

## Supplementary materials

### Anti-Mycobacterial Natural Products and Mechanisms of Action

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**Table S1 Antitubercular compounds in clinical pipeline**

| No. | Compound                | Phase        | Chemical class                  | Target                                     | MIC (μg/mL)   | Ref.          |
|-----|-------------------------|--------------|---------------------------------|--------------------------------------------|---------------|---------------|
| 1   | Sanfetrinem             | Pre-Clinical | Trinem beta-lactam              | Cell wall                                  | 2.9–5 μM      | <sup>1</sup>  |
| 2   | TBAJ-876                | Pre-Clinical | Diarylquinoline                 | ATPase                                     | 0.004–0.006   | <sup>2</sup>  |
| 3   | GSK-286                 | Pre-Clinical | -                               | Cholesterol catabolism                     | NA            | <sup>3</sup>  |
| 4   | TBAJ-587                | Pre-Clinical | Diarylquinoline                 | ATPase                                     | 0.006         | <sup>2</sup>  |
| 5   | Spectinamide 1810       | Pre-Clinical | Spectinamide                    | Rv1258c                                    | 1.6           | <sup>4</sup>  |
| 6   | GSK839                  | Pre-Clinical | Tetrazole                       | Tryptophan Synthase                        | NA            | <sup>3</sup>  |
| 7   | TBI-223                 | Phase 1      | Oxazolidinone                   | N-formylmethionyl-tRNA                     | NA            | <sup>3</sup>  |
| 8   | BTZ-043                 | Phase 1      | Benzothiazinone                 | DprE1                                      | 0.001         | <sup>5</sup>  |
| 9   | SPR720                  | Phase 1      | Ethyl urea benzimidazole        | DNA gyrase GyrB                            | 0.03–0.25     | <sup>6</sup>  |
| 10  | OPC-167832              | Phase 1      | 3,4-dihydrocarbostyryl          | DprE1                                      | 0.00024–0.002 | <sup>3</sup>  |
| 11  | TBA-7371                | Phase 1      | Azaindole                       | DprE1                                      | 0.78–3.12 μM  | <sup>3</sup>  |
| 12  | Macozinone              | Phase 1      | Benzothiazinone                 | DprE1                                      | 0.0003        | <sup>7</sup>  |
| 13  | TBI-166                 | Phase 1      | Riminophenazines                | NA                                         | 0.016         | <sup>8</sup>  |
| 14  | Auranofin               | Phase 2      | Thiosugar and triethylphosphine | Thioredoxin reductase: trxB2               | 0.5           | <sup>9</sup>  |
| 15  | Nitazoxanide            | Phase 2      | Nitrothiazolyl-salicylamide     | NA                                         | 12–28         | <sup>10</sup> |
| 16  | Delpazolid (LCB01-0371) | Phase 2      | Oxazolidinone                   | 23S rRNA                                   | 0.5           | <sup>11</sup> |
| 17  | GSK070 (GSK-3036656)    | Phase 2      | Oxaborole                       | Leucyl-tRNA Synthetase (LeuRS)             | 0.024         | <sup>12</sup> |
| 18  | Telacebec (Q203)        | Phase 2      | Imidazopyridine amide           | qcrB subunit of the cytochrome bc1 complex | 0.0027 μM     | <sup>13</sup> |
| 19  | SQ109                   | Phase 2      | Ethylenediamine                 | MmpL3                                      | 1.56 μM       | <sup>14</sup> |
| 20  | Sutezolid               | Phase 2      | Oxazolidinone                   | 23S rRNA of the 50S subunit                | 0.5           | <sup>15</sup> |
| 21  | Contezolid (MRX-1)      | Phase 3      | Oxazolidinone                   | 23S rRNA                                   | 0.03-8        | <sup>16</sup> |

**Table S2 Druggable targets of *M. tuberculosis***

| No. | SSGCID ID      | Annotation                                                                                                                                                                                                                                                |
|-----|----------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1   | MytuD.00001.ra | Thi-box riboswitch (responds to TPP)                                                                                                                                                                                                                      |
| 2   | MytuD.00010.a  | 3-ketoacyl-(acyl-carrier-protein) reductase                                                                                                                                                                                                               |
| 3   | MytuD.00010.b  | Putative oxidoreductase Rv1856c                                                                                                                                                                                                                           |
| 4   | MytuD.00014.a  | Isocitrate lyase (Rv0467)                                                                                                                                                                                                                                 |
| 5   | MytuD.00030.a  | ATP-dependent Clp protease ATP-binding subunit ClpX                                                                                                                                                                                                       |
| 6   | MytuD.00050.a  | Udp-glucose 4-epimerase GALE1 (galactowaldenase) (udp-galactose 4-epimerase) (uridine diphosphate galactose 4-epimerase) (uridine diphospho-galactose 4-epimerase)                                                                                        |
| 7   | MytuD.00058.a  | Thioredoxin-disulfide reductase (TrxR)                                                                                                                                                                                                                    |
