

Supplementary Table S5. Complete list of KEGG pathways in the identified acetylated proteins.

mra01100 Metabolic pathways - Mycobacterium tuberculosis H37Ra (59)

| | | | |
|--------------|----------|--------|--|
| gi 148659759 | MRA_0002 | dnaN; | DNA polymerase III subunit beta |
| gi 148659826 | MRA_0068 | icd2; | isocitrate dehydrogenase (NADP) Icd2 |
| gi 148659921 | MRA_0165 | pntB; | NAD(P) transhydrogenase subunit beta |
| gi 148659975 | MRA_0219 | pckA; | phosphoenolpyruvate carboxykinase |
| gi 148659995 | MRA_0239 | fadE4; | acyl-CoA dehydrogenase |
| gi 148660007 | MRA_0251 | fabG; | 3-ketoacyl-ACP reductase |
| gi 148660013 | MRA_0257 | sdhA; | succinate dehydrogenase flavoprotein subunit |
| gi 148660129 | MRA_0372 | fba; | fructose-bisphosphate aldolase |
| gi 148660228 | MRA_0468 | lpd; | dihydrolipoamide dehydrogenase |
| gi 148660233 | MRA_0473 | icl; | isocitrate lyase Icl |
| gi 148660256 | MRA_0496 | gpmA; | phosphoglyceromutase |
| gi 148660441 | MRA_0676 | rpoB; | DNA-directed RNA polymerase subunit beta |
| gi 148660442 | MRA_0677 | rpoC; | DNA-directed RNA polymerase subunit beta' |
| gi 148660529 | MRA_0762 | mmsA; | MmsA |
| gi 148660593 | MRA_0825 | cysA2; | thiosulfate sulfurtransferase CysA2 |
| gi 148660636 | MRA_0867 | fadA; | acetyl-CoA acetyltransferase |
| gi 148660637 | MRA_0868 | fadB; | fatty oxidation complex subunit alpha |
| gi 148660661 | MRA_0891 | serC; | phosphoserine aminotransferase |
| gi 148660667 | MRA_0897 | citA; | citrate synthase 2 |
| gi 148660674 | MRA_0904 | gltA; | type II citrate synthase |
| gi 148660730 | MRA_0958 | sucC; | succinyl-CoA synthetase subunit beta |
| gi 148660731 | MRA_0959 | sucD; | succinyl-CoA synthetase subunit alpha |
| gi 148660799 | MRA_1025 | prsA; | ribose-phosphate pyrophosphokinase |
| gi 148660879 | MRA_1104 | glyA; | serine hydroxymethyltransferase |
| gi 148660884 | MRA_1109 | fumC; | fumarate hydratase |
| gi 148660908 | MRA_1131 | gnd2; | 6-phosphogluconate dehydrogenase |
| gi 148660988 | MRA_1210 | | tetrahydrodipicolinate N-succinyltransferase |
| gi 148661027 | MRA_1249 | mdh; | malate dehydrogenase |

