Supplemental Table S8. Complete list of KEGG pathways in the identified succinylated proteins.

mtu01100 Metabolic pathways - Mycobacterium tuberculosis H37Rv (222)

ncbi-gi:1560714	mtu:Rv0002	dnaN	DNA polymerase III (beta chain) DnaN (DNA nucleotidyltransferase)
ncbi-gi:1560720	mtu:Rv0066c	icd2	Probable isocitrate dehydrogenase [NADP] Icd2 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1560727	mtu:Rv0131c	fadE1	Probable acyl-CoA dehydrogenase FadE1
ncbi-gi:1560729	mtu:Rv0154c	fadE2	Probable acyl-CoA dehydrogenase FadE2
ncbi-gi:1560729	mtu:Rv0155	pntAa	Probable N catalytic part] (pyridine nucleotide transhydrogenase subunit alpha) (nicotinamide nucleotide transhydrogenase subunit alpha)
ncbi-gi:1560733	mtu:Rv0189c	ilvD	Probable dihydroxy-acid dehydratase IlvD (dad)
ncbi-gi:1560735	mtu:Rv0211	pckA	Probable iron-regulated phosphoenolpyruvate carboxykinase [GTP] PckA (phosphoenolpyruvate carboxylase) (PEPCK)(pep carboxykinase)
ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560737	mtu:Rv0231	fadE4	Probable acyl-CoA dehydrogenase FadE4
ncbi-gi:5711670	mtu:Rv0234c	gabD1	Succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD1
ncbi-gi:1560738	mtu:Rv0242c	fabG4	Probable 3-oxoacyl-[acyl-carrier protein] reductase FabG4 (3-ketoacyl-acyl carrier protein reductase)
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560738	mtu:Rv0247c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560738	mtu:Rv0248c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560747	mtu:Rv0334	rmlA	Alpha-D-glucose-1-phosphate thymidylyltransferase RmlA (dTDP-glucose synthase) (dTDP-glucose pyrophosphorylase)
ncbi-gi:1560749	mtu:Rv0357c	purA	Probable adenylosuccinate synthetase PurA (imp--aspartate ligase) (ADSS) (ampsase)
ncbi-gi:1560750	mtu:Rv0363c	fba	Probable fructose-bisphosphate aldolase Fba
ncbi-gi:1560753	mtu:Rv0389	purT	Probable phosphoribosylglycinamide formyltransferase 2 PurT (GART 2) (gar transformylase 2) (5'-phosphoribosylglycinamide transformylase 2) (formate-dependent gar transformylase)
ncbi-gi:1560753	mtu:Rv0391	metZ	Probable O-succinylhomoserine sulfhydrylase MetZ (OSH sulfhydrylase)
ncbi-gi:1560754	mtu:Rv0400c	fadE7	Acyl-CoA dehydrogenase FadE7
ncbi-gi:1560754	mtu:Rv0408	pta	Probable phosphate acetyltransferase Pta (phosphotransacetylase)
ncbi-gi:1560756	mtu:Rv0422c	thiD	Probable phosphomethylpyrimidine kinase ThiD (HMP-phosphate kinase) (HMP-P kinase)
ncbi-gi:1560756	mtu:Rv0423c	thiC	Probable thiamine biosynthesis protein ThiC
ncbi-gi:1560760	mtu:Rv0462	lpdC	Dihydrolipoamide dehydrogenase LpdC (lipoamide reductase (NADH)) (lipoyl dehydrogenase) (dihydrolipoyl dehydrogenase) (diaphorase)
ncbi-gi:5711673	mtu:Rv0467	icl1	Isocitrate lyase Icl (isocitrase) (isocitratase)
ncbi-gi:1560760	mtu:Rv0468	fadB2	3-hydroxybutyryl-CoA dehydrogenase FadB2 (beta-hydroxybutyryl-CoA dehydrogenase) (BHBD)
ncbi-gi:1560762	mtu:Rv0482	murB	Probable UDP-N-acetylenolpyruvoylglucosamine reductase MurB (UDP-N-acetylmuramate dehydrogenase)
ncbi-gi:5711673	mtu:Rv0489	gpm1	Probable phosphoglycerate mutase 1 Gpm1 (phosphoglyceromutase) (PGAM) (BPG-dependent PGAM)
ncbi-gi:1560764	mtu:Rv0500	proC	Probable pyrroline-5-carboxylate reductase ProC (P5CR) (P5C reductase)
ncbi-gi:1560765	mtu:Rv0510	hemC	Probable porphobilinogen deaminase HemC (PBG) (hydroxymethylbilane synthase) (HMBS) (pre-uroporphyrinogen synthase)
ncbi-gi:5711674	mtu:Rv0511	hemD	Probable uroporphyrin-III C-methyltransferase HemD (uroporphyrinogen III methylase) (urogen III methylase) (SUMT) (urogen III methylase) (UROM)
ncbi-gi:1560768	mtu:Rv0548c	menB	Naphthoate synthase MenB (dihydroxynaphthoic acid synthetase) (DHNA synthetase)
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560780	mtu:Rv0667	rpoB	DNA-directed RNA polymerase (beta chain) RpoB (transcriptase beta chain) (RNA polymerase beta subunit)
ncbi-gi:1560780	mtu:Rv0668	rpoC	DNA-directed RNA polymerase (beta' chain) RpoC (transcriptase beta' chain) (RNA polymerase beta' subunit)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560787	mtu:Rv0733	adk	Adenylate kinase Adk (ATP-AMP transphosphorylase)
ncbi-gi:1560789	mtu:Rv0753c	mmsA	Probable methylmalonate-semialdehyde dehydrogenase MmsA (methylmalonic acid semialdehyde dehydrogenase) (MMSDH)
ncbi-gi:1560790	mtu:Rv0760c		hypothetical protein
ncbi-gi:5711677	mtu:Rv0761c	adhB	Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB
ncbi-gi:1560791	mtu:Rv0772	purD	Probable phosphoribosylamine--glycine ligase PurD (GARS) (glycinamide ribonucleotide synthetase) (phosphoribosylglycinamide synthetase) (5'-phosphoribosylglycinamide synthetase)
ncbi-gi:1560791	mtu:Rv0773c	ggtA	Probable bifunctional acylase GgtA: cephalosporin acylase (GL-7ACA acylase) + gamma-glutamyltranspeptidase (GGT)
ncbi-gi:5711678	mtu:Rv0794c	lpdB	Probable oxidoreductase
ncbi-gi:1560794	mtu:Rv0809	purM	Probable phosphoribosylformylglycinamidine CYCLO-ligase PurM (AIRS) (phosphoribosyl-aminoimidazole synthetase) (air synthase)
ncbi-gi:1560795	mtu:Rv0815c	cysA2	Probable thiosulfate sulfurtransferase CysA2 (rhodanese-like protein) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)
ncbi-gi:1560799	mtu:Rv0858c	dapC	Probable N-succinyldiaminopimelate aminotransferase DapC (DAP-at)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560802	mtu:Rv0884c	serC	Possible phosphoserine aminotransferase SerC (PSAT)
ncbi-gi:1560802	mtu:Rv0889c	citA	Probable citrate synthase II CitA
ncbi-gi:1560803	mtu:Rv0896	gltA2	Probable citrate synthase I GltA2
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560808	mtu:Rv0946c	pgi	Probable glucose-6-phosphate isomerase Pgi (GPI) (phosphoglucose isomerase) (phosphohexose isomerase) (phi)
ncbi-gi:1560809	mtu:Rv0951	sucC	Probable succinyl-CoA synthetase (beta chain) SucC (SCS-beta)
ncbi-gi:1560809	mtu:Rv0952	sucD	Probable succinyl-CoA synthetase (alpha chain) SucD (SCS-alpha)
ncbi-gi:1560809	mtu:Rv0957	purH	Probable bifunctional purine biosynthesis protein PurH: phosphoribosylaminoimidazolecarboxamide formyltransferase (AICAR transformylase) (5'-phosphoribosyl-5-aminoimidazole-4-carboxamide formyltransferase) + inosinemonophosphate cyclohydrolase (imp cyclohydrolase) (inosinicase) (imp synthetase) (ATIC)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560815	mtu:Rv1017c	prsA	Probable ribose-phosphate pyrophosphokinase PrsA (phosphoribosyl pyrophosphate synthetase) (PRPP synthetase)
ncbi-gi:1560815	mtu:Rv1018c	glmU	Probable UDP-N-acetylglucosamine pyrophosphorylase GlmU
ncbi-gi:1560816	mtu:Rv1023	eno	Probable enolase Eno
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:5711682	mtu:Rv1077	cbs	Probable cystathionine beta-synthase Cbs (serine sulfhydrase) (beta-thionase) (hemoprotein H-450)
ncbi-gi:1560821	mtu:Rv1079	metB	Cystathionine gamma-synthase MetB (CGS) (O-succinylhomoserine [thiol]-lyase)
ncbi-gi:4488247	mtu:Rv1093	glyA1	Serine hydroxymethyltransferase 1 GlyA1
ncbi-gi:1560823	mtu:Rv1098c	fum	Probable fumarase Fum (fumarate hydratase)
ncbi-gi:4488247	mtu:Rv1099c	glpX	Fructose 1,6-bisphosphatase GlpX
ncbi-gi:5711682	mtu:Rv1110	lytB2	Probable LYTB-related protein LytB2
ncbi-gi:5711683	mtu:Rv1121	zwf1	Probable glucose-6-phosphate 1-dehydrogenase Zwf1 (G6PD)
ncbi-gi:1560826	mtu:Rv1122	gnd2	Probable 6-phosphogluconate dehydrogenase,decarboxylating Gnd2
ncbi-gi:1560827	mtu:Rv1133c	metE	Probable 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase MetE (methionine synthase, vitamin-B12 independent isozyme)
ncbi-gi:1560828	mtu:Rv1143	mcr	Probable alpha-methylacyl-CoA racemase Mcr (2-methylacyl-CoA racemase) (2-arylpropionyl-CoA epimerase)
ncbi-gi:1560834	mtu:Rv1201c	dapD	Tetrahydrodipicolinate N-succinyltransferase DapD
ncbi-gi:1560838	mtu:Rv1240	mdh	Probable malate dehydrogenase Mdh
ncbi-gi:1560843	mtu:Rv1295	thrC	Threonine synthase ThrC (ts)
ncbi-gi:1560844	mtu:Rv1306	atpF	Probable ATP synthase B chain AtpF
ncbi-gi:1560844	mtu:Rv1307	atpH	Probable ATP synthase delta chain AtpH
ncbi-gi:1560844	mtu:Rv1308	atpA	Probable ATP synthase alpha chain AtpA
ncbi-gi:1560844	mtu:Rv1309	atpG	Probable ATP synthase gamma chain AtpG
ncbi-gi:1560845	mtu:Rv1310	atpD	Probable ATP synthase beta chain AtpD

ncbi-gi:1560845	mtu:Rv1311	atpC	Probable ATP synthase epsilon chain AtpC
ncbi-gi:1560845	mtu:Rv1315	murA	Probable UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560846	mtu:Rv1328	glgP	Probable glycogen phosphorylase GlgP
ncbi-gi:1560849	mtu:Rv1350	fabG2	Probable 3-oxoacyl-[acyl-carrier protein] reductase FabG2 (3-ketoacyl-acyl carrier protein reductase)
ncbi-gi:1560851	mtu:Rv1379	pyrR	Probable pyrimidine operon regulatory protein PyrR
ncbi-gi:1560852	mtu:Rv1380	pyrB	Probable aspartate carbamoyltransferase PyrB (ATCase) (aspartate transcarbamylase)
ncbi-gi:1560852	mtu:Rv1383	carA	Probable carbamoyl-phosphate synthase small chain CarA (carbamoyl-phosphate synthetase glutamine chain)
ncbi-gi:5711685	mtu:Rv1384	carB	Probable carbamoyl-phosphate synthase large chain CarB (carbamoyl-phosphate synthetase ammonia chain)
ncbi-gi:1560853	mtu:Rv1391	dfp	Probable DNA/pantothenate metabolism flavoprotein homolog Dfp
ncbi-gi:1560853	mtu:Rv1392	metK	Probable S-adenosylmethionine synthetase MetK (mat) (AdoMet synthetase) (methionine adenosyltransferase)
ncbi-gi:4488247	mtu:Rv1416	ribH	Probable riboflavin synthase beta chain RibH (6,7-dimethyl-8-ribityllumazine synthase) (DMRL synthase) (lumazine synthase)
ncbi-gi:1560857	mtu:Rv1436	gap	Probable glyceraldehyde 3-phosphate dehydrogenase Gap (GAPDH)
ncbi-gi:1560857	mtu:Rv1437	pgk	Probable phosphoglycerate kinase Pgk
ncbi-gi:1560857	mtu:Rv1438	tpi	Probable triosephosphate isomerase Tpi (TIM)
ncbi-gi:1560858	mtu:Rv1448c	tal	Probable transaldolase Tal
ncbi-gi:1560858	mtu:Rv1449c	tkt	Transketolase Tkt (TK)
ncbi-gi:1560861	mtu:Rv1475c	acn	Probable iron-regulated aconitate hydratase Acn (citrate hydro-lyase) (aconitase)
ncbi-gi:1560863	mtu:Rv1492	mutA	Probable methylmalonyl-CoA mutase small subunit MutA (MCM)
ncbi-gi:1560863	mtu:Rv1493	mutB	Probable methylmalonyl-CoA mutase large subunit MutB (MCM)
ncbi-gi:1560869	mtu:Rv1559	ilvA	Probable threonine dehydratase IlvA
ncbi-gi:1560873	mtu:Rv1596	nadC	Probable nicotinate-nucleotide pyrophosphatase NadC
ncbi-gi:1560873	mtu:Rv1601	hisB	Probable imidazole glycerol-phosphate dehydratase HisB
ncbi-gi:1560874	mtu:Rv1603	hisA	Probable phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA
ncbi-gi:1560874	mtu:Rv1611	trpC	Probable indole-3-glycerol phosphate synthase TrpC
ncbi-gi:1560875	mtu:Rv1617	pykA	Probable pyruvate kinase PykA
ncbi-gi:1560876	mtu:Rv1629	polA	Probable DNA polymerase I PolA
ncbi-gi:1560876	mtu:Rv1631	coaE	Probable dephospho-CoA kinase CoaE (dephosphocoenzyme a kinase)
ncbi-gi:1560879	mtu:Rv1654	argB	Probable acetylglutamate kinase ArgB
ncbi-gi:1560879	mtu:Rv1655	argD	Probable acetylornithine aminotransferase ArgD
ncbi-gi:1560879	mtu:Rv1656	argF	Probable ornithine carbamoyltransferase, anabolic ArgF
ncbi-gi:1560883	mtu:Rv1695	ppnK	Inorganic polyphosphate/ATP-NAD kinase PpnK (poly(P)/ATP NAD kinase)
ncbi-gi:1560883	mtu:Rv1699	pyrG	Probable CTP synthase PyrG
ncbi-gi:4488247	mtu:Rv1703c		Probable catechol-O-methyltransferase
ncbi-gi:5711690	mtu:Rv1731	gabD2	Possible succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD2
ncbi-gi:1560896	mtu:Rv1832	gcvB	Probable glycine dehydrogenase GcvB (glycine decarboxylase) (glycine cleavage system P-protein)
ncbi-gi:1560897	mtu:Rv1837c	glcB	Malate synthase G GlcB
ncbi-gi:1560898	mtu:Rv1843c	guaB1	Probable inosine-5'-monophosphate dehydrogenase GuaB1(imp dehydrogenase) (IMPDH) (IMPD)
ncbi-gi:1560900	mtu:Rv1872c	lldD2	Possible L-lactate dehydrogenase (cytochrome) LldD2
ncbi-gi:1560904	mtu:Rv1908c	katG	Catalase-peroxidase-peroxynitritase T KatG
ncbi-gi:1560913	mtu:Rv2002	fabG3	Possible 20-beta-hydroxysteroid dehydrogenase FabG3 (cortisone reductase) ((R)-20-hydroxysteroid dehydrogenase)
ncbi-gi:1560916	mtu:Rv2029c	pfkB	6-phosphofructokinase PfkB (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1560919	mtu:Rv2054		hypothetical protein
ncbi-gi:1560925	mtu:Rv2121c	hisG	ATP phosphoribosyltransferase HisG
ncbi-gi:1560931	mtu:Rv2178c	aroG	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase AroG (DAHP synthetase, phenylalanine-repressible)
ncbi-gi:1560931	mtu:Rv2182c		1-acylglycerol-3-phosphate O-acyltransferase
ncbi-gi:1560932	mtu:Rv2187	fadD15	Long-chain-fatty-acid-CoA ligase FadD15 (fatty-acid-CoA synthetase) (fatty-acid-CoA synthase)
ncbi-gi:1560933	mtu:Rv2195	qcrA	Probable rieske iron-sulfur protein QcrA
ncbi-gi:1560933	mtu:Rv2196	qcrB	Probable ubiquinol-cytochrome C reductase QcrB (cytochrome B subunit)
ncbi-gi:1560933	mtu:Rv2200c	ctaC	Probable transmembrane cytochrome C oxidase (subunit II) CtaC
ncbi-gi:1560933	mtu:Rv2202c	adoK	Adenosine kinase
ncbi-gi:1560934	mtu:Rv2210c	ilvE	Branched-chain amino acid transaminase IlvE
ncbi-gi:1560934	mtu:Rv2211c	gcvT	Probable aminomethyltransferase GcvT (glycine cleavage system T protein)
ncbi-gi:1560935	mtu:Rv2213	pepB	Probable aminopeptidase PepB
ncbi-gi:1560935	mtu:Rv2215	dlaT	DlaT, dihydrolipoamide acyltransferase, E2 component of pyruvate dehydrogenase
ncbi-gi:1560935	mtu:Rv2220	glnA1	Glutamine synthetase GlnA1 (glutamine synthase) (GS-I)
ncbi-gi:1560935	mtu:Rv2222c	glnA2	Probable glutamine synthetase GlnA2 (glutamine synthase) (GS-II)
ncbi-gi:4488247	mtu:Rv2241	aceE	Pyruvate dehydrogenase E1 component AceE (pyruvate decarboxylase) (pyruvate dehydrogenase) (pyruvic dehydrogenase)
ncbi-gi:1560943	mtu:Rv2296		Probable haloalkane dehalogenase
ncbi-gi:5711697	mtu:Rv2334	cysK1	Cysteine synthase a CysK1 (O-acetylserine sulfhydrylase A) (O-acetylserine (thiol)-lyase A) (CSASE A)
ncbi-gi:1560952	mtu:Rv2391	sirA	Ferredoxin-dependent sulfite reductase SirA
ncbi-gi:1560955	mtu:Rv2419c	gpgP	Glucosyl-3-phosphoglycerate phosphatase GpgP
ncbi-gi:5711699	mtu:Rv2438c	nadE	Glutamine-dependent NAD(+) synthetase NadE (NAD(+) synthase [glutamine-hydrolysing])
ncbi-gi:1560959	mtu:Rv2454c		Probable oxidoreductase (beta subunit)
ncbi-gi:1560959	mtu:Rv2455c		Probable oxidoreductase (alpha subunit)
ncbi-gi:5711699	mtu:Rv2465c	rpiB	Ribose-5-phosphate isomerase
ncbi-gi:5711699	mtu:Rv2467	pepN	Probable aminopeptidase N PepN (Lysyl aminopeptidase) (LYS-AP) (alanine aminopeptidase)
ncbi-gi:1560961	mtu:Rv2476c	gdh	Probable NAD-dependent glutamate dehydrogenase Gdh (NAD-Gdh) (NAD-dependent glutamic dehydrogenase)
ncbi-gi:1560963	mtu:Rv2495c	bkdC	Probable branched-chain keto acid dehydrogenase E2 component BkdC
ncbi-gi:1560963	mtu:Rv2501c	accA1	Probable acetyl-/propionyl-coenzyme A carboxylase alpha chain (alpha subunit) AccA1: biotin carboxylase + biotin carboxyl carrier protein (BCCP)
ncbi-gi:1560963	mtu:Rv2502c	accD1	Probable acetyl-/propionyl-CoA carboxylase (beta subunit) AccD1
ncbi-gi:1560966	mtu:Rv2524c	fas	Probable fatty acid synthase Fas (fatty acid synthetase)
ncbi-gi:1560967	mtu:Rv2537c	aroD	3-dehydroquinate dehydratase AroD (AROQ) (3-dehydroquinase) (type II dhqase)
ncbi-gi:1560967	mtu:Rv2538c	aroB	3-dehydroquinate synthase AroB
ncbi-gi:1560967	mtu:Rv2540c	aroF	Probable chorismate synthase AroF (5-enolpyruvylshikimate-3-phosphate phospholyase)
ncbi-gi:1560972	mtu:Rv2589	gabT	4-aminobutyrate aminotransferase GabT (gamma-amino-N-butyrate transaminase) (GABA transaminase) (glutamate:succinic semialdehyde transaminase) (GABA aminotransferase) (GABA-at)
ncbi-gi:1560974	mtu:Rv2607	pdxH	Probable pyridoxamine 5'-phosphate oxidase PdxH (PNP/PMP oxidase) (pyridoxinephosphate oxidase) (PNPOX) (pyridoxine 5'-phosphate oxidase)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560983	mtu:Rv2697c	dut	Probable deoxyuridine 5'-triphosphate nucleotidohydrolase Dut (dUTPase) (dUTP pyrophosphatase) (deoxyuridine 5'-triphosphatase) (dUTP diphosphatase) (deoxyuridine-triphosphatase)
ncbi-gi:1560985	mtu:Rv2713	sthA	Probable soluble pyridine nucleotide transhydrogenase SthA (STH) (NAD(P)(+) transhydrogenase [B-specific]) (nicotinamide nucleotide transhydrogenase)
ncbi-gi:1560986	mtu:Rv2726c	dapF	Probable diaminopimelate epimerase DapF (DAP epimerase)
ncbi-gi:1560989	mtu:Rv2753c	dapA	Probable dihydrodipicolinate synthase DapA (DHDPS) (dihydrodipicolinate synthetase)
ncbi-gi:1560990	mtu:Rv2765		Probable alanine rich hydrolase
ncbi-gi:1560991	mtu:Rv2773c	dapB	Dihydrodipicolinate reductase DapB (DHPR)
ncbi-gi:1560991	mtu:Rv2780	ald	Secreted L-alanine dehydrogenase Ald (40 kDa antigen) (TB43)
ncbi-gi:1560992	mtu:Rv2786c	ribF	Probable bifunctional FAD synthetase/riboflavin biosynthesis protein RibF: riboflavin kinase (flavokinase) + FMN adenylyltransferase (FAD pyrophosphorylase) (FAD synthetase)(FAD diphosphorylase) (flavin adenine dinucleotide synthetase)