| 8   | MytuD.00066.a  | DNA-directed RNA polymerase subunit alpha Rv3457c                                                                                                                                                                                                         |
| 9   | MytuD.00084.a  | Enolase                                                                                                                                                                                                                                                   |
| 10  | MytuD.00095.a  | Oxidoreductase                                                                                                                                                                                                                                            |
| 11  | MytuD.00095.b  | Putative non-heme bromoperoxidase BpoC (EC 1.11.1.18) (Rv0554)                                                                                                                                                                                            |
| 12  | MytuD.00105.a  | Uncharacterized protein Rv1367c/MT1414                                                                                                                                                                                                                    |
| 13  | MytuD.00111.a  | Probable glutamine synthetase GlnA4 (Glutamine synthase) (GS-II) (Rv2860c)                                                                                                                                                                                |
| 14  | MytuD.00113.a  | Probable polyketide synthase PKS15                                                                                                                                                                                                                        |
| 15  | MytuD.00114.a  | Uncharacterized protein Rv0525                                                                                                                                                                                                                            |
| 16  | MytuD.00145.a  | aspartyl-tRNA synthetase                                                                                                                                                                                                                                  |
| 17  | MytuD.00145.b  | Aspartate--tRNA ligase EC=6.1.1.12                                                                                                                                                                                                                        |
| 18  | MytuD.00148.a  | Site-specific tyrosine recombinase XerD                                                                                                                                                                                                                   |
| 19  | MytuD.00148.b  | Site-specific tyrosine recombinase XerC                                                                                                                                                                                                                   |
| 20  | MytuD.00148.c  | Integrase, putative                                                                                                                                                                                                                                       |
| 21  | MytuD.00148.d  | PROBABLE INTEGRASE                                                                                                                                                                                                                                        |
| 22  | MytuD.00149.a  | Cyclopropane mycolic acid synthase MmaA2 (CMAS) (EC 2.1.1.79) (Cyclopropane-fatty-acyl--phospholipid synthase) (CFA synthase) (Mycolic acid methyltransferase) (MA-MT) (S--adenosylmethionine-dependent methyltransferase) (AdoMet-MT) (SAM-MT) (Rv0644c) |
| 23  | MytuD.00149.b  | S-adenosylmethionine-dependent methyltransferase UmaA (SAM-dependent methyltransferase UmaA) (EC 2.1.1.-) (Rv0469)                                                                                                                                        |
| 24  | MytuD.00151.a  | Probable polyketide synthase pks17                                                                                                                                                                                                                        |
| 25  | MytuD.00155.a  | Probable ATP-dependent DNA helicase II UvrD2                                                                                                                                                                                                              |
| 26  | MytuD.00163.a  | Phenylalanyl-tRNA synthetase subunit alpha                                                                                                                                                                                                                |

|    |                               |                                                                                                                                               |
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| 27 | <a href="#">MytuD.00168.a</a> | 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase Rv3582c (IspD)                                                                         |
| 28 | <a href="#">MytuD.00184.a</a> | Phosphoglyceromutase                                                                                                                          |
| 29 | <a href="#">MytuD.00185.a</a> | Probable acyl-CoA dehydrogenase fadE25                                                                                                        |
| 30 | <a href="#">MytuD.00185.b</a> | Probable acyl-CoA dehydrogenase fadE25                                                                                                        |
