxy-scyllo-inosamine dehydrogenase (SAM-dependent)	yellow complex
K12663	ECH1 Delta3,5-Delta2,4-dienoyl-CoA isomerase	yellow complex
K07706	agrC, blpH, fsrC two-component system, LytTR family, sensor histidine kinase AgrC	yellow complex
K01699	pduC propanediol dehydratase large subunit	yellow complex
K03825	yhhY putative acetyltransferase	yellow complex
K11209	yghU, yfcG GSH-dependent disulfide-bond oxidoreductase	yellow complex
K02791	PTS-MalGlc-EIIC, malX PTS system, maltose/glucose-specific IIC component	yellow complex
K10681	saeS two-component system, OmpR family, sensor histidine kinase SaeS	yellow complex
K03697	clpE ATP-dependent Clp protease ATP-binding subunit ClpE	yellow complex
K08660	CNDP2 cytosolic nonspecific dipeptidase	yellow complex
K01541	E3.6.3.10 H+/K+-exchanging ATPase	yellow complex
K01261	pepA glutamyl aminopeptidase	yellow complex
K01215	dexB glucan 1,6-alpha-glucosidase	yellow complex
K01230	MAN1 mannosyl-oligosaccharide alpha-1,2-mannosidase	yellow complex
K02614	paaI acyl-CoA thioesterase	yellow complex
K02788	PTS-Lac-EIIC, lacE PTS system, lactose-specific IIC component	yellow complex
K00158	E1.2.3.3, poxL pyruvate oxidase	yellow complex
K11204	GCLC glutamate--cysteine ligase catalytic subunit	yellow complex

K00690	E2.4.1.7 sucrose phosphorylase	yellow complex
K03095	sprL SprT-like protein	yellow complex
K02236	comC leader peptidase (prepilin peptidase) / N-methyltransferase	yellow complex
K00669	AANAT arylalkylamine N-acetyltransferase	yellow complex
K00687	pbp2B, penA penicillin-binding protein 2B	yellow complex
K01598	PPCDC, coaC phosphopantothenoylcysteine decarboxylase	yellow complex
K05593	aadK aminoglycoside 6-adenylyltransferase	yellow complex
K13522	K13522, nadM bifunctional NMN adenylyltransferase/nudix hydrolase	yellow complex
K12996	rgpA rhamnosyltransferase	yellow complex
K11067	NAGS N-acetylglutamate synthase	yellow complex
K00105	E1.1.3.21 alpha-glycerophosphate oxidase	yellow complex
K12554	murN alanine adding enzyme	yellow complex
K01922	PPCS, COAB phosphopantothenate---cysteine ligase (ATP)	yellow complex
K00093	mdh methanol dehydrogenase	yellow complex
K02745	PTS-Aga-EIIB, agaV PTS system, N-acetylgalactosamine-specific IIB component	yellow complex
K01150	endA deoxyribonuclease I	yellow complex
K00897	aphA kanamycin kinase	yellow complex
K02747	PTS-Aga-EIID, agaE PTS system, N-acetylgalactosamine-specific IID component	yellow complex
K03827	yjaB putative acetyltransferase	yellow complex