ncbi-gi:4488247	mtu:Rv2790c	ltp1	Probable lipid-transfer protein Ltp1
ncbi-gi:1561000	mtu:Rv2868c	gcpE	Probable GcpE protein
ncbi-gi:1561010	mtu:Rv2965c	kdtB	Probable phosphopantetheine adenylyltransferase KdtB (pantetheine-phosphate adenylyltransferase) (PPAT) (dephospho-CoA pyrophosphorylase)
ncbi-gi:1561010	mtu:Rv2967c	pca	Probable pyruvate carboxylase Pca (pyruvic carboxylase)
ncbi-gi:5711704	mtu:Rv2992c	gltS	Glutamyl-tRNA synthetase GltS (glutamate--tRNA ligase) (glutamyl-tRNA synthase) (GLURS)
ncbi-gi:1561013	mtu:Rv2995c	leuB	Probable 3-isopropylmalate dehydrogenase LeuB (beta-IPM dehydrogenase) (IMDH) (3-IPM-DH)
ncbi-gi:5711704	mtu:Rv2996c	serA1	Probable D-3-phosphoglycerate dehydrogenase SerA1 (PGDH)
ncbi-gi:4488247	mtu:Rv3001c	ilvC	Probable KETOL-acid reductoisomerase IlvC (acetohydroxy-acid isomeroreductase) (alpha-keto-beta-hydroxylacil reductoisomerase)
ncbi-gi:1561013	mtu:Rv3002c	ilvN	Probable acetolactate synthase (small subunit) IlvN (acetohydroxy-acid synthase) (AHAS) (ALS)
ncbi-gi:5711704	mtu:Rv3003c	ilvB1	Acetolactate synthase (large subunit) IlvB1 (acetohydroxy-acid synthase)
ncbi-gi:1561014	mtu:Rv3009c	gatB	Probable glutamyl-tRNA(GLN) amidotransferase (subunit B) GatB (Glu-ADT subunit B)
ncbi-gi:1561014	mtu:Rv3010c	pfkA	Probable 6-phosphofructokinase PfkA (phosphohexokinase) (phosphofructokinase)
ncbi-gi:4488247	mtu:Rv3011c	gatA	Probable glutamyl-tRNA(GLN) amidotransferase (subunit A) GatA (Glu-ADT subunit A)
ncbi-gi:5711705	mtu:Rv3048c	nrdF2	Ribonucleoside-diphosphate reductase (beta chain) NrdF2 (ribonucleotide reductase small subunit) (R2F protein)
ncbi-gi:1561018	mtu:Rv3051c	nrdE	Ribonucleoside-diphosphate reductase (alpha chain) NrdE (ribonucleotide reductase small subunit) (R1F protein)
ncbi-gi:1561022	mtu:Rv3086	adhD	Probable zinc-type alcohol dehydrogenase AdhD (aldehyde reductase)
ncbi-gi:1561027	mtu:Rv3140	fadE23	Probable acyl-CoA dehydrogenase FadE23
ncbi-gi:1561028	mtu:Rv3149	nuoE	Probable NADH dehydrogenase I (chain E) NuoE (NADH-ubiquinone oxidoreductase chain E)
ncbi-gi:1561028	mtu:Rv3150	nuoF	Probable NADH dehydrogenase I (chain F) NuoF (NADH-ubiquinone oxidoreductase chain F)
ncbi-gi:1561035	mtu:Rv3215	entC	Probable isochorismate synthase EntC (isochorismate hydroxymutase) (enterochelin biosynthesis)
ncbi-gi:1561036	mtu:Rv3227	aroA	3-phosphoshikimate 1-carboxyvinyltransferase AroA (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS)
ncbi-gi:1561038	mtu:Rv3248c	sahH	Probable adenosylhomocysteinase SahH (S-adenosyl-L-homocysteine hydrolase) (adohcyase)
ncbi-gi:1561039	mtu:Rv3255c	manA	Probable mannose-6-phosphate isomerase ManA (phosphomannose isomerase) (phosphomannoisomerase) (PMI) (phosphohexoisomerase) (phosphohexomutase)
ncbi-gi:5711708	mtu:Rv3264c	manB	D-alpha-D-mannose-1-phosphate guanylyltransferase ManB (D-alpha-D-heptose-1-phosphate guanylyltransferase)
ncbi-gi:1561041	mtu:Rv3275c	purE	Probable phosphoribosylaminoimidazole carboxylase catalytic subunit PurE (air carboxylase) (AIRC)
ncbi-gi:1561041	mtu:Rv3276c	purK	Probable phosphoribosylaminoimidazole carboxylase ATPase subunit PurK (air carboxylase) (AIRC)
ncbi-gi:1561041	mtu:Rv3280	accD5	Probable propionyl-CoA carboxylase beta chain 5 AccD5 (pccase) (propanoyl-CoA:carbon dioxide ligase)
ncbi-gi:1561041	mtu:Rv3283	sseA	Probable thiosulfate sulfurtransferase SseA (rhodanese) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)
ncbi-gi:1561042	mtu:Rv3285	accA3	Probable bifunctional protein acetyl-/propionyl-coenzyme A carboxylase (alpha chain) AccA3: biotin carboxylase + biotin carboxyl carrier protein (BCCP)
ncbi-gi:1561045	mtu:Rv3318	sdhA	Probable succinate dehydrogenase (flavoprotein subunit) SdhA (succinic dehydrogenase) (fumarate reductase) (fumarate dehydrogenase) (fumaric hydrogenase)
ncbi-gi:1561047	mtu:Rv3339c	icd1	Probable isocitrate dehydrogenase [NADP] Icd1 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1561047	mtu:Rv3340	metC	Probable O-acetylhomoserine sulfhydrylase MetC (homocysteine synthase) (O-acetylhomoserine (thiol)-lyase) (OAH sulfhydrylase) (O-acetyl-L-homoserine sulfhydrylase)
ncbi-gi:1561049	mtu:Rv3356c	folD	Probable bifunctional protein FolD: methylenetetrahydrofolate dehydrogenase + methenyltetrahydrofolate cyclohydrolase
ncbi-gi:1561053	mtu:Rv3396c	guaA	Probable GMP synthase [glutamine-hydrolyzing] GuaA (glutamine amidotransferase) (GMP synthetase)
ncbi-gi:1561054	mtu:Rv3410c	guaB3	Probable inosine-5'-monophosphate dehydrogenase GuaB3 (imp dehydrogenase) (inosinic acid dehydrogenase) (inosinate dehydrogenase) (imp oxidoreductase) (inosine-5'-monophosphate oxidoreductase) (IMPDH) (IMPD)
ncbi-gi:1561056	mtu:Rv3432c	gadB	Probable glutamate decarboxylase GadB
ncbi-gi:1561057	mtu:Rv3436c	glmS	Probable glucosamine--fructose-6-phosphate aminotransferase [isomerizing] GlmS (hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (glucosamine-6-phosphate synthase)
ncbi-gi:1561059	mtu:Rv3457c	rpoA	Probable DNA-directed RNA polymerase (alpha chain) RpoA (transcriptase alpha chain) (RNA polymerase alpha subunit) (DNA-directed RNA nucleotidyltransferase)
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561067	mtu:Rv3535c	hsaG	Probable acetaldehyde dehydrogenase (acetaldehyde dehydrogenase [acetylating])
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:5711712	mtu:Rv3566c	nat	Arylamine N-acetyltransferase Nat (arylamine acetylase)
ncbi-gi:1561070	mtu:Rv3568c	hsaC	3,4-DHSA dioxygenase
ncbi-gi:1561070	mtu:Rv3569c	hsaD	4,9-DHSA hydrolase
ncbi-gi:1561070	mtu:Rv3570c	hsaA	Possible oxidoreductase Possible 3-hydroxy-9,10-seconandrost-1,3,5(10)-triene-9,17-dione hydroxylase
ncbi-gi:1561071	mtu:Rv3581c	ispF	Probable 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF (MECPS)
ncbi-gi:1561073	mtu:Rv3600c		hypothetical protein
ncbi-gi:1561074	mtu:Rv3609c	folE	GTP cyclohydrolase I FolE (GTP-ch-I)
ncbi-gi:5711713	mtu:Rv3634c	galE1	UDP-glucose 4-epimerase GalE1 (galactowaldenase) (UDP-galactose 4-epimerase) (uridine diphosphate galactose 4-epimerase) (uridine diphospho-galactose 4-epimerase)
ncbi-gi:1561080	mtu:Rv3667	acs	Acetyl-coenzyme A synthetase Acs (acetate--CoA ligase) (acetyl-CoA synthetase) (acetyl-CoA synthase) (acyl-activating enzyme) (acetate thiokinase) (acetyl-activating enzyme) (acetate--coenzyme A ligase) (acetyl-coenzyme A synthase)
ncbi-gi:3454620	mtu:Rv3710	leuA	2-isopropylmalate synthase LeuA (alpha-isopropylmalate synthase) (alpha-IPM synthetase) (IPMS)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561097	mtu:Rv3838c	pheA	Prephenate dehydratase PheA
ncbi-gi:1561099	mtu:Rv3858c	gltD	Probable NADH-dependent glutamate synthase (small subunit) GltD (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH)) (GLTS beta chain) (NADPH-GOGAT)
ncbi-gi:1561099	mtu:Rv3859c	gltB	Probable ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH))(NADPH-GOGAT)

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ncbi-gi:1560720	mtu:Rv0066c	icd2	Probable isocitrate dehydrogenase [NADP] Icd2 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1560727	mtu:Rv0131c	fadE1	Probable acyl-CoA dehydrogenase FadE1
ncbi-gi:1560729	mtu:Rv0154c	fadE2	Probable acyl-CoA dehydrogenase FadE2
ncbi-gi:1560733	mtu:Rv0189c	ilvD	Probable dihydroxy-acid dehydratase IlvD (dad)
ncbi-gi:1560735	mtu:Rv0211	pckA	Probable iron-regulated phosphoenolpyruvate carboxykinase [GTP] PckA (phosphoenolpyruvate carboxylase) (PEPCK)(pep carboxykinase)
ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560736	mtu:Rv0223c		Probable aldehyde dehydrogenase
ncbi-gi:1560737	mtu:Rv0231	fadE4	Probable acyl-CoA dehydrogenase FadE4
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560738	mtu:Rv0244c	fadE5	Probable acyl-CoA dehydrogenase FadE5
ncbi-gi:1560738	mtu:Rv0247c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560738	mtu:Rv0248c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560741	mtu:Rv0271c	fadE6	Probable acyl-CoA dehydrogenase FadE6
ncbi-gi:1560747	mtu:Rv0334	rmlA	Alpha-D-glucose-1-phosphate thymidylyltransferase RmlA (dTDP-glucose synthase) (dTDP-glucose pyrophosphorylase)
ncbi-gi:1560750	mtu:Rv0363c	fba	Probable fructose-bisphosphate aldolase Fba
ncbi-gi:1560753	mtu:Rv0389	purT	Probable phosphoribosylglycinamide formyltransferase 2 PurT (GART 2) (gar transformylase 2) (5'-phosphoribosylglycinamide transformylase 2) (formate-dependent gar transformylase)
ncbi-gi:1560760	mtu:Rv0462	lpdC	Dihydrolipoamide dehydrogenase LpdC (lipoamide reductase (NADH)) (lipoyl dehydrogenase) (dihydrolipoyl dehydrogenase) (diaphorase)
ncbi-gi:5711673	mtu:Rv0489	gpm1	Probable phosphoglycerate mutase 1 Gpm1 (phosphoglyceromutase) (PGAM) (BPG-dependent PGAM)
ncbi-gi:1560764	mtu:Rv0500	proC	Probable pyrroline-5-carboxylate reductase ProC (P5CR) (P5C reductase)
ncbi-gi:1560765	mtu:Rv0510	hemC	Probable porphobilinogen deaminase HemC (PBG) (hydroxymethylbilane synthase) (HMBS) (pre-uroporphyrinogen synthase)
ncbi-gi:5711674	mtu:Rv0511	hemD	Probable uroporphyrin-III C-methyltransferase HemD (uroporphyrinogen III methylase) (urogen III methylase) (SUMT) (urogen III methylase) (UROM)
ncbi-gi:1560768	mtu:Rv0548c	menB	Naphthoate synthase MenB (dihydroxynaphthoic acid synthetase) (DHNA synthetase)
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560787	mtu:Rv0733	adk	Adenylate kinase Adk (ATP-AMP transphosphorylase)
ncbi-gi:1560789	mtu:Rv0752c	fadE9	Probable acyl-CoA dehydrogenase FadE9
ncbi-gi:5711677	mtu:Rv0761c	adhB	Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB

ncbi-gi:1560791	mtu:Rv0772	purD	Probable phosphoribosylamine--glycine ligase PurD (GARS) (glycinamide ribonucleotide synthetase) (phosphoribosylglycinamide synthetase) (5'-phosphoribosylglycinamide synthetase)
ncbi-gi:5711678	mtu:Rv0794c	lpdB	Probable oxidoreductase
ncbi-gi:1560794	mtu:Rv0809	purM	Probable phosphoribosylformylglycinamidine CYCLO-ligase PurM (AIRS) (phosphoribosyl-aminoimidazole synthetase) (air synthase)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560801	mtu:Rv0873	fadE10	Probable acyl-CoA dehydrogenase FadE10
ncbi-gi:1560802	mtu:Rv0889c	citA	Probable citrate synthase II CitA
ncbi-gi:1560803	mtu:Rv0896	gltA2	Probable citrate synthase I GltA2
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560808	mtu:Rv0946c	pgi	Probable glucose-6-phosphate isomerase Pgi (GPI) (phosphoglucose isomerase) (phosphohexose isomerase) (phi)
ncbi-gi:1560809	mtu:Rv0951	sucC	Probable succinyl-CoA synthetase (beta chain) SucC (SCS-beta)
ncbi-gi:1560809	mtu:Rv0952	sucD	Probable succinyl-CoA synthetase (alpha chain) SucD (SCS-alpha)
ncbi-gi:1560809	mtu:Rv0957	purH	Probable bifunctional purine biosynthesis protein PurH: phosphoribosylaminoimidazolecarboxamide formyltransferase (AICAR transformylase) (5'-phosphoribosyl-5-aminoimidazole-4-carboxamide formyltransferase) + inosinemonophosphate cyclohydrolase (imp cyclohydrolase) (inosinicase) (imp synthetase) (ATIC)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0972c	fadE12	Acyl-CoA dehydrogenase FadE12
ncbi-gi:1560815	mtu:Rv1017c	prsA	Probable ribose-phosphate pyrophosphokinase PrsA (phosphoribosyl pyrophosphate synthetase) (PRPP synthetase)
ncbi-gi:1560815	mtu:Rv1018c	glmU	Probable UDP-N-acetylglucosamine pyrophosphorylase GlmU
ncbi-gi:1560816	mtu:Rv1023	eno	Probable enolase Eno
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560821	mtu:Rv1079	metB	Cystathionine gamma-synthase MetB (CGS) (O-succinylhomoserine [thiol]-lyase)
ncbi-gi:4488247	mtu:Rv1093	glyA1	Serine hydroxymethyltransferase 1 GlyA1
ncbi-gi:1560823	mtu:Rv1098c	fum	Probable fumarase Fum (fumarate hydratase)
ncbi-gi:4488247	mtu:Rv1099c	glpX	Fructose 1,6-bisphosphatase GlpX
ncbi-gi:5711682	mtu:Rv1110	lytB2	Probable LYTB-related protein LytB2
ncbi-gi:5711683	mtu:Rv1121	zwf1	Probable glucose-6-phosphate 1-dehydrogenase Zwf1 (G6PD)
ncbi-gi:1560826	mtu:Rv1122	gnd2	Probable 6-phosphogluconate dehydrogenase,decarboxylating Gnd2
ncbi-gi:1560827	mtu:Rv1133c	metE	Probable 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase MetE (methionine synthase, vitamin-B12 independent isozyme)
ncbi-gi:1560838	mtu:Rv1240	mdh	Probable malate dehydrogenase Mdh
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560846	mtu:Rv1328	glgP	Probable glycogen phosphorylase GlgP
ncbi-gi:1560848	mtu:Rv1346	mbtN	Acyl-CoA dehydrogenase MbtN
ncbi-gi:1560853	mtu:Rv1392	metK	Probable S-adenosylmethionine synthetase MetK (mat) (AdoMet synthetase) (methionine adenosyltransferase)
ncbi-gi:1560857	mtu:Rv1436	gap	Probable glyceraldehyde 3-phosphate dehydrogenase Gap (GAPDH)
ncbi-gi:1560857	mtu:Rv1437	pgk	Probable phosphoglycerate kinase Pgk
ncbi-gi:1560857	mtu:Rv1438	tpi	Probable triosephosphate isomerase Tpi (TIM)
ncbi-gi:1560858	mtu:Rv1448c	tal	Probable transaldolase Tal
ncbi-gi:1560858	mtu:Rv1449c	tkt	Transketolase Tkt (TK)
ncbi-gi:1560860	mtu:Rv1467c	fadE15	Probable acyl-CoA dehydrogenase FadE15
ncbi-gi:1560861	mtu:Rv1475c	acn	Probable iron-regulated aconitate hydratase Acn (citrate hydro-lyase) (aconitase)
ncbi-gi:1560869	mtu:Rv1559	ilvA	Probable threonine dehydratase IlvA
ncbi-gi:1560873	mtu:Rv1601	hisB	Probable imidazole glycerol-phosphate dehydratase HisB
ncbi-gi:1560874	mtu:Rv1603	hisA	Probable phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA
ncbi-gi:1560874	mtu:Rv1611	trpC	Probable indole-3-glycerol phosphate synthase TrpC
ncbi-gi:1560875	mtu:Rv1617	pykA	Probable pyruvate kinase PykA
ncbi-gi:1560879	mtu:Rv1654	argB	Probable acetylglutamate kinase ArgB
ncbi-gi:1560879	mtu:Rv1655	argD	Probable acetylornithine aminotransferase ArgD
ncbi-gi:1560879	mtu:Rv1656	argF	Probable ornithine carbamoyltransferase, anabolic ArgF
ncbi-gi:1560898	mtu:Rv1843c	guaB1	Probable inosine-5'-monophosphate dehydrogenase GuaB1(imp dehydrogenase) (IMPDH) (IMPD)
ncbi-gi:1560916	mtu:Rv2029c	pfkB	6-phosphofructokinase PfkB (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1560919	mtu:Rv2054		hypothetical protein
ncbi-gi:1560925	mtu:Rv2121c	hisG	ATP phosphoribosyltransferase HisG
ncbi-gi:1560931	mtu:Rv2178c	aroG	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase AroG (DAHP synthetase, phenylalanine-repressible)
ncbi-gi:1560934	mtu:Rv2210c	ilvE	Branched-chain amino acid transaminase IlvE
ncbi-gi:1560935	mtu:Rv2215	dlaT	DlaT, dihydrolipoamide acyltransferase, E2 component of pyruvate dehydrogenase
ncbi-gi:4488247	mtu:Rv2241	aceE	Pyruvate dehydrogenase E1 component AceE (pyruvate decarboxylase) (pyruvate dehydrogenase) (pyruvic dehydrogenase)
ncbi-gi:1560955	mtu:Rv2419c	gpgP	Glucosyl-3-phosphoglycerate phosphatase GpgP
ncbi-gi:5711699	mtu:Rv2465c	rpiB	Ribose-5-phosphate isomerase
ncbi-gi:1560963	mtu:Rv2495c	bkdC	Probable branched-chain keto acid dehydrogenase E2 component BkdC
ncbi-gi:1560963	mtu:Rv2498c	citE	Probable citrate (pro-3S)-lyase (beta subunit) CitE (citrase) (citratase) (citritase) (citridesmolase) (citrase aldolase)
ncbi-gi:1560967	mtu:Rv2537c	aroD	3-dehydroquinate dehydratase AroD (AROQ) (3-dehydroquinase) (type II dhqase)
ncbi-gi:1560967	mtu:Rv2538c	aroB	3-dehydroquinate synthase AroB
ncbi-gi:1560967	mtu:Rv2540c	aroF	Probable chorismate synthase AroF (5-enolpyruvylshikimate-3-phosphate phospholyase)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560986	mtu:Rv2726c	dapF	Probable diaminopimelate epimerase DapF (DAP epimerase)
ncbi-gi:1560989	mtu:Rv2753c	dapA	Probable dihydrodipicolinate synthase DapA (DHDPS) (dihydrodipicolinate synthetase)
ncbi-gi:1560990	mtu:Rv2765		Probable alanine rich hydrolase
ncbi-gi:1560991	mtu:Rv2773c	dapB	Dihydrodipicolinate reductase DapB (DHPR)
ncbi-gi:1560992	mtu:Rv2789c	fadE21	Probable acyl-CoA dehydrogenase FadE21
ncbi-gi:4488247	mtu:Rv2790c	ltp1	Probable lipid-transfer protein Ltp1
ncbi-gi:1561000	mtu:Rv2868c	gcpE	Probable GcpE protein
ncbi-gi:5711704	mtu:Rv2992c	gltS	Glutamyl-tRNA synthetase GltS (glutamate--tRNA ligase) (glutamyl-tRNA synthase) (GLURS)
ncbi-gi:1561013	mtu:Rv2995c	leuB	Probable 3-isopropylmalate dehydrogenase LeuB (beta-IPM dehydrogenase) (IMDH) (3-IPM-DH)
ncbi-gi:4488247	mtu:Rv3001c	ilvC	Probable KETOL-acid reductoisomerase IlvC (acetohydroxy-acid isomeroreductase) (alpha-keto-beta-hydroxylacil reductoisomerase)
ncbi-gi:1561013	mtu:Rv3002c	ilvN	Probable acetolactate synthase (small subunit) IlvN (acetohydroxy-acid synthase) (AHAS) (ALS)
ncbi-gi:5711704	mtu:Rv3003c	ilvB1	Acetolactate synthase (large subunit) IlvB1 (acetohydroxy-acid synthase)
ncbi-gi:1561014	mtu:Rv3010c	pfkA	Probable 6-phosphofructokinase PfkA (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1561021	mtu:Rv3075c		hypothetical protein
ncbi-gi:1561022	mtu:Rv3086	adhD	Probable zinc-type alcohol dehydrogenase AdhD (aldehyde reductase)
ncbi-gi:1561027	mtu:Rv3139	fadE24	Probable acyl-CoA dehydrogenase FadE24
ncbi-gi:1561027	mtu:Rv3140	fadE23	Probable acyl-CoA dehydrogenase FadE23
ncbi-gi:1561035	mtu:Rv3215	entC	Probable isochorismate synthase EntC (isochorismate hydroxymutase) (enterochelin biosynthesis)
ncbi-gi:1561036	mtu:Rv3227	aroA	3-phosphoshikimate 1-carboxyvinyltransferase AroA (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS)
ncbi-gi:1561039	mtu:Rv3255c	manA	Probable mannose-6-phosphate isomerase ManA (phosphomannose isomerase) (phosphomannoisomerase) (PMI) (phosphohexoisomerase) (phosphohexomutase)
ncbi-gi:5711708	mtu:Rv3264c	manB	D-alpha-D-mannose-1-phosphate guanylyltransferase ManB (D-alpha-D-heptose-1-phosphate guanylyltransferase)