| | | | |
|--------------|----------|----------|---|
| gi 148661094 | MRA_1314 | atpF; | ATP synthase F0F1 subunit B |
| gi 148661096 | MRA_1316 | atpA; | ATP synthase F0F1 subunit alpha |
| gi 148661098 | MRA_1318 | atpD; | ATP synthase F0F1 subunit beta |
| gi 148661112 | MRA_1331 | fadA4; | acetyl-CoA acetyltransferase |
| gi 148661183 | MRA_1401 | metK; | S-adenosylmethionine synthetase |
| gi 148661240 | MRA_1457 | tal; | transaldolase |
| gi 148661268 | MRA_1485 | acn; | aconitate hydratase |
| gi 148661454 | MRA_1669 | argG; | argininosuccinate synthase |
| gi 148661496 | MRA_1708 | pyrG; | CTP synthetase |
| gi 148661529 | MRA_1741 | gabD2; | succinic semialdehyde dehydrogenase |
| gi 148661643 | MRA_1848 | glcB; | malate synthase G |
| gi 148661816 | MRA_2018 | fabG3-1; | 20-beta-hydroxysteroid dehydrogenase FabG3 |
| gi 148662003 | MRA_2202 | fadD15; | long-chain-fatty-acid--CoA ligase |
| gi 148662013 | MRA_2212 | qcrB; | ubiquinol-cytochrome C reductase QcrB |
| gi 148662028 | MRA_2227 | gcvT; | glycine cleavage system aminomethyltransferase T |
| gi 148662032 | MRA_2231 | dlaT; | dihydrolipoamide acetyltransferase |
| gi 148662038 | MRA_2237 | glnA1; | glutamine synthetase |
| gi 148662062 | MRA_2261 | aceE; | pyruvate dehydrogenase subunit E1 |
| gi 148662311 | MRA_2501 | gdh; | NAD-dependent glutamate dehydrogenase Gdh |
| gi 148662842 | MRA_3021 | gltX; | glutamyl-tRNA synthetase |
| gi 148662852 | MRA_3031 | ilvC; | ketol-acid reductoisomerase |
| gi 148662940 | MRA_3118 | adhD; | zinc-type alcohol dehydrogenase AdhD |
| gi 148662971 | MRA_3149 | cysA3; | thiosulfate sulfurtransferase CysA3 |
| gi 148662995 | MRA_3173 | fadE23; | acyl-CoA dehydrogenase |
| gi 148663007 | MRA_3185 | nuoH; | NADH dehydrogenase subunit H |
| gi 148663076 | MRA_3254 | entC; | isochorismate synthase EntC |
| gi 148663111 | MRA_3289 | sahH; | S-adenosyl-L-homocysteine hydrolase |
| gi 148663322 | MRA_3498 | rpoA; | DNA-directed RNA polymerase subunit alpha |
| gi 148663419 | MRA_3595 | fadA6; | acetyl-CoA acetyltransferase |
| gi 148663433 | MRA_3608 | bphD; | 2-hydroxy-6-phenylhexa-2,4-dienoic acid hydrolase |
| gi 148663642 | MRA_3814 | echA21; | enoyl-CoA hydratase |

mra01110 Biosynthesis of secondary metabolites - Mycobacterium tuberculosis H37Ra (36)

| | | | |
|--------------|----------|--------|--|
| gi 148659826 | MRA_0068 | icd2; | isocitrate dehydrogenase (NADP) Icd2 |
| gi 148659975 | MRA_0219 | pckA; | phosphoenolpyruvate carboxykinase |
| gi 148659995 | MRA_0239 | fadE4; | acyl-CoA dehydrogenase |
| gi 148660009 | MRA_0253 | fadE5; | acyl-CoA dehydrogenase |
| gi 148660013 | MRA_0257 | sdhA; | succinate dehydrogenase flavoprotein subunit |
| gi 148660036 | MRA_0279 | fadE6; | acyl-CoA dehydrogenase |
| gi 148660129 | MRA_0372 | fba; | fructose-bisphosphate aldolase |
| gi 148660228 | MRA_0468 | lpd; | dihydrolipoamide dehydrogenase |
| gi 148660256 | MRA_0496 | gpmA; | phosphoglyceromutase |
| gi 148660331 | MRA_0569 | grcC1; | polyprenyl-diphosphate synthase GrcC1 |
| gi 148660636 | MRA_0867 | fadA; | acetyl-CoA acetyltransferase |
| gi 148660637 | MRA_0868 | fadB; | fatty oxidation complex subunit alpha |
| gi 148660667 | MRA_0897 | citA; | citrate synthase 2 |
| gi 148660674 | MRA_0904 | gltA; | type II citrate synthase |
| gi 148660730 | MRA_0958 | sucC; | succinyl-CoA synthetase subunit beta |
| gi 148660731 | MRA_0959 | sucD; | succinyl-CoA synthetase subunit alpha |
| gi 148660799 | MRA_1025 | prsA; | ribose-phosphate pyrophosphokinase |
| gi 148660879 | MRA_1104 | glyA; | serine hydroxymethyltransferase |
| gi 148660884 | MRA_1109 | fumC; | fumarate hydratase |
| gi 148660908 | MRA_1131 | gnd2; | 6-phosphogluconate dehydrogenase |
| gi 148661027 | MRA_1249 | mdh; | malate dehydrogenase |
| gi 148661112 | MRA_1331 | fadA4; | acetyl-CoA acetyltransferase |
| gi 148661183 | MRA_1401 | metK; | S-adenosylmethionine synthetase |
| gi 148661240 | MRA_1457 | tal; | transaldolase |
| gi 148661268 | MRA_1485 | acn; | aconitate hydratase |
| gi 148661454 | MRA_1669 | argG; | argininosuccinate synthase |
| gi 148662032 | MRA_2231 | dlaT; | dihydrolipoamide acetyltransferase |
| gi 148662062 | MRA_2261 | aceE; | pyruvate dehydrogenase subunit E1 |
| gi 148662842 | MRA_3021 | gltX; | glutamyl-tRNA synthetase |
| gi 148662852 | MRA_3031 | ilvC; | ketol-acid reductoisomerase |
| gi 148662940 | MRA_3118 | adhD; | zinc-type alcohol dehydrogenase AdhD |