| 31 | <a href="#">MytuD.00185.c</a> | Probable acyl-CoA dehydrogenase fadE25                                                                                                        |
| 32 | <a href="#">MytuD.00191.a</a> | NADH dehydrogenase subunit D                                                                                                                  |
| 33 | <a href="#">MytuD.00200.a</a> | Arginine/ornithine transport system ATPase                                                                                                    |
| 34 | <a href="#">MytuD.00212.a</a> | Probable rubredoxin RubA                                                                                                                      |
| 35 | <a href="#">MytuD.00213.a</a> | Enoyl-CoA hydratase                                                                                                                           |
| 36 | <a href="#">MytuD.00236.a</a> | Probable conserved ATP-binding protein ABC transporter                                                                                        |
| 37 | <a href="#">MytuD.00247.a</a> | Probable acyl-CoA dehydrogenase FadE20                                                                                                        |
| 38 | <a href="#">MytuD.00249.a</a> | Thymidylate synthase Rv2764c                                                                                                                  |
| 39 | <a href="#">MytuD.00250.a</a> | Possible oxidoreductase                                                                                                                       |
| 40 | <a href="#">MytuD.00262.a</a> | GTPase Era                                                                                                                                    |
| 41 | <a href="#">MytuD.00272.a</a> | 8-amino-7-oxononanoate synthase                                                                                                               |
| 42 | <a href="#">MytuD.00277.a</a> | Possible esterase LipW                                                                                                                        |
| 43 | <a href="#">MytuD.00289.a</a> | Deoxyribose-phosphate aldolase                                                                                                                |
| 44 | <a href="#">MytuD.00295.a</a> | Probable zinc-type alcohol dehydrogenase (E subunit) ADHE                                                                                     |
| 45 | <a href="#">MytuD.00304.a</a> | Probable cysteine desulfurase CSD                                                                                                             |
| 46 | <a href="#">MytuD.00305.a</a> | Enoyl-CoA hydratase                                                                                                                           |
| 47 | <a href="#">MytuD.00309.a</a> | Probable acyl-CoA dehydrogenase FadE2                                                                                                         |
| 48 | <a href="#">MytuD.00317.a</a> | Triosephosphate isomerase                                                                                                                     |
| 49 | <a href="#">MytuD.00328.a</a> | 50S ribosomal protein L1                                                                                                                      |
| 50 | <a href="#">MytuD.00337.a</a> | Short chain dehydrogenase                                                                                                                     |
| 51 | <a href="#">MytuD.00340.a</a> | Enoyl-CoA hydratase                                                                                                                           |
| 52 | <a href="#">MytuD.00358.a</a> | Enoyl-CoA hydratase                                                                                                                           |
| 53 | <a href="#">MytuD.00382.a</a> | Possible para-nitrobenzyl esterase (fragment)                                                                                                 |
| 54 | <a href="#">MytuD.00384.a</a> | Probable cytoplasmic peptidase PepQ                                                                                                           |
| 55 | <a href="#">MytuD.00386.a</a> | Enoyl-CoA hydratase                                                                                                                           |
| 56 | <a href="#">MytuD.00391.a</a> | Short chain dehydrogenase                                                                                                                     |
| 57 | <a href="#">MytuD.00392.a</a> | Putative cell division ATP-binding protein FtsE (septation component-transport ATP-binding protein ABC transporter)                           |
| 58 | <a href="#">MytuD.00398.a</a> | ATP-dependent Clp protease proteolytic subunit 1                                                                                              |
| 59 | <a href="#">MytuD.00398.b</a> | ATP-dependent Clp protease proteolytic subunit 2                                                                                              |
| 60 | <a href="#">MytuD.00403.a</a> | Deoxyuridine 5'-triphosphate nucleotidohydrolase                                                                                              |
| 61 | <a href="#">MytuD.00404.a</a> | Probable DNA-3-methyladenine glycosylase I TagA (Tag I) (3-methyladenine-DNA glycosylase I, constitutive) (DNA-3-methyladenine glycosidase I) |
| 62 | <a href="#">MytuD.00414.a</a> | Short chain dehydrogenase                                                                                                                     |
| 63 | <a href="#">MytuD.00416.a</a> | Probable molybdenum-transport ATP-binding protein ABC transporter ModC                                                                        |
| 64 | <a href="#">MytuD.00427.a</a> | UPF0079 ATP-binding protein Rv3422c/MT3531                                                                                                    |