ncbi-gi:1561041	mtu:Rv3274c	fadE25	Probable acyl-CoA dehydrogenase FadE25
ncbi-gi:1561041	mtu:Rv3275c	purE	Probable phosphoribosylaminoimidazole carboxylase catalytic subunit PurE (air carboxylase) (AIRC)
ncbi-gi:1561041	mtu:Rv3276c	purK	Probable phosphoribosylaminoimidazole carboxylase ATPase subunit PurK (air carboxylase) (AIRC)
ncbi-gi:1561045	mtu:Rv3318	sdhA	Probable succinate dehydrogenase (flavoprotein subunit) SdhA (succinic dehydrogenase) (fumarate reductase) (fumarate dehydrogenase) (fumaric hydrogenase)
ncbi-gi:1561047	mtu:Rv3339c	icd1	Probable isocitrate dehydrogenase [NADP] Icd1 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1561054	mtu:Rv3410c	guaB3	Probable inosine-5'-monophosphate dehydrogenase GuaB3 (imp dehydrogenase) (inosinic acid dehydrogenase) (inosinate dehydrogenase) (imp oxidoreductase) (inosine-5'-monophosphate oxidoreductase) (IMPDH) (IMPD)
ncbi-gi:1561056	mtu:Rv3432c	gadB	Probable glutamate decarboxylase GadB
ncbi-gi:1561057	mtu:Rv3436c	glmS	Probable glucosamine--fructose-6-phosphate aminotransferase [isomerizing] GlmS (hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (glucosamine-6-phosphate synthase)
ncbi-gi:1561064	mtu:Rv3504	fadE26	Probable acyl-CoA dehydrogenase FadE26
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561069	mtu:Rv3563	fadE32	Probable acyl-CoA dehydrogenase FadE32
ncbi-gi:5711712	mtu:Rv3566c	nat	Arylamine N-acetyltransferase Nat (arylamine acetylase)
ncbi-gi:1561071	mtu:Rv3581c	ispF	Probable 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF (MECPS)
ncbi-gi:5711713	mtu:Rv3634c	galE1	UDP-glucose 4-epimerase GalE1 (galactowaldenase) (UDP-galactose 4-epimerase) (uridine diphosphate galactose 4-epimerase) (uridine diphospho-galactose 4-epimerase)
ncbi-gi:1561080	mtu:Rv3667	acs	Acetyl-coenzyme A synthetase Acs (acetate--CoA ligase) (acetyl-CoA synthetase) (acetyl-CoA synthase) (acyl-activating enzyme) (acetate thiokinase) (acetyl-activating enzyme) (acetate--coenzyme A ligase) (acetyl-coenzyme A synthase)
ncbi-gi:3454620	mtu:Rv3710	leuA	2-isopropylmalate synthase LeuA (alpha-isopropylmalate synthase) (alpha-IPM synthetase) (IPMS)
ncbi-gi:1561089	mtu:Rv3761c	fadE36	Possible acyl-CoA dehydrogenase FadE36
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561097	mtu:Rv3838c	pheA	Prephenate dehydratase PheA
ncbi-gi:1561099	mtu:Rv3858c	gltD	Probable NADH-dependent glutamate synthase (small subunit) GltD (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH)) (GLTS beta chain) (NADPH-GOGAT)
ncbi-gi:1561099	mtu:Rv3859c	gltB	Probable ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH))(NADPH-GOGAT)

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ncbi-gi:1560720	mtu:Rv0066c	icd2	Probable isocitrate dehydrogenase [NADP] Icd2 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1560735	mtu:Rv0211	pckA	Probable iron-regulated phosphoenolpyruvate carboxykinase [GTP] PckA (phosphoenolpyruvate carboxylase) (PEPCK)(pep carboxykinase)
ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560736	mtu:Rv0223c		Probable aldehyde dehydrogenase
ncbi-gi:5711670	mtu:Rv0234c	gabD1	Succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD1
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560738	mtu:Rv0247c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560738	mtu:Rv0248c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560750	mtu:Rv0363c	fba	Probable fructose-bisphosphate aldolase Fba
ncbi-gi:1560754	mtu:Rv0408	pta	Probable phosphate acetyltransferase Pta (phosphotransacetylase)
ncbi-gi:1560760	mtu:Rv0462	lpdC	Dihydrolipoamide dehydrogenase LpdC (lipoamide reductase (NADH)) (lipoyl dehydrogenase) (dihydrolipoyl dehydrogenase) (diaphorase)
ncbi-gi:5711673	mtu:Rv0467	icl1	Isocitrate lyase Icl (isocitrase) (isocitratase)
ncbi-gi:1560760	mtu:Rv0468	fadB2	3-hydroxybutyryl-CoA dehydrogenase FadB2 (beta-hydroxybutyryl-CoA dehydrogenase) (BHBD)
ncbi-gi:5711673	mtu:Rv0489	gpm1	Probable phosphoglycerate mutase 1 Gpm1 (phosphoglyceromutase) (PGAM) (BPG-dependent PGAM)
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560790	mtu:Rv0760c		hypothetical protein
ncbi-gi:5711677	mtu:Rv0761c	adhB	Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB
ncbi-gi:5711678	mtu:Rv0794c	lpdB	Probable oxidoreductase
ncbi-gi:1560795	mtu:Rv0815c	cysA2	Probable thiosulfate sulfurtransferase CysA2 (rhodanese-like protein) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)
ncbi-gi:1560799	mtu:Rv0858c	dapC	Probable N-succinyldiaminopimelate aminotransferase DapC (DAP-at)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560802	mtu:Rv0884c	serC	Possible phosphoserine aminotransferase SerC (PSAT)
ncbi-gi:1560802	mtu:Rv0889c	citA	Probable citrate synthase II CitA
ncbi-gi:1560803	mtu:Rv0896	gltA2	Probable citrate synthase I GltA2
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560808	mtu:Rv0946c	pgi	Probable glucose-6-phosphate isomerase Pgi (GPI) (phosphoglucose isomerase) (phosphohexose isomerase) (phi)
ncbi-gi:1560809	mtu:Rv0951	sucC	Probable succinyl-CoA synthetase (beta chain) SucC (SCS-beta)
ncbi-gi:1560809	mtu:Rv0952	sucD	Probable succinyl-CoA synthetase (alpha chain) SucD (SCS-alpha)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560815	mtu:Rv1017c	prsA	Probable ribose-phosphate pyrophosphokinase PrsA (phosphoribosyl pyrophosphate synthetase) (PRPP synthetase)
ncbi-gi:1560816	mtu:Rv1023	eno	Probable enolase Eno
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:4488247	mtu:Rv1093	glyA1	Serine hydroxymethyltransferase 1 GlyA1
ncbi-gi:1560823	mtu:Rv1098c	fum	Probable fumarase Fum (fumarate hydratase)
ncbi-gi:4488247	mtu:Rv1099c	glpX	Fructose 1,6-bisphosphatase GlpX
ncbi-gi:5711683	mtu:Rv1121	zwf1	Probable glucose-6-phosphate 1-dehydrogenase Zwf1 (G6PD)
ncbi-gi:1560826	mtu:Rv1122	gnd2	Probable 6-phosphogluconate dehydrogenase,decarboxylating Gnd2
ncbi-gi:1560834	mtu:Rv1201c	dapD	Tetrahydrodipicolinate N-succinyltransferase DapD
ncbi-gi:1560838	mtu:Rv1240	mdh	Probable malate dehydrogenase Mdh
ncbi-gi:1560843	mtu:Rv1295	thrC	Threonine synthase ThrC (ts)
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560857	mtu:Rv1436	gap	Probable glyceraldehyde 3-phosphate dehydrogenase Gap (GAPDH)
ncbi-gi:1560857	mtu:Rv1437	pgk	Probable phosphoglycerate kinase Pgk
ncbi-gi:1560857	mtu:Rv1438	tpi	Probable triosephosphate isomerase Tpi (TIM)
ncbi-gi:1560858	mtu:Rv1448c	tal	Probable transaldolase Tal
ncbi-gi:1560858	mtu:Rv1449c	tkt	Transketolase Tkt (TK)
ncbi-gi:1560861	mtu:Rv1475c	acn	Probable iron-regulated aconitate hydratase Acn (citrate hydro-lyase) (aconitase)
ncbi-gi:1560863	mtu:Rv1492	mutA	Probable methylmalonyl-CoA mutase small subunit MutA (MCM)
ncbi-gi:1560863	mtu:Rv1493	mutB	Probable methylmalonyl-CoA mutase large subunit MutB (MCM)
ncbi-gi:1560875	mtu:Rv1617	pykA	Probable pyruvate kinase PykA
ncbi-gi:5711690	mtu:Rv1731	gabD2	Possible succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD2
ncbi-gi:1560897	mtu:Rv1837c	glcB	Malate synthase G GlcB
ncbi-gi:1560916	mtu:Rv2029c	pfkB	6-phosphofructokinase PfkB (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1560919	mtu:Rv2054		hypothetical protein
ncbi-gi:1560935	mtu:Rv2215	dlaT	DlaT, dihydrolipoamide acyltransferase, E2 component of pyruvate dehydrogenase
ncbi-gi:1560935	mtu:Rv2220	glnA1	Glutamine synthetase GlnA1 (glutamine synthase) (GS-I)

ncbi-gi:1560935	mtu:Rv2222c	glnA2	Probable glutamine synthetase GlnA2 (glutamine synthase) (GS-II)
ncbi-gi:4488247	mtu:Rv2241	aceE	Pyruvate dehydrogenase E1 component AceE (pyruvate decarboxylase) (pyruvate dehydrogenase) (pyruvic dehydrogenase)
ncbi-gi:1560943	mtu:Rv2296		Probable haloalkane dehalogenase
ncbi-gi:5711697	mtu:Rv2334	cysK1	Cysteine synthase a CysK1 (O-acetylserine sulfhydrylase A) (O-acetylserine (thiol)-lyase A) (CSASE A)
ncbi-gi:1560952	mtu:Rv2391	sirA	Ferredoxin-dependent sulfite reductase SirA
ncbi-gi:1560955	mtu:Rv2419c	gpgP	Glucosyl-3-phosphoglycerate phosphatase GpgP
ncbi-gi:1560959	mtu:Rv2454c		Probable oxidoreductase (beta subunit)
ncbi-gi:1560959	mtu:Rv2455c		Probable oxidoreductase (alpha subunit)
ncbi-gi:5711699	mtu:Rv2465c	rpiB	Ribose-5-phosphate isomerase
ncbi-gi:1560963	mtu:Rv2495c	bkdC	Probable branched-chain keto acid dehydrogenase E2 component BkdC
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560986	mtu:Rv2726c	dapF	Probable diaminopimelate epimerase DapF (DAP epimerase)
ncbi-gi:1560989	mtu:Rv2753c	dapA	Probable dihydrodipicolinate synthase DapA (DHDPS) (dihydrodipicolinate synthetase)
ncbi-gi:1560990	mtu:Rv2765		Probable alanine rich hydrolase
ncbi-gi:1560991	mtu:Rv2773c	dapB	Dihydrodipicolinate reductase DapB (DHPR)
ncbi-gi:4488247	mtu:Rv2790c	ltp1	Probable lipid-transfer protein Ltp1
ncbi-gi:5711703	mtu:Rv2922A	acyP	Probable acylphosphatase AcyP (acylphosphate phosphohydrolase)
ncbi-gi:1561010	mtu:Rv2967c	pca	Probable pyruvate carboxylase Pca (pyruvic carboxylase)
ncbi-gi:5711704	mtu:Rv2996c	serA1	Probable D-3-phosphoglycerate dehydrogenase SerA1 (PGDH)
ncbi-gi:1561014	mtu:Rv3010c	pfkA	Probable 6-phosphofructokinase PfkA (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1561022	mtu:Rv3086	adhD	Probable zinc-type alcohol dehydrogenase AdhD (aldehyde reductase)
ncbi-gi:1561041	mtu:Rv3280	accD5	Probable propionyl-CoA carboxylase beta chain 5 AccD5 (pccase) (propanoyl-CoA:carbon dioxide ligase)
ncbi-gi:1561041	mtu:Rv3283	sseA	Probable thiosulfate sulfurtransferase SseA (rhodanese) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)
ncbi-gi:1561045	mtu:Rv3318	sdhA	Probable succinate dehydrogenase (flavoprotein subunit) SdhA (succinic dehydrogenase) (fumarate reductase) (fumarate dehydrogenase) (fumaric hydrogenase)
ncbi-gi:1561047	mtu:Rv3339c	icd1	Probable isocitrate dehydrogenase [NADP] Icd1 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1561049	mtu:Rv3356c	folD	Probable bifunctional protein FolD: methylenetetrahydrofolate dehydrogenase + methenyltetrahydrofolate cyclohydrolase
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561067	mtu:Rv3535c	hsaG	Probable acetaldehyde dehydrogenase (acetaldehyde dehydrogenase [acetylating])
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:5711712	mtu:Rv3566c	nat	Arylamine N-acetyltransferase Nat (arylamine acetylase)
ncbi-gi:1561070	mtu:Rv3568c	hsaC	3,4-DHSA dioxygenase
ncbi-gi:1561070	mtu:Rv3569c	hsaD	4,9-DHSA hydrolase
ncbi-gi:1561070	mtu:Rv3570c	hsaA	Possible oxidoreductase Possible 3-hydroxy-9,10-seconandrost-1,3,5(10)-triene-9,17-dione hydroxylase
ncbi-gi:1561080	mtu:Rv3667	acs	Acetyl-coenzyme A synthetase Acs (acetate--CoA ligase) (acetyl-CoA synthetase) (acetyl-CoA synthase) (acyl-activating enzyme) (acetate thiokinase) (acetyl-activating enzyme) (acetate--coenzyme A ligase) (acetyl-coenzyme A synthase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561099	mtu:Rv3858c	gltD	Probable NADH-dependent glutamate synthase (small subunit) GltD (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH)) (GLTS beta chain) (NADPH-GOGAT)
ncbi-gi:1561099	mtu:Rv3859c	gltB	Probable ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH))(NADPH-GOGAT)

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ncbi-gi:1560720	mtu:Rv0066c	icd2	Probable isocitrate dehydrogenase [NADP] Icd2 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560738	mtu:Rv0247c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560738	mtu:Rv0248c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560750	mtu:Rv0363c	fba	Probable fructose-bisphosphate aldolase Fba
ncbi-gi:1560754	mtu:Rv0408	pta	Probable phosphate acetyltransferase Pta (phosphotransacetylase)
ncbi-gi:1560760	mtu:Rv0462	lpdC	Dihydrolipoamide dehydrogenase LpdC (lipoamide reductase (NADH)) (lipoyl dehydrogenase) (dihydrolipoyl dehydrogenase) (diaphorase)
ncbi-gi:5711673	mtu:Rv0467	icl1	Isocitrate lyase Icl (isocitrase) (isocitratase)
ncbi-gi:5711673	mtu:Rv0489	gpm1	Probable phosphoglycerate mutase 1 Gpm1 (phosphoglyceromutase) (PGAM) (BPG-dependent PGAM)
ncbi-gi:5711677	mtu:Rv0761c	adhB	Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB
ncbi-gi:5711678	mtu:Rv0794c	lpdB	Probable oxidoreductase
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560802	mtu:Rv0884c	serC	Possible phosphoserine aminotransferase SerC (PSAT)
ncbi-gi:1560802	mtu:Rv0889c	citA	Probable citrate synthase II CitA
ncbi-gi:1560803	mtu:Rv0896	gltA2	Probable citrate synthase I GltA2
ncbi-gi:1560808	mtu:Rv0946c	pgi	Probable glucose-6-phosphate isomerase Pgi (GPI) (phosphoglucose isomerase) (phosphohexose isomerase) (phi)
ncbi-gi:1560809	mtu:Rv0951	sucC	Probable succinyl-CoA synthetase (beta chain) SucC (SCS-beta)
ncbi-gi:1560809	mtu:Rv0952	sucD	Probable succinyl-CoA synthetase (alpha chain) SucD (SCS-alpha)
ncbi-gi:1560815	mtu:Rv1017c	prsA	Probable ribose-phosphate pyrophosphokinase PrsA (phosphoribosyl pyrophosphate synthetase) (PRPP synthetase)
ncbi-gi:1560816	mtu:Rv1023	eno	Probable enolase Eno
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:4488247	mtu:Rv1093	glyA1	Serine hydroxymethyltransferase 1 GlyA1
ncbi-gi:1560823	mtu:Rv1098c	fum	Probable fumarase Fum (fumarate hydratase)
ncbi-gi:4488247	mtu:Rv1099c	glpX	Fructose 1,6-bisphosphatase GlpX
ncbi-gi:5711683	mtu:Rv1121	zwf1	Probable glucose-6-phosphate 1-dehydrogenase Zwf1 (G6PD)
ncbi-gi:1560826	mtu:Rv1122	gnd2	Probable 6-phosphogluconate dehydrogenase,decarboxylating Gnd2
ncbi-gi:1560838	mtu:Rv1240	mdh	Probable malate dehydrogenase Mdh
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560857	mtu:Rv1436	gap	Probable glyceraldehyde 3-phosphate dehydrogenase Gap (GAPDH)
ncbi-gi:1560857	mtu:Rv1437	pgk	Probable phosphoglycerate kinase Pgk
ncbi-gi:1560857	mtu:Rv1438	tpi	Probable triosephosphate isomerase Tpi (TIM)
ncbi-gi:1560858	mtu:Rv1448c	tal	Probable transaldolase Tal
ncbi-gi:1560858	mtu:Rv1449c	tkt	Transketolase Tkt (TK)
ncbi-gi:1560861	mtu:Rv1475c	acn	Probable iron-regulated aconitate hydratase Acn (citrate hydro-lyase) (aconitase)
ncbi-gi:1560863	mtu:Rv1492	mutA	Probable methylmalonyl-CoA mutase small subunit MutA (MCM)
ncbi-gi:1560863	mtu:Rv1493	mutB	Probable methylmalonyl-CoA mutase large subunit MutB (MCM)
ncbi-gi:1560869	mtu:Rv1559	ilvA	Probable threonine dehydratase IlvA
ncbi-gi:1560875	mtu:Rv1617	pykA	Probable pyruvate kinase PykA
ncbi-gi:1560896	mtu:Rv1832	gcvB	Probable glycine dehydrogenase GcvB (glycine decarboxylase) (glycine cleavage system P-protein)
ncbi-gi:1560897	mtu:Rv1837c	glcB	Malate synthase G GlcB
ncbi-gi:1560916	mtu:Rv2029c	pfkB	6-phosphofructokinase PfkB (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1560934	mtu:Rv2211c	gcvT	Probable aminomethyltransferase GcvT (glycine cleavage system T protein)
ncbi-gi:1560935	mtu:Rv2215	dlaT	DlaT, dihydrolipoamide acyltransferase, E2 component of pyruvate dehydrogenase
ncbi-gi:4488247	mtu:Rv2241	aceE	Pyruvate dehydrogenase E1 component AceE (pyruvate decarboxylase) (pyruvate dehydrogenase) (pyruvic dehydrogenase)

ncbi-gi:5711697	mtu:Rv2334	cysK1	Cysteine synthase a CysK1 (O-acetylserine sulfhydrylase A) (O-acetylserine (thiol)-lyase A) (CSASE A)
ncbi-gi:1560955	mtu:Rv2419c	gpgP	Glucosyl-3-phosphoglycerate phosphatase GpgP
ncbi-gi:1560959	mtu:Rv2454c		Probable oxidoreductase (beta subunit)
ncbi-gi:1560959	mtu:Rv2455c		Probable oxidoreductase (alpha subunit)
ncbi-gi:5711699	mtu:Rv2465c	rpiB	Ribose-5-phosphate isomerase
ncbi-gi:1560963	mtu:Rv2495c	bkdC	Probable branched-chain keto acid dehydrogenase E2 component BkdC
ncbi-gi:1561010	mtu:Rv2967c	pca	Probable pyruvate carboxylase Pca (pyruvic carboxylase)
ncbi-gi:5711704	mtu:Rv2996c	serA1	Probable D-3-phosphoglycerate dehydrogenase SerA1 (PGDH)
ncbi-gi:1561014	mtu:Rv3010c	pfkA	Probable 6-phosphofructokinase PfkA (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1561022	mtu:Rv3086	adhD	Probable zinc-type alcohol dehydrogenase AdhD (aldehyde reductase)
ncbi-gi:1561041	mtu:Rv3280	accD5	Probable propionyl-CoA carboxylase beta chain 5 AccD5 (pccase) (propanoyl-CoA:carbon dioxide ligase)
ncbi-gi:1561045	mtu:Rv3318	sdhA	Probable succinate dehydrogenase (flavoprotein subunit) SdhA (succinic dehydrogenase) (fumarate reductase) (fumarate dehydrogenase) (fumaric hydrogenase)
ncbi-gi:1561047	mtu:Rv3339c	icd1	Probable isocitrate dehydrogenase [NADP] Icd1 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1561049	mtu:Rv3356c	folD	Probable bifunctional protein FolD: methylenetetrahydrofolate dehydrogenase + methenyltetrahydrofolate cyclohydrolase
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561080	mtu:Rv3667	acs	Acetyl-coenzyme A synthetase Acs (acetate--CoA ligase) (acetyl-CoA synthetase) (acetyl-CoA synthase) (acyl-activating enzyme) (acetate thiokinase) (acetyl-activating enzyme) (acetate--coenzyme A ligase) (acetyl-coenzyme A synthase)