gi|148662995 MRA_3173 fadE23; acyl-CoA dehydrogenase
gi|148663076 MRA_3254 entC; isochorismate synthase EntC
gi|148663137 MRA_3315 fadE25; acyl-CoA dehydrogenase
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra01120 Microbial metabolism in diverse environments - Mycobacterium tuberculosis H37Ra (32)

gi|148659826 MRA_0068 icd2; isocitrate dehydrogenase (NADP) Icd2
gi|148659975 MRA_0219 pckA; phosphoenolpyruvate carboxykinase
gi|148660013 MRA_0257 sdhA; succinate dehydrogenase flavoprotein subunit
gi|148660129 MRA_0372 fba; fructose-bisphosphate aldolase
gi|148660228 MRA_0468 lpd; dihydrolipoamide dehydrogenase
gi|148660233 MRA_0473 icl; isocitrate lyase Icl
gi|148660256 MRA_0496 gpmA; phosphoglyceromutase
gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha
gi|148660661 MRA_0891 serC; phosphoserine aminotransferase
gi|148660667 MRA_0897 citA; citrate synthase 2
gi|148660674 MRA_0904 gltA; type II citrate synthase
gi|148660730 MRA_0958 sucC; succinyl-CoA synthetase subunit beta
gi|148660731 MRA_0959 sucD; succinyl-CoA synthetase subunit alpha
gi|148660799 MRA_1025 prsA; ribose-phosphate pyrophosphokinase
gi|148660879 MRA_1104 glyA; serine hydroxymethyltransferase
gi|148660884 MRA_1109 fumC; fumarate hydratase
gi|148660908 MRA_1131 gnd2; 6-phosphogluconate dehydrogenase
gi|148660988 MRA_1210 tetrahydrodipicolinate N-succinyltransferase
gi|148661027 MRA_1249 mdh; malate dehydrogenase
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148661240 MRA_1457 tal; transaldolase
gi|148661268 MRA_1485 acn; aconitate hydratase
gi|148661529 MRA_1741 gabD2; succinic semialdehyde dehydrogenase
gi|148661643 MRA_1848 glcB; malate synthase G

gi|148662032 MRA_2231 dlaT; dihydrolipoamide acetyltransferase
gi|148662038 MRA_2237 glnA1; glutamine synthetase
gi|148662062 MRA_2261 aceE; pyruvate dehydrogenase subunit E1
gi|148662940 MRA_3118 adhD; zinc-type alcohol dehydrogenase AdhD
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase
gi|148663433 MRA_3608 bphD; 2-hydroxy-6-phenylhexa-2,4-dienoic acid hydrolase
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra00020 Citrate cycle (TCA cycle) - Mycobacterium tuberculosis H37Ra (13)