| 65 | <a href="#">MytuD.00429.a</a> | 6-phosphofructokinase                                                                                                                         |
| 66 | <a href="#">MytuD.00441.a</a> | Probable pyruvate dehydrogenase E1 component (beta subunit) PDHB (pyruvate decarboxylase) (pyruvate dehydrogenase) (pyruvic dehydrogenase)    |
| 67 | <a href="#">MytuD.00448.a</a> | Nicotinic acid mononucleotide adenyltransferase                                                                                               |
| 68 | <a href="#">MytuD.00458.a</a> | Probable acyl-CoA thioesterase II TesB2 (TEII)                                                                                                |
| 69 | <a href="#">MytuD.00463.a</a> | Probable ornithine aminotransferase (C-terminus part) RocD2 (ornithine--oxo-acid aminotransferase)                                            |
| 70 | <a href="#">MytuD.00471.a</a> | Possible 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (HHDD isomerase)                                                                       |
| 71 | <a href="#">MytuD.00472.a</a> | Probable short-chain type dehydrogenase/reductase                                                                                             |
| 72 | <a href="#">MytuD.00489.a</a> | Possible enoyl-CoA hydratase                                                                                                                  |
| 73 | <a href="#">MytuD.00495.a</a> | Cytidine deaminase                                                                                                                            |
| 74 | <a href="#">MytuD.00504.a</a> | Possible dehydrogenase                                                                                                                        |
| 75 | <a href="#">MytuD.00516.a</a> | Chromosome partitioning protein                                                                                                               |
| 76 | <a href="#">MytuD.00519.a</a> | Probable serine acetyltransferase cysE (SAT)                                                                                                  |
| 77 | <a href="#">MytuD.00541.a</a> | Succinyl-CoA synthetase subunit beta                                                                                                          |
| 78 | <a href="#">MytuD.00549.a</a> | Molybdenum cofactor biosynthesis protein A                                                                                                    |
| 79 | <a href="#">MytuD.00554.a</a> | Probable short-chain type dehydrogenase/reductase                                                                                             |
| 80 | <a href="#">MytuD.00556.a</a> | Succinyl-CoA synthetase subunit alpha                                                                                                         |
| 81 | <a href="#">MytuD.00560.a</a> | Probable proline iminopeptidase Pip (prolyl aminopeptidase) (Pap)                                                                             |
| 82 | <a href="#">MytuD.00572.a</a> | Probable tetraonasin-transport ATP-binding protein ABC transporter                                                                            |
| 83 | <a href="#">MytuD.00577.a</a> | Probable ornithine aminotransferase (N-terminus part) RocD1 (ornithine--oxo-acid aminotransferase)                                            |
| 84 | <a href="#">MytuD.00587.a</a> | Mycobacterial persistence regulator MrpA (two component response transcriptional regulatory protein)                                          |
| 85 | <a href="#">MytuD.00609.a</a> | Probable glutamine-transport ATP-binding protein ABC transporter                                                                              |
| 86 | <a href="#">MytuD.00609.b</a> | Probable glutamine-transport ATP-binding protein ABC transporter GlnQ                                                                         |
| 87 | <a href="#">MytuD.00612.a</a> | Lysine--tRNA ligase 1 (LysS) (LysS1) (Rv3598c)                                                                                                |
| 88 | <a href="#">MytuD.00620.a</a> | Cytokinin riboside 5'-monophosphate phosphoribohydrolase (Protein Lonely Guy homolog) (LOG homologue)                                         |
| 89 | <a href="#">MytuD.00625.a</a> | Hypothetical protein                                                                                                                          |
| 90 | <a href="#">MytuD.00629.a</a> | Acyl-CoA synthetase                                                                                                                           |
| 91 | <a href="#">MytuD.00629.b</a> | Probable fatty-acid-CoA ligase FadD7 (fatty-acid-CoA synthetase) (fatty-acid-CoA synthase)                                                    |
| 92 | <a href="#">MytuD.00629.c</a> | Probable fatty-acid-CoA ligase fadd8 (fatty-acid-CoA synthetase) (fatty-acid-CoA synthase)                                                    |
| 93 | <a href="#">MytuD.00629.d</a> | Bifunctional enzyme MbtA: salicyl-AMP ligase (SAL-AMP ligase) + salicyl-S-ArCP synthetase (Enterobactin synthase subunit E)                   |

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|-----|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 94  | <a href="#">MytuD.00640.a</a> | Acetate kinase                                                                                                                                                                                                                                     |
| 95  | <a href="#">MytuD.00654.a</a> | Acetyl-CoA acetyltransferase                                                                                                                                                                                                                       |
| 96  | <a href="#">MytuD.00656.a</a> | Possible ribonucleotide-transport ATP-binding protein ABC transporter Mkl                                                                                                                                                                          |