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ncbi-gi:1560720	mtu:Rv0066c	icd2	Probable isocitrate dehydrogenase [NADP] Icd2 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1560733	mtu:Rv0189c	ilvD	Probable dihydroxy-acid dehydratase IlvD (dad)
ncbi-gi:1560750	mtu:Rv0363c	fba	Probable fructose-bisphosphate aldolase Fba
ncbi-gi:5711673	mtu:Rv0489	gpm1	Probable phosphoglycerate mutase 1 Gpm1 (phosphoglyceromutase) (PGAM) (BPG-dependent PGAM)
ncbi-gi:1560764	mtu:Rv0500	proC	Probable pyrroline-5-carboxylate reductase ProC (P5CR) (P5C reductase)
ncbi-gi:1560799	mtu:Rv0858c	dapC	Probable N-succinyldiaminopimelate aminotransferase DapC (DAP-at)
ncbi-gi:1560802	mtu:Rv0884c	serC	Possible phosphoserine aminotransferase SerC (PSAT)
ncbi-gi:1560802	mtu:Rv0889c	citA	Probable citrate synthase II CitA
ncbi-gi:1560803	mtu:Rv0896	gltA2	Probable citrate synthase I GltA2
ncbi-gi:1560815	mtu:Rv1017c	prsA	Probable ribose-phosphate pyrophosphokinase PrsA (phosphoribosyl pyrophosphate synthetase) (PRPP synthetase)
ncbi-gi:1560816	mtu:Rv1023	eno	Probable enolase Eno
ncbi-gi:5711682	mtu:Rv1077	cbs	Probable cystathionine beta-synthase Cbs (serine sulfhydrase) (beta-thionase) (hemoprotein H-450)
ncbi-gi:1560821	mtu:Rv1079	metB	Cystathionine gamma-synthase MetB (CGS) (O-succinylhomoserine [thiol]-lyase)
ncbi-gi:4488247	mtu:Rv1093	glyA1	Serine hydroxymethyltransferase 1 GlyA1
ncbi-gi:1560827	mtu:Rv1133c	metE	Probable 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase MetE (methionine synthase, vitamin-B12 independent isozyme)
ncbi-gi:1560834	mtu:Rv1201c	dapD	Tetrahydrodipicolinate N-succinyltransferase DapD
ncbi-gi:1560843	mtu:Rv1295	thrC	Threonine synthase ThrC (ts)
ncbi-gi:1560853	mtu:Rv1392	metK	Probable S-adenosylmethionine synthetase MetK (mat) (AdoMet synthetase) (methionine adenosyltransferase)
ncbi-gi:1560857	mtu:Rv1436	gap	Probable glyceraldehyde 3-phosphate dehydrogenase Gap (GAPDH)
ncbi-gi:1560857	mtu:Rv1437	pgk	Probable phosphoglycerate kinase Pgk
ncbi-gi:1560857	mtu:Rv1438	tpi	Probable triosephosphate isomerase Tpi (TIM)
ncbi-gi:1560858	mtu:Rv1448c	tal	Probable transaldolase Tal
ncbi-gi:1560858	mtu:Rv1449c	tkt	Transketolase Tkt (TK)
ncbi-gi:1560861	mtu:Rv1475c	acn	Probable iron-regulated aconitate hydratase Acn (citrate hydro-lyase) (aconitase)
ncbi-gi:1560869	mtu:Rv1559	ilvA	Probable threonine dehydratase IlvA
ncbi-gi:1560873	mtu:Rv1601	hisB	Probable imidazole glycerol-phosphate dehydratase HisB
ncbi-gi:1560874	mtu:Rv1603	hisA	Probable phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA
ncbi-gi:1560874	mtu:Rv1611	trpC	Probable indole-3-glycerol phosphate synthase TrpC
ncbi-gi:1560875	mtu:Rv1617	pykA	Probable pyruvate kinase PykA
ncbi-gi:1560879	mtu:Rv1654	argB	Probable acetylglutamate kinase ArgB
ncbi-gi:1560879	mtu:Rv1655	argD	Probable acetylornithine aminotransferase ArgD
ncbi-gi:1560879	mtu:Rv1656	argF	Probable ornithine carbamoyltransferase, anabolic ArgF
ncbi-gi:1560916	mtu:Rv2029c	pfkB	6-phosphofructokinase PfkB (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1560925	mtu:Rv2121c	hisG	ATP phosphoribosyltransferase HisG
ncbi-gi:1560931	mtu:Rv2178c	aroG	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase AroG (DAHP synthetase, phenylalanine-repressible)
ncbi-gi:1560934	mtu:Rv2210c	ilvE	Branched-chain amino acid transaminase IlvE
ncbi-gi:1560935	mtu:Rv2220	glnA1	Glutamine synthetase GlnA1 (glutamine synthase) (GS-I)
ncbi-gi:1560935	mtu:Rv2222c	glnA2	Probable glutamine synthetase GlnA2 (glutamine synthase) (GS-II)
ncbi-gi:5711697	mtu:Rv2334	cysK1	Cysteine synthase a CysK1 (O-acetylserine sulfhydrylase A) (O-acetylserine (thiol)-lyase A) (CSASE A)
ncbi-gi:1560955	mtu:Rv2419c	gpgP	Glucosyl-3-phosphoglycerate phosphatase GpgP
ncbi-gi:5711699	mtu:Rv2465c	rpiB	Ribose-5-phosphate isomerase
ncbi-gi:1560967	mtu:Rv2537c	aroD	3-dehydroquinate dehydratase AroD (AROQ) (3-dehydroquinase) (type II dhqase)
ncbi-gi:1560967	mtu:Rv2538c	aroB	3-dehydroquinate synthase AroB
ncbi-gi:1560967	mtu:Rv2540c	aroF	Probable chorismate synthase AroF (5-enolpyruvylshikimate-3-phosphate phospholyase)
ncbi-gi:1560986	mtu:Rv2726c	dapF	Probable diaminopimelate epimerase DapF (DAP epimerase)
ncbi-gi:1560989	mtu:Rv2753c	dapA	Probable dihydrodipicolinate synthase DapA (DHDPS) (dihydrodipicolinate synthetase)
ncbi-gi:1560991	mtu:Rv2773c	dapB	Dihydrodipicolinate reductase DapB (DHPR)
ncbi-gi:1561010	mtu:Rv2967c	pca	Probable pyruvate carboxylase Pca (pyruvic carboxylase)
ncbi-gi:1561013	mtu:Rv2995c	leuB	Probable 3-isopropylmalate dehydrogenase LeuB (beta-IPM dehydrogenase) (IMDH) (3-IPM-DH)
ncbi-gi:5711704	mtu:Rv2996c	serA1	Probable D-3-phosphoglycerate dehydrogenase SerA1 (PGDH)
ncbi-gi:4488247	mtu:Rv3001c	ilvC	Probable KETOL-acid reductoisomerase IlvC (acetohydroxy-acid isomeroreductase) (alpha-keto-beta-hydroxylacil reductoisomerase)
ncbi-gi:1561013	mtu:Rv3002c	ilvN	Probable acetolactate synthase (small subunit) IlvN (acetohydroxy-acid synthase) (AHAS) (ALS)
ncbi-gi:5711704	mtu:Rv3003c	ilvB1	Acetolactate synthase (large subunit) IlvB1 (acetohydroxy-acid synthase)
ncbi-gi:1561014	mtu:Rv3010c	pfkA	Probable 6-phosphofructokinase PfkA (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1561036	mtu:Rv3227	aroA	3-phosphoshikimate 1-carboxyvinyltransferase AroA (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS)
ncbi-gi:1561047	mtu:Rv3339c	icd1	Probable isocitrate dehydrogenase [NADP] Icd1 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:3454620	mtu:Rv3710	leuA	2-isopropylmalate synthase LeuA (alpha-isopropylmalate synthase) (alpha-IPM synthetase) (IPMS)
ncbi-gi:1561097	mtu:Rv3838c	pheA	Prephenate dehydratase PheA
ncbi-gi:1561099	mtu:Rv3858c	gltD	Probable NADH-dependent glutamate synthase (small subunit) GltD (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH)) (GLTS beta chain) (NADPH-GOGAT)
ncbi-gi:1561099	mtu:Rv3859c	gltB	Probable ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH))(NADPH-GOGAT)

mtu03010 Ribosome - Mycobacterium tuberculosis H37Rv (36)

ncbi-gi:1560719	mtu:Rv0053	rpsF	30S ribosomal protein S6 RpsF
ncbi-gi:5711668	mtu:Rv0055	rpsR1	30S ribosomal protein S18-1 RpsR1

ncbi-gi:1560719	mtu:Rv0056	rplI	50S ribosomal protein L9 RplI
ncbi-gi:5711676	mtu:Rv0634B	rpmG2	50S ribosomal protein L33 RpmG2
ncbi-gi:1560778	mtu:Rv0640	rplK	50S ribosomal protein L11 RplK
ncbi-gi:1560778	mtu:Rv0641	rplA	50S ribosomal protein L1 RplA
ncbi-gi:1560779	mtu:Rv0651	rplJ	50S ribosomal protein L10 RplJ
ncbi-gi:1560779	mtu:Rv0652	rplL	50S ribosomal protein L7/L12 RplL (SA1)
ncbi-gi:1560782	mtu:Rv0683	rpsG	30S ribosomal protein S7 RpsG
ncbi-gi:1560784	mtu:Rv0700	rpsJ	30S ribosomal protein S10 RpsJ (transcription antitermination factor NusE)
ncbi-gi:1560784	mtu:Rv0701	rplC	50S ribosomal protein L3 RplC
ncbi-gi:1560784	mtu:Rv0702	rplD	50S ribosomal protein L4 RplD
ncbi-gi:1560784	mtu:Rv0704	rplB	50S ribosomal protein L2 RplB
ncbi-gi:1560784	mtu:Rv0705	rpsS	30S ribosomal protein S19 RpsS
ncbi-gi:1560784	mtu:Rv0706	rplV	50S ribosomal protein L22 RplV
ncbi-gi:1560784	mtu:Rv0707	rpsC	30S ribosomal protein S3 RpsC
ncbi-gi:1560785	mtu:Rv0714	rplN	50S ribosomal protein L14 RplN
ncbi-gi:1560785	mtu:Rv0715	rplX	50S ribosomal protein L24 RplX
ncbi-gi:1560785	mtu:Rv0716	rplE	50S ribosomal protein L5 RplE
ncbi-gi:1560785	mtu:Rv0718	rpsH	30S ribosomal protein S8 RpsH
ncbi-gi:1560785	mtu:Rv0719	rplF	50S ribosomal protein L6 RplF
ncbi-gi:1560786	mtu:Rv0722	rpmD	50S ribosomal protein L30 RpmD
ncbi-gi:1560786	mtu:Rv0723	rplO	50S ribosomal protein L15 RplO
ncbi-gi:5711680	mtu:Rv0979A	rpmF	50S ribosomal protein L32 RpmF
ncbi-gi:1560815	mtu:Rv1015c	rplY	50S ribosomal protein L25 RplY
ncbi-gi:1560876	mtu:Rv1630	rpsA	30S ribosomal protein S1 RpsA
ncbi-gi:1560954	mtu:Rv2412	rpsT	30S ribosomal protein S20 RpsT
ncbi-gi:1560957	mtu:Rv2442c	rplU	50S ribosomal protein L21 RplU
ncbi-gi:1560992	mtu:Rv2785c	rpsO	30S ribosomal protein S15 RpsO
ncbi-gi:1561002	mtu:Rv2890c	rpsB	30S ribosomal protein S2 RpsB
ncbi-gi:1561004	mtu:Rv2904c	rplS	50S ribosomal protein L19 RplS
ncbi-gi:1561004	mtu:Rv2909c	rpsP	30S ribosomal protein S16 RpsP
ncbi-gi:1561057	mtu:Rv3442c	rpsI	30S ribosomal protein S9 RpsI
ncbi-gi:1561057	mtu:Rv3443c	rplM	50S ribosomal protein L13 RplM
ncbi-gi:1561059	mtu:Rv3458c	rpsD	30S ribosomal protein S4 RpsD
ncbi-gi:1561059	mtu:Rv3459c	rpsK	30S ribosomal protein S11 RpsK

mtu00280 Valine, leucine and isoleucine degradation - Mycobacterium tuberculosis H37Rv (32)

ncbi-gi:1560727	mtu:Rv0131c	fadE1	Probable acyl-CoA dehydrogenase FadE1
ncbi-gi:1560729	mtu:Rv0154c	fadE2	Probable acyl-CoA dehydrogenase FadE2
ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560737	mtu:Rv0231	fadE4	Probable acyl-CoA dehydrogenase FadE4
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560760	mtu:Rv0462	lpdC	Dihydrolipoamide dehydrogenase LpdC (lipoamide reductase (NADH)) (lipoyl dehydrogenase) (dihydrolipoyl dehydrogenase) (diaphorase)
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560789	mtu:Rv0753c	mmsA	Probable methylmalonate-semialdehyde dehydrogenase MmsA (methylmalonic acid semialdehyde dehydrogenase) (MMSDH)
ncbi-gi:5711678	mtu:Rv0794c	lpdB	Probable oxidoreductase
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560863	mtu:Rv1492	mutA	Probable methylmalonyl-CoA mutase small subunit MutA (MCM)
ncbi-gi:1560863	mtu:Rv1493	mutB	Probable methylmalonyl-CoA mutase large subunit MutB (MCM)
ncbi-gi:1560934	mtu:Rv2210c	ilvE	Branched-chain amino acid transaminase IlvE
ncbi-gi:1560963	mtu:Rv2502c	accD1	Probable acetyl-/propionyl-CoA carboxylase (beta subunit) AccD1
ncbi-gi:1560964	mtu:Rv2503c	scoB	Probable succinyl-CoA:3-ketoacid-coenzyme A transferase (beta subunit) ScoB (3-oxo-acid:CoA transferase) (OXCT B) (succinyl CoA:3-oxoacid CoA-transferase)
ncbi-gi:1560964	mtu:Rv2504c	scoA	Probable succinyl-CoA:3-ketoacid-coenzyme A transferase (alpha subunit) ScoA (3-oxo acid:CoA transferase) (OXCT A) (succinyl-CoA:3-oxoacid-coenzyme A transferase)
ncbi-gi:1560972	mtu:Rv2589	gabT	4-aminobutyrate aminotransferase GabT (gamma-amino-N-butyrate transaminase) (GABA transaminase) (glutamate:succinic semialdehyde transaminase) (GABA aminotransferase) (GABA-at)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:4488247	mtu:Rv2790c	ltp1	Probable lipid-transfer protein Ltp1
ncbi-gi:1561027	mtu:Rv3140	fadE23	Probable acyl-CoA dehydrogenase FadE23
ncbi-gi:1561041	mtu:Rv3280	accD5	Probable propionyl-CoA carboxylase beta chain 5 AccD5 (pccase) (propanoyl-CoA:carbon dioxide ligase)
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00640 Propanoate metabolism - Mycobacterium tuberculosis H37Rv (29)

ncbi-gi:1560727	mtu:Rv0131c	fadE1	Probable acyl-CoA dehydrogenase FadE1
ncbi-gi:1560729	mtu:Rv0154c	fadE2	Probable acyl-CoA dehydrogenase FadE2
ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560737	mtu:Rv0231	fadE4	Probable acyl-CoA dehydrogenase FadE4
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560754	mtu:Rv0408	pta	Probable phosphate acetyltransferase Pta (phosphotransacetylase)
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560789	mtu:Rv0753c	mmsA	Probable methylmalonate-semialdehyde dehydrogenase MmsA (methylmalonic acid semialdehyde dehydrogenase) (MMSDH)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

ncbi-gi:1560809	mtu:Rv0951	sucC	Probable succinyl-CoA synthetase (beta chain) SucC (SCS-beta)
ncbi-gi:1560809	mtu:Rv0952	sucD	Probable succinyl-CoA synthetase (alpha chain) SucD (SCS-alpha)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560863	mtu:Rv1492	mutA	Probable methylmalonyl-CoA mutase small subunit MutA (MCM)
ncbi-gi:1560863	mtu:Rv1493	mutB	Probable methylmalonyl-CoA mutase large subunit MutB (MCM)
ncbi-gi:1560972	mtu:Rv2589	gabT	4-aminobutyrate aminotransferase GabT (gamma-amino-N-butyrate transaminase) (GABA transaminase) (glutamate:succinic semialdehyde transaminase) (GABA aminotransferase) (GABA-at)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561027	mtu:Rv3140	fadE23	Probable acyl-CoA dehydrogenase FadE23
ncbi-gi:1561041	mtu:Rv3280	accD5	Probable propionyl-CoA carboxylase beta chain 5 AccD5 (pccase) (propanoyl-CoA:carbon dioxide ligase)
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561080	mtu:Rv3667	acs	Acetyl-coenzyme A synthetase Acs (acetate--CoA ligase) (acetyl-CoA synthetase) (acetyl-CoA synthase) (acyl-activating enzyme) (acetate thiokinase) (acetyl-activating enzyme) (acetate--coenzyme A ligase) (acetyl-coenzyme A synthase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00650 Butanoate metabolism - Mycobacterium tuberculosis H37Rv (29)

ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711670	mtu:Rv0234c	gabD1	Succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD1
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560738	mtu:Rv0247c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560738	mtu:Rv0248c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560760	mtu:Rv0468	fadB2	3-hydroxybutyryl-CoA dehydrogenase FadB2 (beta-hydroxybutyryl-CoA dehydrogenase) (BHBD)
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:5711690	mtu:Rv1731	gabD2	Possible succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD2
ncbi-gi:1560964	mtu:Rv2503c	scoB	Probable succinyl-CoA:3-ketoacid-coenzyme A transferase (beta subunit) ScoB (3-oxo-acid:CoA transferase) (OXCT B) (succinyl CoA:3-oxoacid CoA-transferase)
ncbi-gi:1560964	mtu:Rv2504c	scoA	Probable succinyl-CoA:3-ketoacid-coenzyme A transferase (alpha subunit) ScoA (3-oxo acid:CoA transferase) (OXCT A) (succinyl-CoA:3-oxoacid-coenzyme A transferase)
ncbi-gi:1560972	mtu:Rv2589	gabT	4-aminobutyrate aminotransferase GabT (gamma-amino-N-butyrate transaminase) (GABA transaminase) (glutamate:succinic semialdehyde transaminase) (GABA aminotransferase) (GABA-at)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561013	mtu:Rv3002c	ilvN	Probable acetolactate synthase (small subunit) IlvN (acetohydroxy-acid synthase) (AHAS) (ALS)
ncbi-gi:5711704	mtu:Rv3003c	ilvB1	Acetolactate synthase (large subunit) IlvB1 (acetohydroxy-acid synthase)
ncbi-gi:1561045	mtu:Rv3318	sdhA	Probable succinate dehydrogenase (flavoprotein subunit) SdhA (succinic dehydrogenase) (fumarate reductase) (fumarate dehydrogenase) (fumaric hydrogenase)
ncbi-gi:1561056	mtu:Rv3432c	gadB	Probable glutamate decarboxylase GadB
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561067	mtu:Rv3535c	hsaG	Probable acetaldehyde dehydrogenase (acetaldehyde dehydrogenase [acetylating])
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu01212 Fatty acid metabolism - Mycobacterium tuberculosis H37Rv (29)

ncbi-gi:1560727	mtu:Rv0131c	fadE1	Probable acyl-CoA dehydrogenase FadE1
ncbi-gi:1560729	mtu:Rv0154c	fadE2	Probable acyl-CoA dehydrogenase FadE2
ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560737	mtu:Rv0231	fadE4	Probable acyl-CoA dehydrogenase FadE4
ncbi-gi:1560738	mtu:Rv0242c	fabG4	Probable 3-oxoacyl-[acyl-carrier protein] reductase FabG4 (3-ketoacyl-acyl carrier protein reductase)
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711678	mtu:Rv0824c	desA1	Probable acyl-[acyl-carrier protein] desaturase DesA1 (acyl-[ACP] desaturase) (stearoyl-ACP desaturase) (protein Des)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560823	mtu:Rv1094	desA2	Possible acyl-[acyl-carrier protein] desaturase DesA2 (acyl-[ACP] desaturase) (stearoyl-ACP desaturase)
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560849	mtu:Rv1350	fabG2	Probable 3-oxoacyl-[acyl-carrier protein] reductase FabG2 (3-ketoacyl-acyl carrier protein reductase)
ncbi-gi:1560932	mtu:Rv2187	fadD15	Long-chain-fatty-acid-CoA ligase FadD15 (fatty-acid-CoA synthetase) (fatty-acid-CoA synthase)
ncbi-gi:1560963	mtu:Rv2501c	accA1	Probable acetyl-/propionyl-coenzyme A carboxylase alpha chain (alpha subunit) AccA1: biotin carboxylase + biotin carboxyl carrier protein (BCCP)
ncbi-gi:1560966	mtu:Rv2524c	fas	Probable fatty acid synthase Fas (fatty acid synthetase)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:4488247	mtu:Rv2790c	ltp1	Probable lipid-transfer protein Ltp1
ncbi-gi:1561027	mtu:Rv3140	fadE23	Probable acyl-CoA dehydrogenase FadE23
ncbi-gi:1561042	mtu:Rv3285	accA3	Probable bifunctional protein acetyl-/propionyl-coenzyme A carboxylase (alpha chain) AccA3: biotin carboxylase + biotin carboxyl carrier protein (BCCP)
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00281 Geraniol degradation - Mycobacterium tuberculosis H37Rv (26)

ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560736	mtu:Rv0223c		Probable aldehyde dehydrogenase
ncbi-gi:1560738	mtu:Rv0244c	fadE5	Probable acyl-CoA dehydrogenase FadE5
ncbi-gi:1560741	mtu:Rv0271c	fadE6	Probable acyl-CoA dehydrogenase FadE6
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560789	mtu:Rv0752c	fadE9	Probable acyl-CoA dehydrogenase FadE9
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560801	mtu:Rv0873	fadE10	Probable acyl-CoA dehydrogenase FadE10
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0972c	fadE12	Acyl-CoA dehydrogenase FadE12
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560848	mtu:Rv1346	mbtN	Acyl-CoA dehydrogenase MbtN
ncbi-gi:1560860	mtu:Rv1467c	fadE15	Probable acyl-CoA dehydrogenase FadE15
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560992	mtu:Rv2789c	fadE21	Probable acyl-CoA dehydrogenase FadE21
ncbi-gi:4488247	mtu:Rv2790c	ltp1	Probable lipid-transfer protein Ltp1
ncbi-gi:1561027	mtu:Rv3139	fadE24	Probable acyl-CoA dehydrogenase FadE24
ncbi-gi:1561041	mtu:Rv3274c	fadE25	Probable acyl-CoA dehydrogenase FadE25
ncbi-gi:1561064	mtu:Rv3504	fadE26	Probable acyl-CoA dehydrogenase FadE26
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561069	mtu:Rv3563	fadE32	Probable acyl-CoA dehydrogenase FadE32
ncbi-gi:1561089	mtu:Rv3761c	fadE36	Possible acyl-CoA dehydrogenase FadE36
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00071 Fatty acid degradation - Mycobacterium tuberculosis H37Rv (25)

ncbi-gi:1560727	mtu:Rv0131c	fadE1	Probable acyl-CoA dehydrogenase FadE1
ncbi-gi:1560729	mtu:Rv0154c	fadE2	Probable acyl-CoA dehydrogenase FadE2
ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560737	mtu:Rv0231	fadE4	Probable acyl-CoA dehydrogenase FadE4
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560754	mtu:Rv0400c	fadE7	Acyl-CoA dehydrogenase FadE7
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711677	mtu:Rv0761c	adhB	Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560932	mtu:Rv2187	fadD15	Long-chain-fatty-acid-CoA ligase FadD15 (fatty-acid-CoA synthetase) (fatty-acid-CoA synthase)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:4488247	mtu:Rv2790c	ltp1	Probable lipid-transfer protein Ltp1
ncbi-gi:1561022	mtu:Rv3086	adhD	Probable zinc-type alcohol dehydrogenase AdhD (aldehyde reductase)
ncbi-gi:1561027	mtu:Rv3140	fadE23	Probable acyl-CoA dehydrogenase FadE23
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00020 Citrate cycle (TCA cycle) - Mycobacterium tuberculosis H37Rv (23)

ncbi-gi:1560720	mtu:Rv0066c	icd2	Probable isocitrate dehydrogenase [NADP] Icd2 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1560735	mtu:Rv0211	pckA	Probable iron-regulated phosphoenolpyruvate carboxykinase [GTP] PckA (phosphoenolpyruvate carboxylase) (PEPCK)(pep carboxykinase)
ncbi-gi:1560738	mtu:Rv0247c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560738	mtu:Rv0248c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560760	mtu:Rv0462	lpdC	Dihydrolipoamide dehydrogenase LpdC (lipoamide reductase (NADH)) (lipoyl dehydrogenase) (dihydrolipoyl dehydrogenase) (diaphorase)
ncbi-gi:5711678	mtu:Rv0794c	lpdB	Probable oxidoreductase
ncbi-gi:1560802	mtu:Rv0889c	citA	Probable citrate synthase II CitA
ncbi-gi:1560803	mtu:Rv0896	gltA2	Probable citrate synthase I GltA2
ncbi-gi:1560809	mtu:Rv0951	sucC	Probable succinyl-CoA synthetase (beta chain) SucC (SCS-beta)
ncbi-gi:1560809	mtu:Rv0952	sucD	Probable succinyl-CoA synthetase (alpha chain) SucD (SCS-alpha)
ncbi-gi:1560823	mtu:Rv1098c	fum	Probable fumarase Fum (fumarate hydratase)
ncbi-gi:1560838	mtu:Rv1240	mdh	Probable malate dehydrogenase Mdh
ncbi-gi:1560861	mtu:Rv1475c	acn	Probable iron-regulated aconitate hydratase Acn (citrate hydro-lyase) (aconitase)
ncbi-gi:1560935	mtu:Rv2215	dlaT	DlaT, dihydrolipoamide acyltransferase, E2 component of pyruvate dehydrogenase
ncbi-gi:4488247	mtu:Rv2241	aceE	Pyruvate dehydrogenase E1 component AceE (pyruvate decarboxylase) (pyruvate dehydrogenase) (pyruvic dehydrogenase)
ncbi-gi:1560959	mtu:Rv2454c		Probable oxidoreductase (beta subunit)
ncbi-gi:1560959	mtu:Rv2455c		Probable oxidoreductase (alpha subunit)
ncbi-gi:1560963	mtu:Rv2495c	bkdC	Probable branched-chain keto acid dehydrogenase E2 component BkdC
ncbi-gi:1560963	mtu:Rv2498c	citE	Probable citrate (pro-3S)-lyase (beta subunit) CitE (citrase) (citratase) (citritase) (citridesmolase) (citrase aldolase)
ncbi-gi:1561010	mtu:Rv2967c	pca	Probable pyruvate carboxylase Pca (pyruvic carboxylase)
ncbi-gi:1561021	mtu:Rv3075c		hypothetical protein
ncbi-gi:1561045	mtu:Rv3318	sdhA	Probable succinate dehydrogenase (flavoprotein subunit) SdhA (succinic dehydrogenase) (fumarate reductase) (fumarate dehydrogenase) (fumaric hydrogenase)
ncbi-gi:1561047	mtu:Rv3339c	icd1	Probable isocitrate dehydrogenase [NADP] Icd1 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)

mtu00230 Purine metabolism - Mycobacterium tuberculosis H37Rv (22)

ncbi-gi:1560714	mtu:Rv0002	dnaN	DNA polymerase III (beta chain) DnaN (DNA nucleotidyltransferase)
ncbi-gi:1560749	mtu:Rv0357c	purA	Probable adenylosuccinate synthetase PurA (imp--aspartate ligase) (ADSS) (ampsase)
ncbi-gi:1560753	mtu:Rv0389	purT	Probable phosphoribosylglycinamide formyltransferase 2 PurT (GART 2) (gar transformylase 2) (5'-phosphoribosylglycinamide transformylase 2) (formate-dependent gar transformylase)
ncbi-gi:1560780	mtu:Rv0667	rpoB	DNA-directed RNA polymerase (beta chain) RpoB (transcriptase beta chain) (RNA polymerase beta subunit)
ncbi-gi:1560780	mtu:Rv0668	rpoC	DNA-directed RNA polymerase (beta' chain) RpoC (transcriptase beta' chain) (RNA polymerase beta' subunit)
ncbi-gi:1560787	mtu:Rv0733	adk	Adenylate kinase Adk (ATP-AMP transphosphorylase)
ncbi-gi:1560791	mtu:Rv0772	purD	Probable phosphoribosylamine--glycine ligase PurD (GARS) (glycinamide ribonucleotide synthetase) (phosphoribosylglycinamide synthetase) (5'-phosphoribosylglycinamide synthetase)
ncbi-gi:1560794	mtu:Rv0809	purM	Probable phosphoribosylformylglycinamidine CYCLO-ligase PurM (AIRS) (phosphoribosyl-aminoimidazole synthetase) (air synthase)
ncbi-gi:1560809	mtu:Rv0957	purH	Probable bifunctional purine biosynthesis protein PurH: phosphoribosylaminoimidazolecarboxamide formyltransferase (AICAR transformylase) (5'-phosphoribosyl-5-aminoimidazole-4-carboxamide formyltransferase) + inosinemonophosphate cyclohydrolase (imp cyclohydrolase) (inosinicase) (imp synthetase) (ATIC)
ncbi-gi:1560815	mtu:Rv1017c	prsA	Probable ribose-phosphate pyrophosphokinase PrsA (phosphoribosyl pyrophosphate synthetase) (PRPP synthetase)
ncbi-gi:1560875	mtu:Rv1617	pykA	Probable pyruvate kinase PykA
ncbi-gi:1560876	mtu:Rv1629	polA	Probable DNA polymerase I PolA
ncbi-gi:1560898	mtu:Rv1843c	guaB1	Probable inosine-5'-monophosphate dehydrogenase GuaB1(imp dehydrogenase) (IMPDH) (IMPD)
ncbi-gi:1560933	mtu:Rv2202c	adoK	Adenosine kinase
ncbi-gi:1560992	mtu:Rv2783c	gpsI	Bifunctional protein polyribonucleotide nucleotidyltransferase GpsI: guanosine pentaphosphate synthetase + polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase) (pnpase)
ncbi-gi:5711705	mtu:Rv3048c	nrdF2	Ribonucleoside-diphosphate reductase (beta chain) NrdF2 (ribonucleotide reductase small subunit) (R2F protein)
ncbi-gi:1561018	mtu:Rv3051c	nrdE	Ribonucleoside-diphosphate reductase (alpha chain) NrdE (ribonucleotide reductase small subunit) (R1F protein)
ncbi-gi:1561041	mtu:Rv3275c	purE	Probable phosphoribosylaminoimidazole carboxylase catalytic subunit PurE (air carboxylase) (AIRC)
ncbi-gi:1561041	mtu:Rv3276c	purK	Probable phosphoribosylaminoimidazole carboxylase ATPase subunit PurK (air carboxylase) (AIRC)
ncbi-gi:1561053	mtu:Rv3396c	guaA	Probable GMP synthase [glutamine-hydrolyzing] GuaA (glutamine amidotransferase) (GMP synthetase)
ncbi-gi:1561054	mtu:Rv3410c	guaB3	Probable inosine-5'-monophosphate dehydrogenase GuaB3 (imp dehydrogenase) (inosinic acid dehydrogenase) (inosinate dehydrogenase) (imp oxidoreductase) (inosine-5'-monophosphate oxidoreductase) (IMPDH) (IMPD)
ncbi-gi:1561059	mtu:Rv3457c	rpoA	Probable DNA-directed RNA polymerase (alpha chain) RpoA (transcriptase alpha chain) (RNA polymerase alpha subunit) (DNA-directed RNA nucleotidyltransferase)

mtu00310 Lysine degradation - Mycobacterium tuberculosis H37Rv (20)

ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711670	mtu:Rv0234c	gabD1	Succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD1
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560754	mtu:Rv0400c	fadE7	Acyl-CoA dehydrogenase FadE7
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:5711690	mtu:Rv1731	gabD2	Possible succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD2
ncbi-gi:1560935	mtu:Rv2215	dlaT	DlaT, dihydrolipoamide acyltransferase, E2 component of pyruvate dehydrogenase
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00620 Pyruvate metabolism - Mycobacterium tuberculosis H37Rv (20)

ncbi-gi:1560735	mtu:Rv0211	pckA	Probable iron-regulated phosphoenolpyruvate carboxykinase [GTP] PckA (phosphoenolpyruvate carboxylase) (PEPCK)(pep carboxykinase)
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560754	mtu:Rv0408	pta	Probable phosphate acetyltransferase Pta (phosphotransacetylase)
ncbi-gi:1560760	mtu:Rv0462	lpdC	Dihydrolipoamide dehydrogenase LpdC (lipoamide reductase (NADH)) (lipoyl dehydrogenase) (dihydrolipoyl dehydrogenase) (diaphorase)
ncbi-gi:5711678	mtu:Rv0794c	lpdB	Probable oxidoreductase
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560838	mtu:Rv1240	mdh	Probable malate dehydrogenase Mdh
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560875	mtu:Rv1617	pykA	Probable pyruvate kinase PykA
ncbi-gi:1560897	mtu:Rv1837c	glcB	Malate synthase G GlcB
ncbi-gi:1560900	mtu:Rv1872c	lldD2	Possible L-lactate dehydrogenase (cytochrome) LldD2
ncbi-gi:4488247	mtu:Rv2241	aceE	Pyruvate dehydrogenase E1 component AceE (pyruvate decarboxylase) (pyruvate dehydrogenase) (pyruvic dehydrogenase)
ncbi-gi:1560963	mtu:Rv2495c	bkdC	Probable branched-chain keto acid dehydrogenase E2 component BkdC
ncbi-gi:5711703	mtu:Rv2922A	acyP	Probable acylphosphatase AcyP (acylphosphate phosphohydrolase)
ncbi-gi:1561010	mtu:Rv2967c	pca	Probable pyruvate carboxylase Pca (pyruvic carboxylase)
ncbi-gi:1561067	mtu:Rv3535c	hsaG	Probable acetaldehyde dehydrogenase (acetaldehyde dehydrogenase [acetylating])
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561080	mtu:Rv3667	acs	Acetyl-coenzyme A synthetase Acs (acetate--CoA ligase) (acetyl-CoA synthetase) (acetyl-CoA synthase) (acyl-activating enzyme) (acetate thiokinase) (acetyl-activating enzyme) (acetate--coenzyme A ligase) (acetyl-coenzyme A synthase)
ncbi-gi:3454620	mtu:Rv3710	leuA	2-isopropylmalate synthase LeuA (alpha-isopropylmalate synthase) (alpha-IPM synthetase) (IPMS)

mtu00010 Glycolysis / Gluconeogenesis - Mycobacterium tuberculosis H37Rv (20)

ncbi-gi:1560735	mtu:Rv0211	pckA	Probable iron-regulated phosphoenolpyruvate carboxykinase [GTP] PckA (phosphoenolpyruvate carboxylase) (PEPCK)(pep carboxykinase)
ncbi-gi:1560750	mtu:Rv0363c	fba	Probable fructose-bisphosphate aldolase Fba
ncbi-gi:1560760	mtu:Rv0462	lpdC	Dihydrolipoamide dehydrogenase LpdC (lipoamide reductase (NADH)) (lipoyl dehydrogenase) (dihydrolipoyl dehydrogenase) (diaphorase)
ncbi-gi:5711673	mtu:Rv0489	gpm1	Probable phosphoglycerate mutase 1 Gpm1 (phosphoglyceromutase) (PGAM) (BPG-dependent PGAM)
ncbi-gi:5711677	mtu:Rv0761c	adhB	Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB
ncbi-gi:5711678	mtu:Rv0794c	lpdB	Probable oxidoreductase
ncbi-gi:1560808	mtu:Rv0946c	pgi	Probable glucose-6-phosphate isomerase Pgi (GPI) (phosphoglucose isomerase) (phosphohexose isomerase) (phi)
ncbi-gi:1560816	mtu:Rv1023	eno	Probable enolase Eno
ncbi-gi:4488247	mtu:Rv1099c	glpX	Fructose 1,6-bisphosphatase GlpX
ncbi-gi:1560857	mtu:Rv1436	gap	Probable glyceraldehyde 3-phosphate dehydrogenase Gap (GAPDH)
ncbi-gi:1560857	mtu:Rv1437	pgk	Probable phosphoglycerate kinase Pgk

ncbi-gi:1560857	mtu:Rv1438	tpi	Probable triosephosphate isomerase Tpi (TIM)
ncbi-gi:1560875	mtu:Rv1617	pykA	Probable pyruvate kinase PykA
ncbi-gi:1560916	mtu:Rv2029c	pfkB	6-phosphofructokinase PfkB (phosphohexokinase) (phosphofructokinase)
ncbi-gi:4488247	mtu:Rv2241	aceE	Pyruvate dehydrogenase E1 component AceE (pyruvate decarboxylase) (pyruvate dehydrogenase) (pyruvic dehydrogenase)
ncbi-gi:1560955	mtu:Rv2419c	gpgP	Glucosyl-3-phosphoglycerate phosphatase GpgP
ncbi-gi:1560963	mtu:Rv2495c	bkdC	Probable branched-chain keto acid dehydrogenase E2 component BkdC
ncbi-gi:1561014	mtu:Rv3010c	pfkA	Probable 6-phosphofructokinase PfkA (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1561022	mtu:Rv3086	adhD	Probable zinc-type alcohol dehydrogenase AdhD (aldehyde reductase)
ncbi-gi:1561080	mtu:Rv3667	acs	Acetyl-coenzyme A synthetase Acs (acetate--CoA ligase) (acetyl-CoA synthetase) (acetyl-CoA synthase) (acyl-activating enzyme) (acetate thiokinase) (acetyl-activating enzyme) (acetate--coenzyme A ligase) (acetyl-coenzyme A synthase)

mtu00380 Tryptophan metabolism - Mycobacterium tuberculosis H37Rv (18)

ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560754	mtu:Rv0400c	fadE7	Acyl-CoA dehydrogenase FadE7
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560904	mtu:Rv1908c	katG	Catalase-peroxidase-peroxynitritase T KatG
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00362 Benzoate degradation - Mycobacterium tuberculosis H37Rv (18)

ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560760	mtu:Rv0468	fadB2	3-hydroxybutyryl-CoA dehydrogenase FadB2 (beta-hydroxybutyryl-CoA dehydrogenase) (BHBD)
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:4488247	mtu:Rv2790c	ltp1	Probable lipid-transfer protein Ltp1
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561067	mtu:Rv3535c	hsaG	Probable acetaldehyde dehydrogenase (acetaldehyde dehydrogenase [acetylating])
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00410 beta-Alanine metabolism - Mycobacterium tuberculosis H37Rv (18)

ncbi-gi:1560727	mtu:Rv0131c	fadE1	Probable acyl-CoA dehydrogenase FadE1
ncbi-gi:1560729	mtu:Rv0154c	fadE2	Probable acyl-CoA dehydrogenase FadE2
ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560737	mtu:Rv0231	fadE4	Probable acyl-CoA dehydrogenase FadE4
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560789	mtu:Rv0753c	mmsA	Probable methylmalonate-semialdehyde dehydrogenase MmsA (methylmalonic acid semialdehyde dehydrogenase) (MMSDH)
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560972	mtu:Rv2589	gabT	4-aminobutyrate aminotransferase GabT (gamma-amino-N-butyrate transaminase) (GABA transaminase) (glutamate:succinic semialdehyde transaminase) (GABA aminotransferase) (GABA-at)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561027	mtu:Rv3140	fadE23	Probable acyl-CoA dehydrogenase FadE23
ncbi-gi:1561056	mtu:Rv3432c	gadB	Probable glutamate decarboxylase GadB
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00630 Glyoxylate and dicarboxylate metabolism - Mycobacterium tuberculosis H37Rv (17)

ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:5711673	mtu:Rv0467	icl1	Isocitrate lyase Icl (isocitrase) (isocitratase)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560802	mtu:Rv0889c	citA	Probable citrate synthase II CitA
ncbi-gi:1560803	mtu:Rv0896	gltA2	Probable citrate synthase I GltA2
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:4488247	mtu:Rv1093	glyA1	Serine hydroxymethyltransferase 1 GlyA1

ncbi-gi:1560838	mtu:Rv1240	mdh	Probable malate dehydrogenase Mdh
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560861	mtu:Rv1475c	acn	Probable iron-regulated aconitate hydratase Acn (citrate hydro-lyase) (aconitase)
ncbi-gi:1560863	mtu:Rv1492	mutA	Probable methylmalonyl-CoA mutase small subunit MutA (MCM)
ncbi-gi:1560863	mtu:Rv1493	mutB	Probable methylmalonyl-CoA mutase large subunit MutB (MCM)
ncbi-gi:1560897	mtu:Rv1837c	glcB	Malate synthase G GlcB
ncbi-gi:1560935	mtu:Rv2220	glnA1	Glutamine synthetase GlnA1 (glutamine synthase) (GS-I)
ncbi-gi:1560935	mtu:Rv2222c	glnA2	Probable glutamine synthetase GlnA2 (glutamine synthase) (GS-II)
ncbi-gi:1561041	mtu:Rv3280	accD5	Probable propionyl-CoA carboxylase beta chain 5 AccD5 (pccase) (propanoyl-CoA:carbon dioxide ligase)
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)

mtu00970 Aminoacyl-tRNA biosynthesis - Mycobacterium tuberculosis H37Rv (16)

ncbi-gi:1560843	mtu:Rv1292	argS	Probable arginyl-tRNA synthetase ArgS (ARGRS) (arginine--tRNA ligase)
ncbi-gi:1560867	mtu:Rv1536	ileS	Isoleucyl-tRNA synthetase IleS
ncbi-gi:4488247	mtu:Rv1649	pheS	Probable phenylalanyl-tRNA synthetase, alpha chain PheS
ncbi-gi:1560878	mtu:Rv1650	pheT	Probable phenylalanyl-tRNA synthetase, beta chain PheT
ncbi-gi:1560949	mtu:Rv2357c	glyS	Probable glycyl-tRNA synthetase GlyS (glycine--tRNA ligase) (GLYRS)
ncbi-gi:1560958	mtu:Rv2448c	valS	Probable valyl-tRNA synthase protein ValS (valyl-tRNA synthetase) (valine--tRNA ligase) (valine translase)
ncbi-gi:1560969	mtu:Rv2555c	alaS	Probable alanyl-tRNA synthetase AlaS (alanine--tRNA ligase) (alanine translase) (ALARS)
ncbi-gi:1560970	mtu:Rv2572c	aspS	Probable aspartyl-tRNA synthetase AspS (aspartate--tRNA ligase) (ASPRS) (aspartic acid translase)
ncbi-gi:1560975	mtu:Rv2614c	thrS	Probable threonyl-tRNA synthetase ThrS (threonine-tRNA synthetase)(ThrRS) (threonine-tRNA ligase)
ncbi-gi:1560998	mtu:Rv2845c	proS	Probable prolyl-tRNA synthetase ProS (proline--tRNA ligase) (PRORS) (global RNA synthesis factor) (proline translase)
ncbi-gi:5711704	mtu:Rv2992c	gltS	Glutamyl-tRNA synthetase GltS (glutamate--tRNA ligase) (glutamyl-tRNA synthase) (GLURS)
ncbi-gi:1561014	mtu:Rv3009c	gatB	Probable glutamyl-tRNA(GLN) amidotransferase (subunit B) GatB (Glu-ADT subunit B)
ncbi-gi:4488247	mtu:Rv3011c	gatA	Probable glutamyl-tRNA(GLN) amidotransferase (subunit A) GatA (Glu-ADT subunit A)
ncbi-gi:1561047	mtu:Rv3336c	trpS	Probable tryptophanyl-tRNA synthetase TrpS (tryptophan--tRNA ligase) (TRPRS) (tryptophan translase)
ncbi-gi:5711712	mtu:Rv3580c	cysS1	Cysteinyl-tRNA synthetase 1 CysS1 (cysteine--tRNA ligase 1) (CYSRS 1) (cysteine translase)
ncbi-gi:1561073	mtu:Rv3598c	lysS	Lysyl-tRNA synthetase 1 LysS (lysine--tRNA ligase 1) (LysRS 1) (lysine translase)

mtu00190 Oxidative phosphorylation - Mycobacterium tuberculosis H37Rv (16)

ncbi-gi:1560738	mtu:Rv0247c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560738	mtu:Rv0248c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560844	mtu:Rv1306	atpF	Probable ATP synthase B chain AtpF
ncbi-gi:1560844	mtu:Rv1307	atpH	Probable ATP synthase delta chain AtpH
ncbi-gi:1560844	mtu:Rv1308	atpA	Probable ATP synthase alpha chain AtpA
ncbi-gi:1560844	mtu:Rv1309	atpG	Probable ATP synthase gamma chain AtpG
ncbi-gi:1560845	mtu:Rv1310	atpD	Probable ATP synthase beta chain AtpD
ncbi-gi:1560845	mtu:Rv1311	atpC	Probable ATP synthase epsilon chain AtpC
ncbi-gi:1560933	mtu:Rv2195	qcrA	Probable rieske iron-sulfur protein QcrA
ncbi-gi:1560933	mtu:Rv2196	qcrB	Probable ubiquinol-cytochrome C reductase QcrB (cytochrome B subunit)
ncbi-gi:1560933	mtu:Rv2200c	ctaC	Probable transmembrane cytochrome C oxidase (subunit II) CtaC
ncbi-gi:1561012	mtu:Rv2984	ppk1	Polyphosphate kinase PPK (polyphosphoric acid kinase) (ATP-polyphosphate phosphotransferase)
ncbi-gi:1561028	mtu:Rv3149	nuoE	Probable NADH dehydrogenase I (chain E) NuoE (NADH-ubiquinone oxidoreductase chain E)
ncbi-gi:1561028	mtu:Rv3150	nuoF	Probable NADH dehydrogenase I (chain F) NuoF (NADH-ubiquinone oxidoreductase chain F)
ncbi-gi:1561045	mtu:Rv3318	sdhA	Probable succinate dehydrogenase (flavoprotein subunit) SdhA (succinic dehydrogenase) (fumarate reductase) (fumarate dehydrogenase) (fumaric hydrogenase)
ncbi-gi:1561076	mtu:Rv3628	ppa	Inorganic pyrophosphatase Ppa (pyrophosphate phospho-hydrolase) (PPASE) (inorganic diphosphatase) (diphosphate phospho-hydrolase)

mtu00250 Alanine, aspartate and glutamate metabolism - Mycobacterium tuberculosis H37Rv (15)

ncbi-gi:5711670	mtu:Rv0234c	gabD1	Succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD1
ncbi-gi:1560749	mtu:Rv0357c	purA	Probable adenylosuccinate synthetase PurA (imp--aspartate ligase) (ADSS) (ampsase)
ncbi-gi:1560852	mtu:Rv1380	pyrB	Probable aspartate carbamoyltransferase PyrB (ATCase) (aspartate transcarbamylase)
ncbi-gi:1560852	mtu:Rv1383	carA	Probable carbamoyl-phosphate synthase small chain CarA (carbamoyl-phosphate synthetase glutamine chain)
ncbi-gi:5711685	mtu:Rv1384	carB	Probable carbamoyl-phosphate synthase large chain CarB (carbamoyl-phosphate synthetase ammonia chain)
ncbi-gi:5711690	mtu:Rv1731	gabD2	Possible succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD2
ncbi-gi:1560935	mtu:Rv2220	glnA1	Glutamine synthetase GlnA1 (glutamine synthase) (GS-I)
ncbi-gi:1560935	mtu:Rv2222c	glnA2	Probable glutamine synthetase GlnA2 (glutamine synthase) (GS-II)
ncbi-gi:1560961	mtu:Rv2476c	gdh	Probable NAD-dependent glutamate dehydrogenase Gdh (NAD-Gdh) (NAD-dependent glutamic dehydrogenase)
ncbi-gi:1560972	mtu:Rv2589	gabT	4-aminobutyrate aminotransferase GabT (gamma-amino-N-butyrate transaminase) (GABA transaminase) (glutamate:succinic semialdehyde transaminase) (GABA aminotransferase) (GABA-at)
ncbi-gi:1560991	mtu:Rv2780	ald	Secreted L-alanine dehydrogenase Ald (40 kDa antigen) (TB43)
ncbi-gi:1561056	mtu:Rv3432c	gadB	Probable glutamate decarboxylase GadB
ncbi-gi:1561057	mtu:Rv3436c	glmS	Probable glucosamine--fructose-6-phosphate aminotransferase [isomerizing] GlmS (hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (glucosamine-6-phosphate synthase)
ncbi-gi:1561099	mtu:Rv3858c	gltD	Probable NADH-dependent glutamate synthase (small subunit) GltD (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH)) (GLTS beta chain) (NADPH-GOGAT)
ncbi-gi:1561099	mtu:Rv3859c	gltB	Probable ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH))(NADPH-GOGAT)

mtu00680 Methane metabolism - Mycobacterium tuberculosis H37Rv (15)

ncbi-gi:1560750	mtu:Rv0363c	fba	Probable fructose-bisphosphate aldolase Fba
ncbi-gi:1560754	mtu:Rv0408	pta	Probable phosphate acetyltransferase Pta (phosphotransacetylase)
ncbi-gi:5711673	mtu:Rv0489	gpm1	Probable phosphoglycerate mutase 1 Gpm1 (phosphoglyceromutase) (PGAM) (BPG-dependent PGAM)
ncbi-gi:5711677	mtu:Rv0761c	adhB	Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB
ncbi-gi:1560802	mtu:Rv0884c	serC	Possible phosphoserine aminotransferase SerC (PSAT)
ncbi-gi:1560816	mtu:Rv1023	eno	Probable enolase Eno
ncbi-gi:4488247	mtu:Rv1093	glyA1	Serine hydroxymethyltransferase 1 GlyA1
ncbi-gi:4488247	mtu:Rv1099c	glpX	Fructose 1,6-bisphosphatase GlpX
ncbi-gi:1560838	mtu:Rv1240	mdh	Probable malate dehydrogenase Mdh
ncbi-gi:1560916	mtu:Rv2029c	pfkB	6-phosphofructokinase PfkB (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1560955	mtu:Rv2419c	gpgP	Glucosyl-3-phosphoglycerate phosphatase GpgP
ncbi-gi:5711704	mtu:Rv2996c	serA1	Probable D-3-phosphoglycerate dehydrogenase SerA1 (PGDH)
ncbi-gi:1561014	mtu:Rv3010c	pfkA	Probable 6-phosphofructokinase PfkA (phosphohexokinase) (phosphofructokinase)

ncbi-gi:1561022	mtu:Rv3086	adhD	Probable zinc-type alcohol dehydrogenase AdhD (aldehyde reductase)
ncbi-gi:1561080	mtu:Rv3667	acs	Acetyl-coenzyme A synthetase Acs (acetate--CoA ligase) (acetyl-CoA synthetase) (acetyl-CoA synthase) (acyl-activating enzyme) (acetate thiokinase) (acetyl-activating enzyme) (acetate--coenzyme A ligase) (acetyl-coenzyme A synthase)

mtu02020 Two-component system - Mycobacterium tuberculosis H37Rv (14)

ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560804	mtu:Rv0903c	prrA	Two component response transcriptional regulatory protein PrrA
ncbi-gi:5711680	mtu:Rv0932c	pstS2	Periplasmic phosphate-binding lipoprotein PstS2 (PBP-2) (PstS2)
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560935	mtu:Rv2220	glnA1	Glutamine synthetase GlnA1 (glutamine synthase) (GS-I)
ncbi-gi:1560935	mtu:Rv2222c	glnA2	Probable glutamine synthetase GlnA2 (glutamine synthase) (GS-II)
ncbi-gi:1560963	mtu:Rv2498c	citE	Probable citrate (pro-3S)-lyase (beta subunit) CitE (citrase) (citratase) (citritase) (citridesmolase) (citrase aldolase)
ncbi-gi:1561005	mtu:Rv2919c	glnB	Probable nitrogen regulatory protein P-II GlnB
ncbi-gi:1561021	mtu:Rv3075c		hypothetical protein
ncbi-gi:1561026	mtu:Rv3133c	devR	Two component transcriptional regulatory protein DevR (probably LuxR/UhpA-family)
ncbi-gi:1561038	mtu:Rv3246c	mtrA	Two component sensory transduction transcriptional regulatory protein MtrA
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)

mtu01210 2-Oxocarboxylic acid metabolism - Mycobacterium tuberculosis H37Rv (14)

ncbi-gi:1560720	mtu:Rv0066c	icd2	Probable isocitrate dehydrogenase [NADP] Icd2 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1560733	mtu:Rv0189c	ilvD	Probable dihydroxy-acid dehydratase IlvD (dad)
ncbi-gi:1560802	mtu:Rv0889c	citA	Probable citrate synthase II CitA
ncbi-gi:1560803	mtu:Rv0896	gltA2	Probable citrate synthase I GltA2
ncbi-gi:1560861	mtu:Rv1475c	acn	Probable iron-regulated aconitate hydratase Acn (citrate hydro-lyase) (aconitase)
ncbi-gi:1560879	mtu:Rv1654	argB	Probable acetylglutamate kinase ArgB
ncbi-gi:1560879	mtu:Rv1655	argD	Probable acetylornithine aminotransferase ArgD
ncbi-gi:1560934	mtu:Rv2210c	ilvE	Branched-chain amino acid transaminase IlvE
ncbi-gi:1561013	mtu:Rv2995c	leuB	Probable 3-isopropylmalate dehydrogenase LeuB (beta-IPM dehydrogenase) (IMDH) (3-IPM-DH)
ncbi-gi:4488247	mtu:Rv3001c	ilvC	Probable KETOL-acid reductoisomerase IlvC (acetohydroxy-acid isomeroreductase) (alpha-keto-beta-hydroxylacil reductoisomerase)
ncbi-gi:1561013	mtu:Rv3002c	ilvN	Probable acetolactate synthase (small subunit) IlvN (acetohydroxy-acid synthase) (AHAS) (ALS)
ncbi-gi:5711704	mtu:Rv3003c	ilvB1	Acetolactate synthase (large subunit) IlvB1 (acetohydroxy-acid synthase)
ncbi-gi:1561047	mtu:Rv3339c	icd1	Probable isocitrate dehydrogenase [NADP] Icd1 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:3454620	mtu:Rv3710	leuA	2-isopropylmalate synthase LeuA (alpha-isopropylmalate synthase) (alpha-IPM synthetase) (IPMS)

mtu00240 Pyrimidine metabolism - Mycobacterium tuberculosis H37Rv (14)

ncbi-gi:1560714	mtu:Rv0002	dnaN	DNA polymerase III (beta chain) DnaN (DNA nucleotidyltransferase)
ncbi-gi:1560780	mtu:Rv0667	rpoB	DNA-directed RNA polymerase (beta chain) RpoB (transcriptase beta chain) (RNA polymerase beta subunit)
ncbi-gi:1560780	mtu:Rv0668	rpoC	DNA-directed RNA polymerase (beta' chain) RpoC (transcriptase beta' chain) (RNA polymerase beta' subunit)
ncbi-gi:1560851	mtu:Rv1379	pyrR	Probable pyrimidine operon regulatory protein PyrR
ncbi-gi:1560852	mtu:Rv1380	pyrB	Probable aspartate carbamoyltransferase PyrB (ATCase) (aspartate transcarbamylase)
ncbi-gi:1560852	mtu:Rv1383	carA	Probable carbamoyl-phosphate synthase small chain CarA (carbamoyl-phosphate synthetase glutamine chain)
ncbi-gi:5711685	mtu:Rv1384	carB	Probable carbamoyl-phosphate synthase large chain CarB (carbamoyl-phosphate synthetase ammonia chain)
ncbi-gi:1560876	mtu:Rv1629	polA	Probable DNA polymerase I PolA
ncbi-gi:1560883	mtu:Rv1699	pyrG	Probable CTP synthase PyrG
ncbi-gi:1560983	mtu:Rv2697c	dut	Probable deoxyuridine 5'-triphosphate nucleotidohydrolase Dut (dUTPase) (dUTP pyrophosphatase) (deoxyuridine 5'-triphosphatase) (dUTP diphosphatase) (deoxyuridine-triphosphatase)
ncbi-gi:1560992	mtu:Rv2783c	gpsI	Bifunctional protein polyribonucleotide nucleotidyltransferase GpsI: guanosine pentaphosphate synthetase + polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase) (pnpase)
ncbi-gi:5711705	mtu:Rv3048c	nrdF2	Ribonucleoside-diphosphate reductase (beta chain) NrdF2 (ribonucleotide reductase small subunit) (R2F protein)
ncbi-gi:1561018	mtu:Rv3051c	nrdE	Ribonucleoside-diphosphate reductase (alpha chain) NrdE (ribonucleotide reductase small subunit) (R1F protein)
ncbi-gi:1561059	mtu:Rv3457c	rpoA	Probable DNA-directed RNA polymerase (alpha chain) RpoA (transcriptase alpha chain) (RNA polymerase alpha subunit) (DNA-directed RNA nucleotidyltransferase)

mtu00260 Glycine, serine and threonine metabolism - Mycobacterium tuberculosis H37Rv (12)

ncbi-gi:1560760	mtu:Rv0462	lpdC	Dihydrolipoamide dehydrogenase LpdC (lipoamide reductase (NADH)) (lipoyl dehydrogenase) (dihydrolipoyl dehydrogenase) (diaphorase)
ncbi-gi:5711673	mtu:Rv0489	gpm1	Probable phosphoglycerate mutase 1 Gpm1 (phosphoglyceromutase) (PGAM) (BPG-dependent PGAM)
ncbi-gi:5711678	mtu:Rv0794c	lpdB	Probable oxidoreductase
ncbi-gi:1560802	mtu:Rv0884c	serC	Possible phosphoserine aminotransferase SerC (PSAT)
ncbi-gi:5711682	mtu:Rv1077	cbs	Probable cystathionine beta-synthase Cbs (serine sulfhydrase) (beta-thionase) (hemoprotein H-450)
ncbi-gi:4488247	mtu:Rv1093	glyA1	Serine hydroxymethyltransferase 1 GlyA1
ncbi-gi:1560843	mtu:Rv1295	thrC	Threonine synthase ThrC (ts)
ncbi-gi:1560869	mtu:Rv1559	ilvA	Probable threonine dehydratase IlvA
ncbi-gi:1560896	mtu:Rv1832	gcvB	Probable glycine dehydrogenase GcvB (glycine decarboxylase) (glycine cleavage system P-protein)
ncbi-gi:1560934	mtu:Rv2211c	gcvT	Probable aminomethyltransferase GcvT (glycine cleavage system T protein)
ncbi-gi:1560955	mtu:Rv2419c	gpgP	Glucosyl-3-phosphoglycerate phosphatase GpgP
ncbi-gi:5711704	mtu:Rv2996c	serA1	Probable D-3-phosphoglycerate dehydrogenase SerA1 (PGDH)

mtu00903 Limonene and pinene degradation - Mycobacterium tuberculosis H37Rv (12)

ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560736	mtu:Rv0223c		Probable aldehyde dehydrogenase
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00360 Phenylalanine metabolism - Mycobacterium tuberculosis H37Rv (12)

ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560760	mtu:Rv0468	fadB2	3-hydroxybutyryl-CoA dehydrogenase FadB2 (beta-hydroxybutyryl-CoA dehydrogenase) (BHBD)
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560904	mtu:Rv1908c	katG	Catalase-peroxidase-peroxynitritase T KatG
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00030 Pentose phosphate pathway - Mycobacterium tuberculosis H37Rv (11)

ncbi-gi:1560750	mtu:Rv0363c	fba	Probable fructose-bisphosphate aldolase Fba
ncbi-gi:1560808	mtu:Rv0946c	pgi	Probable glucose-6-phosphate isomerase Pgi (GPI) (phosphoglucose isomerase) (phosphohexose isomerase) (phi)
ncbi-gi:1560815	mtu:Rv1017c	prsA	Probable ribose-phosphate pyrophosphokinase PrsA (phosphoribosyl pyrophosphate synthetase) (PRPP synthetase)
ncbi-gi:4488247	mtu:Rv1099c	glpX	Fructose 1,6-bisphosphatase GlpX
ncbi-gi:5711683	mtu:Rv1121	zwf1	Probable glucose-6-phosphate 1-dehydrogenase Zwf1 (G6PD)
ncbi-gi:1560826	mtu:Rv1122	gnd2	Probable 6-phosphogluconate dehydrogenase,decarboxylating Gnd2
ncbi-gi:1560858	mtu:Rv1448c	tal	Probable transaldolase Tal
ncbi-gi:1560858	mtu:Rv1449c	tkt	Transketolase Tkt (TK)
ncbi-gi:1560916	mtu:Rv2029c	pfkB	6-phosphofructokinase PfkB (phosphohexokinase) (phosphofructokinase)
ncbi-gi:5711699	mtu:Rv2465c	rpiB	Ribose-5-phosphate isomerase
ncbi-gi:1561014	mtu:Rv3010c	pfkA	Probable 6-phosphofructokinase PfkA (phosphohexokinase) (phosphofructokinase)

mtu00930 Caprolactam degradation - Mycobacterium tuberculosis H37Rv (11)

ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00627 Aminobenzoate degradation - Mycobacterium tuberculosis H37Rv (11)

ncbi-gi:1560736	mtu:Rv0222	echA1	Probable enoyl-CoA hydratase EchA1 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560777	mtu:Rv0632c	echA3	Probable enoyl-CoA hydratase EchA3 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711676	mtu:Rv0675	echA5	Probable enoyl-CoA hydratase EchA5 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560804	mtu:Rv0905	echA6	Possible enoyl-CoA hydratase EchA6 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560811	mtu:Rv0971c	echA7	Probable enoyl-CoA hydratase EchA7 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1070c	echA8	Probable enoyl-CoA hydratase EchA8 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560821	mtu:Rv1071c	echA9	Possible enoyl-CoA hydratase EchA9 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1560981	mtu:Rv2679	echA15	Probable enoyl-CoA hydratase EchA15 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:5711703	mtu:Rv2922A	acyP	Probable acylphosphatase AcyP (acylphosphate phosphohydrolase)
ncbi-gi:1561065	mtu:Rv3516	echA19	Possible enoyl-CoA hydratase EchA19 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)
ncbi-gi:1561091	mtu:Rv3774	echA21	Possible enoyl-CoA hydratase EchA21 (enoyl hydrase) (unsaturated acyl-CoA hydratase) (crotonase)

mtu00270 Cysteine and methionine metabolism - Mycobacterium tuberculosis H37Rv (10)

ncbi-gi:1560753	mtu:Rv0391	metZ	Probable O-succinylhomoserine sulfhydrylase MetZ (OSH sulfhydrylase)
ncbi-gi:1560795	mtu:Rv0815c	cysA2	Probable thiosulfate sulfurtransferase CysA2 (rhodanese-like protein) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)
ncbi-gi:5711682	mtu:Rv1077	cbs	Probable cystathionine beta-synthase Cbs (serine sulfhydrase) (beta-thionase) (hemoprotein H-450)
ncbi-gi:1560821	mtu:Rv1079	metB	Cystathionine gamma-synthase MetB (CGS) (O-succinylhomoserine [thiol]-lyase)
ncbi-gi:1560827	mtu:Rv1133c	metE	Probable 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase MetE (methionine synthase, vitamin-B12 independent isozyme)
ncbi-gi:1560853	mtu:Rv1392	metK	Probable S-adenosylmethionine synthetase MetK (mat) (AdoMet synthetase) (methionine adenosyltransferase)
ncbi-gi:5711697	mtu:Rv2334	cysK1	Cysteine synthase a CysK1 (O-acetylserine sulfhydrylase A) (O-acetylserine (thiol)-lyase A) (CSASE A)
ncbi-gi:1561038	mtu:Rv3248c	sahH	Probable adenosylhomocysteinase SahH (S-adenosyl-L-homocysteine hydrolase) (adohcyase)
ncbi-gi:1561041	mtu:Rv3283	sseA	Probable thiosulfate sulfurtransferase SseA (rhodanese) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)
ncbi-gi:1561047	mtu:Rv3340	metC	Probable O-acetylhomoserine sulfhydrylase MetC (homocysteine synthase) (O-acetylhomoserine (thiol)-lyase) (OAH sulfhydrylase) (O-acetyl-L-homoserine sulfhydrylase)

mtu03018 RNA degradation - Mycobacterium tuberculosis H37Rv (9)

ncbi-gi:1560749	mtu:Rv0350	dnaK	Probable chaperone protein DnaK (heat shock protein 70) (heat shock 70 kDa protein) (HSP70)
ncbi-gi:1560758	mtu:Rv0440	groEL2	60 kDa chaperonin 2 GroEL2 (protein CPN60-2) (GroEL protein 2) (65 kDa antigen) (heat shock protein 65) (cell wall protein A) (antigen A)
ncbi-gi:1560816	mtu:Rv1023	eno	Probable enolase Eno
ncbi-gi:1560843	mtu:Rv1297	rho	Probable transcription termination factor Rho homolog
ncbi-gi:1560958	mtu:Rv2444c	rne	Possible ribonuclease E Rne

ncbi-gi:1560992	mtu:Rv2783c	gpsI	Bifunctional protein polyribonucleotide nucleotidyltransferase GpsI: guanosine pentaphosphate synthetase + polyribonucleotide nucleotidyltransferase (polynucleotide phosphorylase) (pnpase)
ncbi-gi:1561012	mtu:Rv2984	ppk1	Polyphosphate kinase PPK (polyphosphoric acid kinase) (ATP-polyphosphate phosphotransferase)
ncbi-gi:1561055	mtu:Rv3417c	groEL1	60 kDa chaperonin 1 GroEL1 (protein CPN60-1) (GroEL protein 1)
ncbi-gi:5711716	mtu:Rv3907c	pcnA	Probable poly(A) polymerase PcnA (polynucleotide adenylyltransferase) (NTP polymerase) (RNA adenylating enzyme) (poly(A) polymerase)

mtu00770 Pantothenate and CoA biosynthesis - Mycobacterium tuberculosis H37Rv (9)

ncbi-gi:1560733	mtu:Rv0189c	ilvD	Probable dihydroxy-acid dehydratase IlvD (dad)
ncbi-gi:1560853	mtu:Rv1391	dfp	Probable DNA/pantothenate metabolism flavoprotein homolog Dfp
ncbi-gi:1560876	mtu:Rv1631	coaE	Probable dephospho-CoA kinase CoaE (dephosphocoenzyme a kinase)
ncbi-gi:1560934	mtu:Rv2210c	ilvE	Branched-chain amino acid transaminase IlvE
ncbi-gi:1561010	mtu:Rv2965c	kdtB	Probable phosphopantetheine adenylyltransferase KdtB (pantetheine-phosphate adenylyltransferase) (PPAT) (dephospho-CoA pyrophosphorylase)
ncbi-gi:4488247	mtu:Rv3001c	ilvC	Probable KETOL-acid reductoisomerase IlvC (acetohydroxy-acid isomeroreductase) (alpha-keto-beta-hydroxylacil reductoisomerase)
ncbi-gi:1561013	mtu:Rv3002c	ilvN	Probable acetolactate synthase (small subunit) IlvN (acetohydroxy-acid synthase) (AHAS) (ALS)
ncbi-gi:5711704	mtu:Rv3003c	ilvB1	Acetolactate synthase (large subunit) IlvB1 (acetohydroxy-acid synthase)
ncbi-gi:1561073	mtu:Rv3600c		hypothetical protein

mtu00520 Amino sugar and nucleotide sugar metabolism - Mycobacterium tuberculosis H37Rv (8)

ncbi-gi:1560762	mtu:Rv0482	murB	Probable UDP-N-acetylenolpyruvoylglucosamine reductase MurB (UDP-N-acetylmuramate dehydrogenase)
ncbi-gi:1560808	mtu:Rv0946c	pgi	Probable glucose-6-phosphate isomerase Pgi (GPI) (phosphoglucose isomerase) (phosphohexose isomerase) (phi)
ncbi-gi:1560815	mtu:Rv1018c	glmU	Probable UDP-N-acetylglucosamine pyrophosphorylase GlmU
ncbi-gi:1560845	mtu:Rv1315	murA	Probable UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
ncbi-gi:1561039	mtu:Rv3255c	manA	Probable mannose-6-phosphate isomerase ManA (phosphomannose isomerase) (phosphomannoisomerase) (PMI) (phosphohexoisomerase) (phosphohexomutase)
ncbi-gi:5711708	mtu:Rv3264c	manB	D-alpha-D-mannose-1-phosphate guanylyltransferase ManB (D-alpha-D-heptose-1-phosphate guanylyltransferase)
ncbi-gi:1561057	mtu:Rv3436c	glmS	Probable glucosamine--fructose-6-phosphate aminotransferase [isomerizing] GlmS (hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (glucosamine-6-phosphate synthase)
ncbi-gi:5711713	mtu:Rv3634c	galE1	UDP-glucose 4-epimerase GalE1 (galactowaldenase) (UDP-galactose 4-epimerase) (uridine diphosphate galactose 4-epimerase) (uridine diphospho-galactose 4-epimerase)

mtu00480 Glutathione metabolism - Mycobacterium tuberculosis H37Rv (8)

ncbi-gi:1560720	mtu:Rv0066c	icd2	Probable isocitrate dehydrogenase [NADP] Icd2 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)
ncbi-gi:1560740	mtu:Rv0266c	oplA	Probable 5-oxoprolinase OplA (5-oxo-L-prolinase) (pyroglutamase) (5-OPASE)
ncbi-gi:1560791	mtu:Rv0773c	ggtA	Probable bifunctional acylase GgtA: cephalosporin acylase (GL-7ACA acylase) + gamma-glutamyltranspeptidase (GGT)
ncbi-gi:5711683	mtu:Rv1121	zwf1	Probable glucose-6-phosphate 1-dehydrogenase Zwf1 (G6PD)
ncbi-gi:1560826	mtu:Rv1122	gnd2	Probable 6-phosphogluconate dehydrogenase,decarboxylating Gnd2
ncbi-gi:1560935	mtu:Rv2213	pepB	Probable aminopeptidase PepB
ncbi-gi:5711699	mtu:Rv2467	pepN	Probable aminopeptidase N PepN (Lysyl aminopeptidase) (LYS-AP) (alanine aminopeptidase)
ncbi-gi:1561047	mtu:Rv3339c	icd1	Probable isocitrate dehydrogenase [NADP] Icd1 (oxalosuccinate decarboxylase) (IDH) (NADP+-specific ICDH) (IDP)

mtu00900 Terpenoid backbone biosynthesis - Mycobacterium tuberculosis H37Rv (8)

ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:5711682	mtu:Rv1110	lytB2	Probable LYTB-related protein LytB2
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1561000	mtu:Rv2868c	gcpE	Probable GcpE protein
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)
ncbi-gi:1561071	mtu:Rv3581c	ispF	Probable 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF (MECPS)

mtu00290 Valine, leucine and isoleucine biosynthesis - Mycobacterium tuberculosis H37Rv (8)

ncbi-gi:1560733	mtu:Rv0189c	ilvD	Probable dihydroxy-acid dehydratase IlvD (dad)
ncbi-gi:1560869	mtu:Rv1559	ilvA	Probable threonine dehydratase IlvA
ncbi-gi:1560934	mtu:Rv2210c	ilvE	Branched-chain amino acid transaminase IlvE
ncbi-gi:1561013	mtu:Rv2995c	leuB	Probable 3-isopropylmalate dehydrogenase LeuB (beta-IPM dehydrogenase) (IMDH) (3-IPM-DH)
ncbi-gi:4488247	mtu:Rv3001c	ilvC	Probable KETOL-acid reductoisomerase IlvC (acetohydroxy-acid isomeroreductase) (alpha-keto-beta-hydroxylacil reductoisomerase)
ncbi-gi:1561013	mtu:Rv3002c	ilvN	Probable acetolactate synthase (small subunit) IlvN (acetohydroxy-acid synthase) (AHAS) (ALS)
ncbi-gi:5711704	mtu:Rv3003c	ilvB1	Acetolactate synthase (large subunit) IlvB1 (acetohydroxy-acid synthase)
ncbi-gi:3454620	mtu:Rv3710	leuA	2-isopropylmalate synthase LeuA (alpha-isopropylmalate synthase) (alpha-IPM synthetase) (IPMS)

mtu00400 Phenylalanine, tyrosine and tryptophan biosynthesis - Mycobacterium tuberculosis H37Rv (8)

ncbi-gi:1560874	mtu:Rv1603	hisA	Probable phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA
ncbi-gi:1560874	mtu:Rv1611	trpC	Probable indole-3-glycerol phosphate synthase TrpC
ncbi-gi:1560931	mtu:Rv2178c	aroG	3-deoxy-D-arabino-heptulosonate 7-phosphate synthase AroG (DAHP synthetase, phenylalanine-repressible)
ncbi-gi:1560967	mtu:Rv2537c	aroD	3-dehydroquinate dehydratase AroD (AROQ) (3-dehydroquinase) (type II dhqase)
ncbi-gi:1560967	mtu:Rv2538c	aroB	3-dehydroquinate synthase AroB
ncbi-gi:1560967	mtu:Rv2540c	aroF	Probable chorismate synthase AroF (5-enolpyruvylshikimate-3-phosphate phospholyase)
ncbi-gi:1561036	mtu:Rv3227	aroA	3-phosphoshikimate 1-carboxyvinyltransferase AroA (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS)
ncbi-gi:1561097	mtu:Rv3838c	pheA	Prephenate dehydratase PheA

mtu00051 Fructose and mannose metabolism - Mycobacterium tuberculosis H37Rv (8)

ncbi-gi:1560750	mtu:Rv0363c	fba	Probable fructose-bisphosphate aldolase Fba
ncbi-gi:4488247	mtu:Rv1099c	glpX	Fructose 1,6-bisphosphatase GlpX
ncbi-gi:1560857	mtu:Rv1438	tpi	Probable triosephosphate isomerase Tpi (TIM)
ncbi-gi:1560916	mtu:Rv2029c	pfkB	6-phosphofructokinase PfkB (phosphohexokinase) (phosphofructokinase)
ncbi-gi:5711699	mtu:Rv2465c	rpiB	Ribose-5-phosphate isomerase

ncbi-gi:1561014	mtu:Rv3010c	pfkA	Probable 6-phosphofructokinase PfkA (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1561039	mtu:Rv3255c	manA	Probable mannose-6-phosphate isomerase ManA (phosphomannose isomerase) (phosphomannoisomerase) (PMI) (phosphohexoisomerase) (phosphohexomutase)
ncbi-gi:5711708	mtu:Rv3264c	manB	D-alpha-D-mannose-1-phosphate guanylyltransferase ManB (D-alpha-D-heptose-1-phosphate guanylyltransferase)

mtu00910 Nitrogen metabolism - Mycobacterium tuberculosis H37Rv (7)

ncbi-gi:1560842	mtu:Rv1284	canA	Beta-carbonic anhydrase
ncbi-gi:1560935	mtu:Rv2220	glnA1	Glutamine synthetase GlnA1 (glutamine synthase) (GS-I)
ncbi-gi:1560935	mtu:Rv2222c	glnA2	Probable glutamine synthetase GlnA2 (glutamine synthase) (GS-II)
ncbi-gi:1560961	mtu:Rv2476c	gdh	Probable NAD-dependent glutamate dehydrogenase Gdh (NAD-Gdh) (NAD-dependent glutamic dehydrogenase)
ncbi-gi:1560991	mtu:Rv2781c		Possible alanine rich oxidoreductase
ncbi-gi:1561099	mtu:Rv3858c	gltD	Probable NADH-dependent glutamate synthase (small subunit) GltD (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH)) (GLTS beta chain) (NADPH-GOGAT)
ncbi-gi:1561099	mtu:Rv3859c	gltB	Probable ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB (L-glutamate synthase) (L-glutamate synthetase) (NADH-glutamate synthase) (glutamate synthase (NADH))(NADPH-GOGAT)

mtu00330 Arginine and proline metabolism - Mycobacterium tuberculosis H37Rv (7)

ncbi-gi:1560764	mtu:Rv0500	proC	Probable pyrroline-5-carboxylate reductase ProC (P5CR) (P5C reductase)
ncbi-gi:1560879	mtu:Rv1654	argB	Probable acetylglutamate kinase ArgB
ncbi-gi:1560879	mtu:Rv1655	argD	Probable acetylornithine aminotransferase ArgD
ncbi-gi:1560879	mtu:Rv1656	argF	Probable ornithine carbamoyltransferase, anabolic ArgF
ncbi-gi:1560935	mtu:Rv2220	glnA1	Glutamine synthetase GlnA1 (glutamine synthase) (GS-I)
ncbi-gi:1560935	mtu:Rv2222c	glnA2	Probable glutamine synthetase GlnA2 (glutamine synthase) (GS-II)
ncbi-gi:1560961	mtu:Rv2476c	gdh	Probable NAD-dependent glutamate dehydrogenase Gdh (NAD-Gdh) (NAD-dependent glutamic dehydrogenase)

mtu00061 Fatty acid biosynthesis - Mycobacterium tuberculosis H37Rv (7)

ncbi-gi:1560738	mtu:Rv0242c	fabG4	Probable 3-oxoacyl-[acyl-carrier protein] reductase FabG4 (3-ketoacyl-acyl carrier protein reductase)
ncbi-gi:5711678	mtu:Rv0824c	desA1	Probable acyl-[acyl-carrier protein] desaturase DesA1 (acyl-[ACP] desaturase) (stearoyl-ACP desaturase) (protein Des)
ncbi-gi:1560823	mtu:Rv1094	desA2	Possible acyl-[acyl-carrier protein] desaturase DesA2 (acyl-[ACP] desaturase) (stearoyl-ACP desaturase)
ncbi-gi:1560849	mtu:Rv1350	fabG2	Probable 3-oxoacyl-[acyl-carrier protein] reductase FabG2 (3-ketoacyl-acyl carrier protein reductase)
ncbi-gi:1560963	mtu:Rv2501c	accA1	Probable acetyl-/propionyl-coenzyme A carboxylase alpha chain (alpha subunit) AccA1: biotin carboxylase + biotin carboxyl carrier protein (BCCP)
ncbi-gi:1560966	mtu:Rv2524c	fas	Probable fatty acid synthase Fas (fatty acid synthetase)
ncbi-gi:1561042	mtu:Rv3285	accA3	Probable bifunctional protein acetyl-/propionyl-coenzyme A carboxylase (alpha chain) AccA3: biotin carboxylase + biotin carboxyl carrier protein (BCCP)

mtu00072 Synthesis and degradation of ketone bodies - Mycobacterium tuberculosis H37Rv (7)

ncbi-gi:1560738	mtu:Rv0243	fadA2	Probable acetyl-CoA acyltransferase FadA2 (3-ketoacyl-CoA thiolase) (beta-ketothiolase)
ncbi-gi:1560799	mtu:Rv0859	fadA	Possible acyl-CoA thiolase FadA
ncbi-gi:1560821	mtu:Rv1074c	fadA3	Probable beta-ketoacyl CoA thiolase FadA3
ncbi-gi:1560846	mtu:Rv1323	fadA4	Probable acetyl-CoA acetyltransferase FadA4 (acetoacetyl-CoA thiolase)
ncbi-gi:1560964	mtu:Rv2503c	scoB	Probable succinyl-CoA:3-ketoacid-coenzyme A transferase (beta subunit) ScoB (3-oxo-acid:CoA transferase) (OXCT B) (succinyl CoA:3-oxoacid CoA-transferase)
ncbi-gi:1560964	mtu:Rv2504c	scoA	Probable succinyl-CoA:3-ketoacid-coenzyme A transferase (alpha subunit) ScoA (3-oxo acid:CoA transferase) (OXCT A) (succinyl-CoA:3-oxoacid-coenzyme A transferase)
ncbi-gi:1561069	mtu:Rv3556c	fadA6	Probable acetyl-CoA acetyltransferase FadA6 (acetoacetyl-CoA thiolase)

mtu00920 Sulfur metabolism - Mycobacterium tuberculosis H37Rv (6)

ncbi-gi:1560753	mtu:Rv0391	metZ	Probable O-succinylhomoserine sulfhydrylase MetZ (OSH sulfhydrylase)
ncbi-gi:1560795	mtu:Rv0815c	cysA2	Probable thiosulfate sulfurtransferase CysA2 (rhodanese-like protein) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)
ncbi-gi:1560821	mtu:Rv1079	metB	Cystathionine gamma-synthase MetB (CGS) (O-succinylhomoserine [thiol]-lyase)
ncbi-gi:5711697	mtu:Rv2334	cysK1	Cysteine synthase a CysK1 (O-acetylserine sulfhydrylase A) (O-acetylserine (thiol)-lyase A) (CSASE A)
ncbi-gi:1560952	mtu:Rv2391	sirA	Ferredoxin-dependent sulfite reductase SirA
ncbi-gi:1561041	mtu:Rv3283	sseA	Probable thiosulfate sulfurtransferase SseA (rhodanese) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)

mtu00760 Nicotinate and nicotinamide metabolism - Mycobacterium tuberculosis H37Rv (5)

ncbi-gi:1560729	mtu:Rv0155	pntAa	Probable N catalytic part] (pyridine nucleotide transhydrogenase subunit alpha) (nicotinamide nucleotide transhydrogenase subunit alpha)
ncbi-gi:1560873	mtu:Rv1596	nadC	Probable nicotinate-nucleotide pyrophosphatase NadC
ncbi-gi:1560883	mtu:Rv1695	ppnK	Inorganic polyphosphate/ATP-NAD kinase PpnK (poly(P)/ATP NAD kinase)
ncbi-gi:5711699	mtu:Rv2438c	nadE	Glutamine-dependent NAD(+) synthetase NadE (NAD(+) synthase [glutamine-hydrolysing])
ncbi-gi:1560985	mtu:Rv2713	sthA	Probable soluble pyridine nucleotide transhydrogenase SthA (STH) (NAD(P)(+) transhydrogenase [B-specific]) (nicotinamide nucleotide transhydrogenase)

mtu00300 Lysine biosynthesis - Mycobacterium tuberculosis H37Rv (5)