gi|148659826 MRA_0068 icd2; isocitrate dehydrogenase (NADP) Icd2
gi|148659975 MRA_0219 pckA; phosphoenolpyruvate carboxykinase
gi|148660013 MRA_0257 sdhA; succinate dehydrogenase flavoprotein subunit
gi|148660228 MRA_0468 lpd; dihydrolipoamide dehydrogenase
gi|148660667 MRA_0897 citA; citrate synthase 2
gi|148660674 MRA_0904 gltA; type II citrate synthase
gi|148660730 MRA_0958 sucC; succinyl-CoA synthetase subunit beta
gi|148660731 MRA_0959 sucD; succinyl-CoA synthetase subunit alpha
gi|148660884 MRA_1109 fumC; fumarate hydratase
gi|148661027 MRA_1249 mdh; malate dehydrogenase
gi|148661268 MRA_1485 acn; aconitate hydratase
gi|148662032 MRA_2231 dlaT; dihydrolipoamide acetyltransferase
gi|148662062 MRA_2261 aceE; pyruvate dehydrogenase subunit E1

mra00640 Propanoate metabolism - Mycobacterium tuberculosis H37Ra (10)

gi|148659995 MRA_0239 fadE4; acyl-CoA dehydrogenase
gi|148660529 MRA_0762 mmsA; MmsA
gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha
gi|148660730 MRA_0958 sucC; succinyl-CoA synthetase subunit beta
gi|148660731 MRA_0959 sucD; succinyl-CoA synthetase subunit alpha
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148662995 MRA_3173 fadE23; acyl-CoA dehydrogenase

gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra00280 Valine, leucine and isoleucine degradation - Mycobacterium tuberculosis H37Ra (9)

gi|148659995 MRA_0239 fadE4; acyl-CoA dehydrogenase
gi|148660228 MRA_0468 lpd; dihydrolipoamide dehydrogenase
gi|148660529 MRA_0762 mmsA; MmsA
gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148662995 MRA_3173 fadE23; acyl-CoA dehydrogenase
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra00071 Fatty acid metabolism - Mycobacterium tuberculosis H37Ra (9)

gi|148659995 MRA_0239 fadE4; acyl-CoA dehydrogenase
gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148662003 MRA_2202 fadD15; long-chain-fatty-acid--CoA ligase
gi|148662940 MRA_3118 adhD; zinc-type alcohol dehydrogenase AdhD
gi|148662995 MRA_3173 fadE23; acyl-CoA dehydrogenase
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra00630 Glyoxylate and dicarboxylate metabolism - Mycobacterium tuberculosis H37Ra (11)

gi|148660233 MRA_0473 icl; isocitrate lyase Icl
gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148660667 MRA_0897 citA; citrate synthase 2
gi|148660674 MRA_0904 gltA; type II citrate synthase
gi|148660879 MRA_1104 glyA; serine hydroxymethyltransferase
gi|148661027 MRA_1249 mdh; malate dehydrogenase

gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148661268 MRA_1485 acn; aconitate hydratase
gi|148661643 MRA_1848 glcB; malate synthase G
gi|148662038 MRA_2237 glnA1; glutamine synthetase
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase

mra00650 Butanoate metabolism - Mycobacterium tuberculosis H37Ra (8)

gi|148660013 MRA_0257 sdhA; succinate dehydrogenase flavoprotein subunit
gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148661529 MRA_1741 gabD2; succinic semialdehyde dehydrogenase
gi|148662062 MRA_2261 aceE; pyruvate dehydrogenase subunit E1
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra00310 Lysine degradation - Mycobacterium tuberculosis H37Ra (6)

gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148662032 MRA_2231 dlaT; dihydrolipoamide acetyltransferase
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra03010 Ribosome - Mycobacterium tuberculosis H37Ra (8)

gi|148660426 MRA_0663 rplL; 50S ribosomal protein L7/L12
gi|148660458 MRA_0692 rpsG; 30S ribosomal protein S7
gi|148660475 MRA_0708 rpsJ; 30S ribosomal protein S10
gi|148661425 MRA_1640 rpsA; 30S ribosomal protein S1
gi|148662734 MRA_2915 rpsB; 30S ribosomal protein S2
gi|148662753 MRA_2934 rpsP; 30S ribosomal protein S16
gi|148662825 MRA_3004 rpmB; 50S ribosomal protein L28