| 97  | <a href="#">MytuD.00663.a</a> | Cytidylate kinase                                                                                                                                                                                                                                  |
| 98  | <a href="#">MytuD.00665.a</a> | Probable conserved ATP-binding protein ABC transporter                                                                                                                                                                                             |
| 99  | <a href="#">MytuD.00680.a</a> | 50S ribosomal protein L22                                                                                                                                                                                                                          |
| 100 | <a href="#">MytuD.00681.a</a> | Probable NAD(P) transhydrogenase (subunit alpha) PntAa [first part; catalytic part] (pyridine nucleotide transhydrogenase subunit alpha) (nicotinamide nucleotide transhydrogenase subunit alpha)                                                  |
| 101 | <a href="#">MytuD.00690.a</a> | Probable unidentified antibiotic-transport ATP-binding protein ABC transporter                                                                                                                                                                     |
| 102 | <a href="#">MytuD.00693.a</a> | NAD-dependent deacetylase                                                                                                                                                                                                                          |
| 103 | <a href="#">MytuD.00698.a</a> | Methylcitrate synthase                                                                                                                                                                                                                             |
| 104 | <a href="#">MytuD.00725.a</a> | 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (CMK) Rv1011 (IspE)                                                                                                                                                                              |
| 105 | <a href="#">MytuD.00738.a</a> | RNA polymerase sigma factor rpoD Rv2703                                                                                                                                                                                                            |
| 106 | <a href="#">MytuD.00746.a</a> | Probable sugar-transport ATP-binding protein ABC transporter SugC                                                                                                                                                                                  |
| 107 | <a href="#">MytuD.00750.a</a> | Phosphate-transport ATP-binding protein ABC transporter PstB                                                                                                                                                                                       |
| 108 | <a href="#">MytuD.00751.a</a> | Probable serine hydroxymethyltransferase glyA2 (serine methylase 2) (SHMT 2)                                                                                                                                                                       |
| 109 | <a href="#">MytuD.00753.a</a> | Probable sugar-transport ATP-binding protein ABC transporter                                                                                                                                                                                       |
| 110 | <a href="#">MytuD.00754.a</a> | Hypothetical HIT-like protein                                                                                                                                                                                                                      |
| 111 | <a href="#">MytuD.00760.a</a> | Uncharacterized protein Rv1708/MT1749                                                                                                                                                                                                              |
| 112 | <a href="#">MytuD.00762.a</a> | Short chain dehydrogenase                                                                                                                                                                                                                          |
| 113 | <a href="#">MytuD.00768.a</a> | Phosphoribosylaminoimidazole synthetase                                                                                                                                                                                                            |
| 114 | <a href="#">MytuD.00774.a</a> | Phosphoribosylglycinamide formyltransferase 2                                                                                                                                                                                                      |
| 115 | <a href="#">MytuD.00778.a</a> | Possible pterin-4-alpha-carbinolamine dehydratase moab2 (PHS) (4-alpha-hydroxy-tetrahydropterin dehydratase) (pterin-4-a-carbinolamine dehydratase) (phenylalanine hydroxylase-stimulating protein) (PHS) (pterin carbinolamine dehydratase) (PCD) |
| 116 | <a href="#">MytuD.00781.a</a> | Acetyl-CoA acetyltransferase                                                                                                                                                                                                                       |
| 117 | <a href="#">MytuD.00783.a</a> | Serine hydroxymethyltransferase                                                                                                                                                                                                                    |
| 118 | <a href="#">MytuD.00786.a</a> | Putative deoxyribonucleotide triphosphate pyrophosphatase                                                                                                                                                                                          |