ncbi-gi:1560799	mtu:Rv0858c	dapC	Probable N-succinyldiaminopimelate aminotransferase DapC (DAP-at)
ncbi-gi:1560834	mtu:Rv1201c	dapD	Tetrahydrodipicolinate N-succinyltransferase DapD
ncbi-gi:1560986	mtu:Rv2726c	dapF	Probable diaminopimelate epimerase DapF (DAP epimerase)
ncbi-gi:1560989	mtu:Rv2753c	dapA	Probable dihydrodipicolinate synthase DapA (DHDPS) (dihydrodipicolinate synthetase)
ncbi-gi:1560991	mtu:Rv2773c	dapB	Dihydrodipicolinate reductase DapB (DHPR)

mtu00430 Taurine and hypotaurine metabolism - Mycobacterium tuberculosis H37Rv (5)

ncbi-gi:1560754	mtu:Rv0408	pta	Probable phosphate acetyltransferase Pta (phosphotransacetylase)
ncbi-gi:1560791	mtu:Rv0773c	ggtA	Probable bifunctional acylase GgtA: cephalosporin acylase (GL-7ACA acylase) + gamma-glutamyltranspeptidase (GGT)
ncbi-gi:1560961	mtu:Rv2476c	gdh	Probable NAD-dependent glutamate dehydrogenase Gdh (NAD-Gdh) (NAD-dependent glutamic dehydrogenase)
ncbi-gi:1560991	mtu:Rv2780	ald	Secreted L-alanine dehydrogenase Ald (40 kDa antigen) (TB43)
ncbi-gi:1561056	mtu:Rv3432c	gadB	Probable glutamate decarboxylase GadB

mtu00350 Tyrosine metabolism - Mycobacterium tuberculosis H37Rv (5)

ncbi-gi:5711670	mtu:Rv0234c	gabD1	Succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD1
ncbi-gi:5711677	mtu:Rv0761c	adhB	Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB
ncbi-gi:4488247	mtu:Rv1703c		Probable catechol-O-methyltransferase
ncbi-gi:5711690	mtu:Rv1731	gabD2	Possible succinate-semialdehyde dehydrogenase [NADP+] dependent (SSDH) GabD2
ncbi-gi:1561022	mtu:Rv3086	adhD	Probable zinc-type alcohol dehydrogenase AdhD (aldehyde reductase)

mtu00670 One carbon pool by folate - Mycobacterium tuberculosis H37Rv (5)

ncbi-gi:1560753	mtu:Rv0389	purT	Probable phosphoribosylglycinamide formyltransferase 2 PurT (GART 2) (gar transformylase 2) (5'-phosphoribosylglycinamide transformylase 2) (formate-dependent gar transformylase)
ncbi-gi:1560809	mtu:Rv0957	purH	Probable bifunctional purine biosynthesis protein PurH: phosphoribosylaminoimidazolecarboxamide formyltransferase (AICAR transformylase) (5'-phosphoribosyl-5-aminoimidazole-4-carboxamide formyltransferase) + inosinemonophosphate cyclohydrolase (imp cyclohydrolase) (inosinicase) (imp synthetase) (ATIC)
ncbi-gi:4488247	mtu:Rv1093	glyA1	Serine hydroxymethyltransferase 1 GlyA1
ncbi-gi:1560934	mtu:Rv2211c	gcvT	Probable aminomethyltransferase GcvT (glycine cleavage system T protein)
ncbi-gi:1561049	mtu:Rv3356c	folD	Probable bifunctional protein FolD: methylenetetrahydrofolate dehydrogenase + methenyltetrahydrofolate cyclohydrolase

mtu01040 Biosynthesis of unsaturated fatty acids - Mycobacterium tuberculosis H37Rv (5)

ncbi-gi:1560738	mtu:Rv0242c	fabG4	Probable 3-oxoacyl-[acyl-carrier protein] reductase FabG4 (3-ketoacyl-acyl carrier protein reductase)
ncbi-gi:5711678	mtu:Rv0824c	desA1	Probable acyl-[acyl-carrier protein] desaturase DesA1 (acyl-[ACP] desaturase) (stearoyl-ACP desaturase) (protein Des)
ncbi-gi:1560800	mtu:Rv0860	fadB	Probable fatty oxidation protein FadB
ncbi-gi:1560823	mtu:Rv1094	desA2	Possible acyl-[acyl-carrier protein] desaturase DesA2 (acyl-[ACP] desaturase) (stearoyl-ACP desaturase)
ncbi-gi:1560849	mtu:Rv1350	fabG2	Probable 3-oxoacyl-[acyl-carrier protein] reductase FabG2 (3-ketoacyl-acyl carrier protein reductase)

mtu00623 Toluene degradation - Mycobacterium tuberculosis H37Rv (5)

ncbi-gi:1560738	mtu:Rv0247c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560738	mtu:Rv0248c		Probable succinate dehydrogenase [iron-sulfur subunit] (succinic dehydrogenase)
ncbi-gi:1560919	mtu:Rv2054		hypothetical protein
ncbi-gi:1560990	mtu:Rv2765		Probable alanine rich hydrolase
ncbi-gi:1561045	mtu:Rv3318	sdhA	Probable succinate dehydrogenase (flavoprotein subunit) SdhA (succinic dehydrogenase) (fumarate reductase) (fumarate dehydrogenase) (fumaric hydrogenase)

mtu05152 Tuberculosis - Mycobacterium tuberculosis H37Rv (5)

ncbi-gi:1560749	mtu:Rv0350	dnaK	Probable chaperone protein DnaK (heat shock protein 70) (heat shock 70 kDa protein) (HSP70)
ncbi-gi:1560755	mtu:Rv0410c	pknG	Serine/threonine-protein kinase PknG (protein kinase G) (STPK G)
ncbi-gi:1560758	mtu:Rv0440	groEL2	60 kDa chaperonin 2 GroEL2 (protein CPN60-2) (GroEL protein 2) (65 kDa antigen) (heat shock protein 65) (cell wall protein A) (antigen A)
ncbi-gi:5711680	mtu:Rv0932c	pstS2	Periplasmic phosphate-binding lipoprotein PstS2 (PBP-2) (PstS2)
ncbi-gi:1561055	mtu:Rv3417c	groEL1	60 kDa chaperonin 1 GroEL1 (protein CPN60-1) (GroEL protein 1)

mtu00750 Vitamin B6 metabolism - Mycobacterium tuberculosis H37Rv (4)

ncbi-gi:1560802	mtu:Rv0884c	serC	Possible phosphoserine aminotransferase SerC (PSAT)
ncbi-gi:1560843	mtu:Rv1295	thrC	Threonine synthase ThrC (ts)
ncbi-gi:1560974	mtu:Rv2606c	snzP	Possible pyridoxine biosynthesis protein SnzP
ncbi-gi:1560974	mtu:Rv2607	pdxH	Probable pyridoxamine 5'-phosphate oxidase PdxH (PNP/PMP oxidase) (pyridoxinephosphate oxidase) (PNPOX) (pyridoxine 5'-phosphate oxidase)

mtu00660 C5-Branched dibasic acid metabolism - Mycobacterium tuberculosis H37Rv (4)

ncbi-gi:1560809	mtu:Rv0951	sucC	Probable succinyl-CoA synthetase (beta chain) SucC (SCS-beta)
ncbi-gi:1560809	mtu:Rv0952	sucD	Probable succinyl-CoA synthetase (alpha chain) SucD (SCS-alpha)
ncbi-gi:1561013	mtu:Rv3002c	ilvN	Probable acetolactate synthase (small subunit) IlvN (acetohydroxy-acid synthase) (AHAS) (ALS)
ncbi-gi:5711704	mtu:Rv3003c	ilvB1	Acetolactate synthase (large subunit) IlvB1 (acetohydroxy-acid synthase)

mtu03440 Homologous recombination - Mycobacterium tuberculosis H37Rv (4)

ncbi-gi:1560714	mtu:Rv0002	dnaN	DNA polymerase III (beta chain) DnaN (DNA nucleotidyltransferase)
ncbi-gi:1560719	mtu:Rv0054	ssb	Single-strand binding protein Ssb (helix-destabilizing protein)
ncbi-gi:1560777	mtu:Rv0631c	recC	Probable exonuclease V (gamma chain) RecC (exodeoxyribonuclease V gamma chain)(exodeoxyribonuclease V polypeptide)
ncbi-gi:1560876	mtu:Rv1629	polA	Probable DNA polymerase I PolA

mtu01220 Degradation of aromatic compounds - Mycobacterium tuberculosis H37Rv (4)

ncbi-gi:5711677	mtu:Rv0761c	adhB	Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB
ncbi-gi:1561022	mtu:Rv3086	adhD	Probable zinc-type alcohol dehydrogenase AdhD (aldehyde reductase)
ncbi-gi:1561070	mtu:Rv3568c	hsaC	3,4-DHSA dioxygenase
ncbi-gi:1561070	mtu:Rv3569c	hsaD	4,9-DHSA hydrolase

mtu00984 Steroid degradation - Mycobacterium tuberculosis H37Rv (4)

ncbi-gi:1560790	mtu:Rv0760c		hypothetical protein
ncbi-gi:1561070	mtu:Rv3568c	hsaC	3,4-DHSA dioxygenase
ncbi-gi:1561070	mtu:Rv3569c	hsaD	4,9-DHSA hydrolase
ncbi-gi:1561070	mtu:Rv3570c	hsaA	Possible oxidoreductase Possible 3-hydroxy-9,10-seconandrost-1,3,5(10)-triene-9,17-dione hydroxylase

mtu03030 DNA replication - Mycobacterium tuberculosis H37Rv (3)

ncbi-gi:1560714	mtu:Rv0002	dnaN	DNA polymerase III (beta chain) DnaN (DNA nucleotidyltransferase)
ncbi-gi:1560719	mtu:Rv0054	ssb	Single-strand binding protein Ssb (helix-destabilizing protein)
ncbi-gi:1560876	mtu:Rv1629	polA	Probable DNA polymerase I PolA

mtu00860 Porphyrin and chlorophyll metabolism - Mycobacterium tuberculosis H37Rv (3)

ncbi-gi:1560765	mtu:Rv0510	hemC	Probable porphobilinogen deaminase HemC (PBG) (hydroxymethylbilane synthase) (HMBS) (pre-uroporphyrinogen synthase)
ncbi-gi:5711674	mtu:Rv0511	hemD	Probable uroporphyrin-III C-methyltransferase HemD (uroporphyrinogen III methylase) (urogen III methylase) (SUMT) (urogen III methylase) (UROM)
ncbi-gi:5711704	mtu:Rv2992c	gltS	Glutamyl-tRNA synthetase GltS (glutamate--tRNA ligase) (glutamyl-tRNA synthase) (GLURS)

mtu00500 Starch and sucrose metabolism - Mycobacterium tuberculosis H37Rv (3)

ncbi-gi:1560726	mtu:Rv0127	mak	Maltokinase Mak
ncbi-gi:1560808	mtu:Rv0946c	pgi	Probable glucose-6-phosphate isomerase Pgi (GPI) (phosphoglucose isomerase) (phosphohexose isomerase) (phi)
ncbi-gi:1560846	mtu:Rv1328	glgP	Probable glycogen phosphorylase GlgP

mtu00625 Chloroalkane and chloroalkene degradation - Mycobacterium tuberculosis H37Rv (3)

ncbi-gi:5711677	mtu:Rv0761c	adhB	Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB
ncbi-gi:1560943	mtu:Rv2296		Probable haloalkane dehalogenase
ncbi-gi:1561022	mtu:Rv3086	adhD	Probable zinc-type alcohol dehydrogenase AdhD (aldehyde reductase)

mtu00626 Naphthalene degradation - Mycobacterium tuberculosis H37Rv (3)

ncbi-gi:1560736	mtu:Rv0223c		Probable aldehyde dehydrogenase
ncbi-gi:5711677	mtu:Rv0761c	adhB	Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB
ncbi-gi:1561022	mtu:Rv3086	adhD	Probable zinc-type alcohol dehydrogenase AdhD (aldehyde reductase)

mtu00052 Galactose metabolism - Mycobacterium tuberculosis H37Rv (3)

ncbi-gi:1560916	mtu:Rv2029c	pfkB	6-phosphofructokinase PfkB (phosphohexokinase) (phosphofructokinase)
ncbi-gi:1561014	mtu:Rv3010c	pfkA	Probable 6-phosphofructokinase PfkA (phosphohexokinase) (phosphofructokinase)
ncbi-gi:5711713	mtu:Rv3634c	galE1	UDP-glucose 4-epimerase GalE1 (galactowaldenase) (UDP-galactose 4-epimerase) (uridine diphosphate galactose 4-epimerase) (uridine diphospho-galactose 4-epimerase)

mtu03020 RNA polymerase - Mycobacterium tuberculosis H37Rv (3)

ncbi-gi:1560780	mtu:Rv0667	rpoB	DNA-directed RNA polymerase (beta chain) RpoB (transcriptase beta chain) (RNA polymerase beta subunit)
ncbi-gi:1560780	mtu:Rv0668	rpoC	DNA-directed RNA polymerase (beta' chain) RpoC (transcriptase beta' chain) (RNA polymerase beta' subunit)
ncbi-gi:1561059	mtu:Rv3457c	rpoA	Probable DNA-directed RNA polymerase (alpha chain) RpoA (transcriptase alpha chain) (RNA polymerase alpha subunit) (DNA-directed RNA nucleotidyltransferase)

mtu00361 Chlorocyclohexane and chlorobenzene degradation - Mycobacterium tuberculosis H37Rv (3)

ncbi-gi:1560919	mtu:Rv2054		hypothetical protein
ncbi-gi:1560943	mtu:Rv2296		Probable haloalkane dehalogenase
ncbi-gi:1560990	mtu:Rv2765		Probable alanine rich hydrolase

mtu00340 Histidine metabolism - Mycobacterium tuberculosis H37Rv (3)

ncbi-gi:1560873	mtu:Rv1601	hisB	Probable imidazole glycerol-phosphate dehydratase HisB
ncbi-gi:1560874	mtu:Rv1603	hisA	Probable phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA
ncbi-gi:1560925	mtu:Rv2121c	hisG	ATP phosphoribosyltransferase HisG

mtu00564 Glycerophospholipid metabolism - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560931	mtu:Rv2182c		1-acylglycerol-3-phosphate O-acyltransferase
ncbi-gi:1561043	mtu:Rv3302c	glpD2	Probable glycerol-3-phosphate dehydrogenase GlpD2

mtu01053 Biosynthesis of siderophore group nonribosomal peptides - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560952	mtu:Rv2384	mbtA	Bifunctional enzyme MbtA: salicyl-AMP ligase (SAL-AMP ligase) + salicyl-S-ArCP synthetase
ncbi-gi:1561035	mtu:Rv3215	entC	Probable isochorismate synthase EntC (isochorismate hydroxymutase) (enterochelin biosynthesis)

mtu03410 Base excision repair - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560781	mtu:Rv0670	end	Probable endonuclease IV End (endodeoxyribonuclease IV) (apurinase)
ncbi-gi:1560876	mtu:Rv1629	polA	Probable DNA polymerase I PolA

mtu04122 Sulfur relay system - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560795	mtu:Rv0815c	cysA2	Probable thiosulfate sulfurtransferase CysA2 (rhodanese-like protein) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)
ncbi-gi:1561041	mtu:Rv3283	sseA	Probable thiosulfate sulfurtransferase SseA (rhodanese) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)

mtu00740 Riboflavin metabolism - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:4488247	mtu:Rv1416	ribH	Probable riboflavin synthase beta chain RibH (6,7-dimethyl-8-ribityllumazine synthase) (DMRL synthase) (lumazine synthase)
ncbi-gi:1560992	mtu:Rv2786c	ribF	Probable bifunctional FAD synthetase/riboflavin biosynthesis protein RibF: riboflavin kinase (flavokinase) + FMN adenylyltransferase (FAD pyrophosphorylase) (FAD synthetase)(FAD diphosphorylase) (flavin adenine dinucleotide synthetase)

mtu03420 Nucleotide excision repair - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560876	mtu:Rv1629	polA	Probable DNA polymerase I PolA
ncbi-gi:1560877	mtu:Rv1638	uvrA	Probable excinuclease ABC (subunit A-DNA-binding ATPase) UvrA

mtu00562 Inositol phosphate metabolism - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560789	mtu:Rv0753c	mmsA	Probable methylmalonate-semialdehyde dehydrogenase MmsA (methylmalonic acid semialdehyde dehydrogenase) (MMSDH)
ncbi-gi:1560857	mtu:Rv1438	tpi	Probable triosephosphate isomerase Tpi (TIM)

mtu00130 Ubiquinone and other terpenoid-quinone biosynthesis - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560768	mtu:Rv0548c	menB	Naphthoate synthase MenB (dihydroxynaphthoic acid synthetase) (DHNA synthetase)
ncbi-gi:1561035	mtu:Rv3215	entC	Probable isochorismate synthase EntC (isochorismate hydroxymutase) (enterochelin biosynthesis)

mtu00460 Cyanoamino acid metabolism - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560791	mtu:Rv0773c	ggtA	Probable bifunctional acylase GgtA: cephalosporin acylase (GL-7ACA acylase) + gamma-glutamyltranspeptidase (GGT)
ncbi-gi:4488247	mtu:Rv1093	glyA1	Serine hydroxymethyltransferase 1 GlyA1

mtu00730 Thiamine metabolism - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560756	mtu:Rv0422c	thiD	Probable phosphomethylpyrimidine kinase ThiD (HMP-phosphate kinase) (HMP-P kinase)
ncbi-gi:1560756	mtu:Rv0423c	thiC	Probable thiamine biosynthesis protein ThiC

mtu00364 Fluorobenzoate degradation - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560919	mtu:Rv2054		hypothetical protein
ncbi-gi:1560990	mtu:Rv2765		Probable alanine rich hydrolase

mtu00550 Peptidoglycan biosynthesis - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560762	mtu:Rv0482	murB	Probable UDP-N-acetylenolpyruvoylglucosamine reductase MurB (UDP-N-acetylmuramate dehydrogenase)
ncbi-gi:1560845	mtu:Rv1315	murA	Probable UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA

mtu00450 Selenocompound metabolism - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560821	mtu:Rv1079	metB	Cystathionine gamma-synthase MetB (CGS) (O-succinylhomoserine [thiol]-lyase)
ncbi-gi:1560827	mtu:Rv1133c	metE	Probable 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase MetE (methionine synthase, vitamin-B12 independent isozyme)

mtu03430 Mismatch repair - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560714	mtu:Rv0002	dnaN	DNA polymerase III (beta chain) DnaN (DNA nucleotidyltransferase)
ncbi-gi:1560719	mtu:Rv0054	ssb	Single-strand binding protein Ssb (helix-destabilizing protein)

mtu00780 Biotin metabolism - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:1560738	mtu:Rv0242c	fabG4	Probable 3-oxoacyl-[acyl-carrier protein] reductase FabG4 (3-ketoacyl-acyl carrier protein reductase)
ncbi-gi:1560849	mtu:Rv1350	fabG2	Probable 3-oxoacyl-[acyl-carrier protein] reductase FabG2 (3-ketoacyl-acyl carrier protein reductase)

mtu00790 Folate biosynthesis - Mycobacterium tuberculosis H37Rv (2)

ncbi-gi:5711668	mtu:Rv0013	trpG	Possible anthranilate synthase component II TrpG (glutamine amidotransferase)
ncbi-gi:1561074	mtu:Rv3609c	folE	GTP cyclohydrolase I FolE (GTP-ch-I)

mtu00642 Ethylbenzene degradation - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:4488247	mtu:Rv2790c	ltp1	Probable lipid-transfer protein Ltp1

mtu00561 Glycerolipid metabolism - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:1560931	mtu:Rv2182c		1-acylglycerol-3-phosphate O-acyltransferase

mtu00622 Xylene degradation - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:1561067	mtu:Rv3535c	hsaG	Probable acetaldehyde dehydrogenase (acetaldehyde dehydrogenase [acetylating])

mtu00521 Streptomycin biosynthesis - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:1560747	mtu:Rv0334	rmlA	Alpha-D-glucose-1-phosphate thymidylyltransferase RmlA (dTDP-glucose synthase) (dTDP-glucose pyrophosphorylase)

mtu00633 Nitrotoluene degradation - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:5711712	mtu:Rv3566c	nat	Arylamine N-acetyltransferase Nat (arylamine acetylase)

mtu03060 Protein export - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:1560895	mtu:Rv1821	secA2	Possible preprotein translocase ATPase SecA2

mtu03070 Bacterial secretion system - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:1560895	mtu:Rv1821	secA2	Possible preprotein translocase ATPase SecA2

mtu00621 Dioxin degradation - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:1561067	mtu:Rv3535c	hsaG	Probable acetaldehyde dehydrogenase (acetaldehyde dehydrogenase [acetylating])

mtu00523 Polyketide sugar unit biosynthesis - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:1560747	mtu:Rv0334	rmlA	Alpha-D-glucose-1-phosphate thymidylyltransferase RmlA (dTDP-glucose synthase) (dTDP-glucose pyrophosphorylase)

mtu03050 Proteasome - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:1560924	mtu:Rv2109c	prcA	Proteasom assembles with beta subunit PrcB

mtu02010 ABC transporters - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:5711680	mtu:Rv0932c	pstS2	Periplasmic phosphate-binding lipoprotein PstS2 (PBP-2) (PstS2)

mtu00592 alpha-Linolenic acid metabolism - Mycobacterium tuberculosis H37Rv (1)

ncbi-gi:4488247	mtu:Rv2790c	ltp1	Probable lipid-transfer protein Ltp1