gi|148663323 MRA_3499 rpsD; 30S ribosomal protein S4

mra00620 Pyruvate metabolism - Mycobacterium tuberculosis H37Ra (8)

gi|148659975 MRA_0219 pckA; phosphoenolpyruvate carboxykinase
gi|148660228 MRA_0468 lpd; dihydrolipoamide dehydrogenase
gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148661027 MRA_1249 mdh; malate dehydrogenase
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148661643 MRA_1848 glcB; malate synthase G
gi|148662062 MRA_2261 aceE; pyruvate dehydrogenase subunit E1
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase

mra00380 Tryptophan metabolism - Mycobacterium tuberculosis H37Ra (5)

gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra00410 beta-Alanine metabolism - Mycobacterium tuberculosis H37Ra (5)

gi|148659995 MRA_0239 fadE4; acyl-CoA dehydrogenase
gi|148660529 MRA_0762 mmsA; MmsA
gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha
gi|148662995 MRA_3173 fadE23; acyl-CoA dehydrogenase
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra00281 Geraniol degradation - Mycobacterium tuberculosis H37Ra (5)

gi|148660009 MRA_0253 fadE5; acyl-CoA dehydrogenase
gi|148660036 MRA_0279 fadE6; acyl-CoA dehydrogenase
gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha
gi|148663137 MRA_3315 fadE25; acyl-CoA dehydrogenase
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra00190 Oxidative phosphorylation - Mycobacterium tuberculosis H37Ra (7)

gi|148660013 MRA_0257 sdhA; succinate dehydrogenase flavoprotein subunit
gi|148661094 MRA_1314 atpF; ATP synthase F0F1 subunit B
gi|148661096 MRA_1316 atpA; ATP synthase F0F1 subunit alpha
gi|148661098 MRA_1318 atpD; ATP synthase F0F1 subunit beta
gi|148662013 MRA_2212 qcrB; ubiquinol-cytochrome C reductase QcrB
gi|148663007 MRA_3185 nuoH; NADH dehydrogenase subunit H
gi|148663491 MRA_3664 ppa; inorganic pyrophosphatase

mra02020 Two-component system - Mycobacterium tuberculosis H37Ra (6)

gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148662038 MRA_2237 glnA1; glutamine synthetase
gi|148662987 MRA_3165 devR; two component transcriptional regulatory protein DevR
gi|148663109 MRA_3287 mtrA; two component sensory transduction transcriptional regulatory protein MtrA
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase

mra00362 Benzoate degradation - Mycobacterium tuberculosis H37Ra (4)

gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra00240 Pyrimidine metabolism - Mycobacterium tuberculosis H37Ra (6)

gi|148659759 MRA_0002 dnaN; DNA polymerase III subunit beta
gi|148660441 MRA_0676 rpoB; DNA-directed RNA polymerase subunit beta
gi|148660442 MRA_0677 rpoC; DNA-directed RNA polymerase subunit beta'
gi|148661496 MRA_1708 pyrG; CTP synthetase
gi|148662625 MRA_2807 gpsI; polynucleotide phosphorylase
gi|148663322 MRA_3498 rpoA; DNA-directed RNA polymerase subunit alpha

mra00010 Glycolysis / Gluconeogenesis - Mycobacterium tuberculosis H37Ra (6)

gi|148659975 MRA_0219 pckA; phosphoenolpyruvate carboxykinase
gi|148660129 MRA_0372 fba; fructose-bisphosphate aldolase
gi|148660228 MRA_0468 lpd; dihydrolipoamide dehydrogenase
gi|148660256 MRA_0496 gpmA; phosphoglyceromutase
gi|148662062 MRA_2261 aceE; pyruvate dehydrogenase subunit E1
gi|148662940 MRA_3118 adhD; zinc-type alcohol dehydrogenase AdhD

mra00230 Purine metabolism - Mycobacterium tuberculosis H37Ra (6)