| 119 | <a href="#">MytuD.00797.a</a> | Probable antibiotic-transport ATP-binding protein ABC transporter                                                                                                                                                                                  |
| 120 | <a href="#">MytuD.00808.a</a> | Probable L-aparaginase ansA                                                                                                                                                                                                                        |
| 121 | <a href="#">MytuD.00814.a</a> | Probable catechol-o-methyltransferase                                                                                                                                                                                                              |
| 122 | <a href="#">MytuD.00829.a</a> | Enoyl-CoA hydratase                                                                                                                                                                                                                                |
| 123 | <a href="#">MytuD.00852.a</a> | GTPase Der                                                                                                                                                                                                                                         |
| 124 | <a href="#">MytuD.00863.a</a> | Putative uncharacterized protein                                                                                                                                                                                                                   |
| 125 | <a href="#">MytuD.00887.a</a> | Hypothetical protein                                                                                                                                                                                                                               |
| 126 | <a href="#">MytuD.00887.b</a> | mRNA interferase MazF6                                                                                                                                                                                                                             |
| 127 | <a href="#">MytuD.00891.a</a> | Probable oxidoreductase                                                                                                                                                                                                                            |
| 128 | <a href="#">MytuD.00896.a</a> | Type II citrate synthase                                                                                                                                                                                                                           |
| 129 | <a href="#">MytuD.00897.a</a> | Glucose-6-phosphate 1-dehydrogenase                                                                                                                                                                                                                |
| 130 | <a href="#">MytuD.00904.a</a> | Peroxidoxin BcpB                                                                                                                                                                                                                                   |
| 131 | <a href="#">MytuD.00906.a</a> | Cystathionine gamma-synthase                                                                                                                                                                                                                       |
| 132 | <a href="#">MytuD.00922.a</a> | 50S ribosomal protein L4                                                                                                                                                                                                                           |
| 133 | <a href="#">MytuD.00937.a</a> | tRNA (guanine-N(1)-)-methyltransferase                                                                                                                                                                                                             |
| 134 | <a href="#">MytuD.00938.a</a> | 2,5-diketo-D-gluconate reductase A                                                                                                                                                                                                                 |
| 135 | <a href="#">MytuD.00950.a</a> | Probable lipoprotein aminopeptidase Lpql                                                                                                                                                                                                           |
| 136 | <a href="#">MytuD.00951.a</a> | Amidase                                                                                                                                                                                                                                            |
| 137 | <a href="#">MytuD.00951.b</a> | Conserved hypothetical protein                                                                                                                                                                                                                     |
| 138 | <a href="#">MytuD.00980.a</a> | Phosphoserine aminotransferase (EC 2.6.1.52) (Phosphohydroxythreonine aminotransferase) (PSAT) (Rv0884c)                                                                                                                                           |
| 139 | <a href="#">MytuD.01007.a</a> | Hypothetical protein                                                                                                                                                                                                                               |
| 140 | <a href="#">MytuD.01019.a</a> | Dihydropteroate synthase 1 (DHPS) (DHPS 1)                                                                                                                                                                                                         |