gi|148659759 MRA_0002 dnaN; DNA polymerase III subunit beta
gi|148660441 MRA_0676 rpoB; DNA-directed RNA polymerase subunit beta
gi|148660442 MRA_0677 rpoC; DNA-directed RNA polymerase subunit beta'
gi|148660799 MRA_1025 prsA; ribose-phosphate pyrophosphokinase
gi|148662625 MRA_2807 gpsI; polynucleotide phosphorylase
gi|148663322 MRA_3498 rpoA; DNA-directed RNA polymerase subunit alpha

mra00680 Methane metabolism - Mycobacterium tuberculosis H37Ra (6)

gi|148660129 MRA_0372 fba; fructose-bisphosphate aldolase
gi|148660256 MRA_0496 gpmA; phosphoglyceromutase
gi|148660661 MRA_0891 serC; phosphoserine aminotransferase
gi|148660879 MRA_1104 glyA; serine hydroxymethyltransferase
gi|148661027 MRA_1249 mdh; malate dehydrogenase
gi|148662940 MRA_3118 adhD; zinc-type alcohol dehydrogenase AdhD

mra00910 Nitrogen metabolism - Mycobacterium tuberculosis H37Ra (5)

gi|148662028 MRA_2227 gcvT; glycine cleavage system aminomethyltransferase T
gi|148662038 MRA_2237 glnA1; glutamine synthetase
gi|148662311 MRA_2501 gdh; NAD-dependent glutamate dehydrogenase Gdh
gi|148662881 MRA_3060 fixA; electron transfer flavoprotein subunit beta
gi|148663007 MRA_3185 nuoH; NADH dehydrogenase subunit H

mra00260 Glycine, serine and threonine metabolism - Mycobacterium tuberculosis H37Ra (5)

gi|148660228 MRA_0468 lpd; dihydrolipoamide dehydrogenase
gi|148660256 MRA_0496 gpmA; phosphoglyceromutase
gi|148660661 MRA_0891 serC; phosphoserine aminotransferase
gi|148660879 MRA_1104 glyA; serine hydroxymethyltransferase
gi|148662028 MRA_2227 gcvT; glycine cleavage system aminomethyltransferase T

mra03018 RNA degradation - Mycobacterium tuberculosis H37Ra (4)

gi|148660116 MRA_0359 dnaK; molecular chaperone DnaK
gi|148660205 MRA_0445 groEL; molecular chaperone GroEL
gi|148662625 MRA_2807 gpsI; polynucleotide phosphorylase
gi|148663281 MRA_3457 groEL; molecular chaperone GroEL

mra00903 Limonene and pinene degradation - Mycobacterium tuberculosis H37Ra (2)

gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra00270 Cysteine and methionine metabolism - Mycobacterium tuberculosis H37Ra (4)

gi|148660593 MRA_0825 cysA2; thiosulfate sulfurtransferase CysA2
gi|148661183 MRA_1401 metK; S-adenosylmethionine synthetase
gi|148662971 MRA_3149 cysA3; thiosulfate sulfurtransferase CysA3
gi|148663111 MRA_3289 sahH; S-adenosyl-L-homocysteine hydrolase

mra00900 Terpenoid backbone biosynthesis - Mycobacterium tuberculosis H37Ra (4)

gi|148660331 MRA_0569 grcC1; polyprenyl-diphosphate synthase GrcC1
gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase

mra00250 Alanine, aspartate and glutamate metabolism - Mycobacterium tuberculosis H37Ra (4)

gi|148661454 MRA_1669 argG; argininosuccinate synthase
gi|148661529 MRA_1741 gabD2; succinic semialdehyde dehydrogenase
gi|148662038 MRA_2237 glnA1; glutamine synthetase

gi|148662311 MRA_2501 gdh; NAD-dependent glutamate dehydrogenase Gdh

mra00030 Pentose phosphate pathway - Mycobacterium tuberculosis H37Ra (4)

gi|148660129 MRA_0372 fba; fructose-bisphosphate aldolase
gi|148660799 MRA_1025 prsA; ribose-phosphate pyrophosphokinase
gi|148660908 MRA_1131 gnd2; 6-phosphogluconate dehydrogenase
gi|148661240 MRA_1457 tal; transaldolase

mra00930 Caprolactam degradation - Mycobacterium tuberculosis H37Ra (2)

gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha
gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra05152 Tuberculosis - Mycobacterium tuberculosis H37Ra (3)

gi|148660116 MRA_0359 dnaK; molecular chaperone DnaK
gi|148660205 MRA_0445 groEL; molecular chaperone GroEL
gi|148663281 MRA_3457 groEL; molecular chaperone GroEL

mra03020 RNA polymerase - Mycobacterium tuberculosis H37Ra (3)

gi|148660441 MRA_0676 rpoB; DNA-directed RNA polymerase subunit beta
gi|148660442 MRA_0677 rpoC; DNA-directed RNA polymerase subunit beta'
gi|148663322 MRA_3498 rpoA; DNA-directed RNA polymerase subunit alpha

mra01040 Biosynthesis of unsaturated fatty acids - Mycobacterium tuberculosis H37Ra (3)

gi|148660007 MRA_0251 fabG; 3-ketoacyl-ACP reductase
gi|148660602 MRA_0834 desA1; fatty acid desaturase
gi|148660637 MRA_0868 fadB; fatty oxidation complex subunit alpha

mra00330 Arginine and proline metabolism - Mycobacterium tuberculosis H37Ra (3)

gi|148661454 MRA_1669 argG; argininosuccinate synthase
gi|148662038 MRA_2237 glnA1; glutamine synthetase
gi|148662311 MRA_2501 gdh; NAD-dependent glutamate dehydrogenase Gdh

mra00970 Aminoacyl-tRNA biosynthesis - Mycobacterium tuberculosis H37Ra (3)

gi|148661080 MRA_1300 argS; arginyl-tRNA synthetase
gi|148662842 MRA_3021 gltX; glutamyl-tRNA synthetase
gi|148663444 MRA_3619 cysS; cysteinyl-tRNA synthetase

mra00072 Synthesis and degradation of ketone bodies - Mycobacterium tuberculosis H37Ra (3)

gi|148660636 MRA_0867 fadA; acetyl-CoA acetyltransferase
gi|148661112 MRA_1331 fadA4; acetyl-CoA acetyltransferase
gi|148663419 MRA_3595 fadA6; acetyl-CoA acetyltransferase

mra00480 Glutathione metabolism - Mycobacterium tuberculosis H37Ra (2)

gi|148659826 MRA_0068 icd2; isocitrate dehydrogenase (NADP) Icd2
gi|148660908 MRA_1131 gnd2; 6-phosphogluconate dehydrogenase

mra00750 Vitamin B6 metabolism - Mycobacterium tuberculosis H37Ra (2)

gi|148660661 MRA_0891 serC; phosphoserine aminotransferase
gi|148662446 MRA_2634 pyridoxal biosynthesis lyase PdxS

mra00660 C5-Branched dibasic acid metabolism - Mycobacterium tuberculosis H37Ra (2)

gi|148660730 MRA_0958 sucC; succinyl-CoA synthetase subunit beta
gi|148660731 MRA_0959 sucD; succinyl-CoA synthetase subunit alpha

mra00061 Fatty acid biosynthesis - Mycobacterium tuberculosis H37Ra (2)

gi|148660007 MRA_0251 fabG; 3-ketoacyl-ACP reductase
gi|148660602 MRA_0834 desA1; fatty acid desaturase

mra00350 Tyrosine metabolism - Mycobacterium tuberculosis H37Ra (2)

gi|148661529 MRA_1741 gabD2; succinic semialdehyde dehydrogenase
gi|148662940 MRA_3118 adhD; zinc-type alcohol dehydrogenase AdhD

mra00670 One carbon pool by folate - Mycobacterium tuberculosis H37Ra (2)

gi|148660879 MRA_1104 glyA; serine hydroxymethyltransferase

gi|148662028 MRA_2227 gcvT; glycine cleavage system aminomethyltransferase T

mra04122 Sulfur relay system - Mycobacterium tuberculosis H37Ra (2)

gi|148660593 MRA_0825 cysA2; thiosulfate sulfurtransferase CysA2

gi|148662971 MRA_3149 cysA3; thiosulfate sulfurtransferase CysA3

mra00300 Lysine biosynthesis - Mycobacterium tuberculosis H37Ra (2)

gi|148660988 MRA_1210 tetrahydrodipicolinate N-succinyltransferase

gi|148661974 MRA_2173 murE; UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase

mra00360 Phenylalanine metabolism - Mycobacterium tuberculosis H37Ra (1)

gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra00627 Aminobenzoate degradation - Mycobacterium tuberculosis H37Ra (1)

gi|148663642 MRA_3814 echA21; enoyl-CoA hydratase

mra03430 Mismatch repair - Mycobacterium tuberculosis H37Ra (1)

gi|148659759 MRA_0002 dnaN; DNA polymerase III subunit beta

mra00460 Cyanoamino acid metabolism - Mycobacterium tuberculosis H37Ra (1)

gi|148660879 MRA_1104 glyA; serine hydroxymethyltransferase

mra00626 Naphthalene degradation - Mycobacterium tuberculosis H37Ra (1)

gi|148662940 MRA_3118 adhD; zinc-type alcohol dehydrogenase AdhD

mra00760 Nicotinate and nicotinamide metabolism - Mycobacterium tuberculosis H37Ra (1)

gi|148659921 MRA_0165 pntB; NAD(P) transhydrogenase subunit beta

mra00860 Porphyrin and chlorophyll metabolism - Mycobacterium tuberculosis H37Ra (1)

gi|148662842 MRA_3021 gltX; glutamyl-tRNA synthetase

mra00623 Toluene degradation - Mycobacterium tuberculosis H37Ra (1)

gi|148660013 MRA_0257 sdhA; succinate dehydrogenase flavoprotein subunit

mra00051 Fructose and mannose metabolism - Mycobacterium tuberculosis H37Ra (1)

gi|148660129 MRA_0372 fba; fructose-bisphosphate aldolase

mra01053 Biosynthesis of siderophore group nonribosomal peptides - Mycobacterium tuberculosis H37Ra (1)

gi|148663076 MRA_3254 entC; isochorismate synthase EntC

mra00625 Chloroalkane and chloroalkene degradation - Mycobacterium tuberculosis H37Ra (1)

gi|148662940 MRA_3118 adhD; zinc-type alcohol dehydrogenase AdhD

mra00984 Steroid degradation - Mycobacterium tuberculosis H37Ra (1)

gi|148663433 MRA_3608 bphD; 2-hydroxy-6-phenylhexa-2,4-dienoic acid hydrolase

mra00130 Ubiquinone and other terpenoid-quinone biosynthesis - Mycobacterium tuberculosis H37Ra (1)

gi|148663076 MRA_3254 entC; isochorismate synthase EntC

mra00780 Biotin metabolism - Mycobacterium tuberculosis H37Ra (1)

gi|148660007 MRA_0251 fabG; 3-ketoacyl-ACP reductase

mra03030 DNA replication - Mycobacterium tuberculosis H37Ra (1)

gi|148659759 MRA_0002 dnaN; DNA polymerase III subunit beta

mra00550 Peptidoglycan biosynthesis - Mycobacterium tuberculosis H37Ra (1)

gi|148661974 MRA_2173 murE; UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase

mra03440 Homologous recombination - Mycobacterium tuberculosis H37Ra (1)

gi|148659759 MRA_0002 dnaN; DNA polymerase III subunit beta

mra00770 Pantothenate and CoA biosynthesis - Mycobacterium tuberculosis H37Ra (1)

gi|148662852 MRA_3031 ilvC; ketol-acid reductoisomerase

mra00562 Inositol phosphate metabolism - Mycobacterium tuberculosis H37Ra (1)

gi|148660529 MRA_0762 mmsA; MmsA

mra00290 Valine, leucine and isoleucine biosynthesis - Mycobacterium tuberculosis H37Ra (1)

gi|148662852 MRA_3031 ilvC; ketol-acid reductoisomerase

mra00430 Taurine and hypotaurine metabolism - Mycobacterium tuberculosis H37Ra (1)

gi|148662311 MRA_2501 gdh; NAD-dependent glutamate dehydrogenase Gdh