| 141 | <a href="#">MytuD.01026.a</a> | 4-aminobutyrate aminotransferase                                                                                                                                                                                                                   |
| 142 | <a href="#">MytuD.01046.a</a> | Glycine cleavage system protein H                                                                                                                                                                                                                  |
| 143 | <a href="#">MytuD.01048.a</a> | Probable acyl-CoA dehydrogenase FadE9                                                                                                                                                                                                              |
| 144 | <a href="#">MytuD.01058.a</a> | Hypothetical protein                                                                                                                                                                                                                               |
| 145 | <a href="#">MytuD.01062.a</a> | Dihydrofolate reductase (DHFR)                                                                                                                                                                                                                     |
| 146 | <a href="#">MytuD.01068.a</a> | Phosphoribosylaminoimidazole-succinocarboxamide synthase                                                                                                                                                                                           |
| 147 | <a href="#">MytuD.01073.a</a> | NADH dehydrogenase subunit C                                                                                                                                                                                                                       |
| 148 | <a href="#">MytuD.01083.a</a> | Probable thiosulfate sulfurtransferase CysA2 (rhodanese-like protein) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)                                                                                                           |
| 149 | <a href="#">MytuD.01097.a</a> | Probable short-chain type dehydrogenase/reductase                                                                                                                                                                                                  |
| 150 | <a href="#">MytuD.01097.b</a> | Uncharacterized oxidoreductase (Rv1543)                                                                                                                                                                                                            |
| 151 | <a href="#">MytuD.01105.a</a> | 50S ribosomal protein L3                                                                                                                                                                                                                           |
| 152 | <a href="#">MytuD.01113.a</a> | Probable cysteine synthase b CysM (CSase B) (O-acetylserine sulphydrylase B) (O-acetylserine (Thiol)-lyase B)                                                                                                                                      |
| 153 | <a href="#">MytuD.01117.a</a> | Probable acyl-CoA dehydrogenase FadE29                                                                                                                                                                                                             |
| 154 | <a href="#">MytuD.01124.a</a> | Probable daunorubicin-DIM-transport ATP-binding protein ABC transporter DrrA                                                                                                                                                                       |
| 155 | <a href="#">MytuD.01125.a</a> | Hypothetical protein                                                                                                                                                                                                                               |
| 156 | <a href="#">MytuD.01147.a</a> | Probable cystathionine beta-synthase CBS (Serine sulphydrase) (Beta-thionase) (Hemoprotein H--450)                                                                                                                                                 |
| 157 | <a href="#">MytuD.01152.a</a> | Uroporphyrinogen decarboxylase                                                                                                                                                                                                                     |
| 158 | <a href="#">MytuD.01155.a</a> | Phosphoserine phosphatase                                                                                                                                                                                                                          |
| 159 | <a href="#">MytuD.01155.b</a> | Uncharacterized protein Rv3661/MT3761                                                                                                                                                                                                              |
| 160 | <a href="#">MytuD.01156.a</a> | O-acetylhomoserine sulphydrylase MetC                                                                                                                                                                                                              |

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| 161 | <a href="#">MytuD.01188.a</a> | Probable dioxygenase                                                                                                                                               |
| 162 | <a href="#">MytuD.01188.b</a> | Probable dioxygenase                                                                                                                                               |
| 163 | <a href="#">MytuD.01189.a</a> | Probable NADPH quinone oxidoreductase FadB4 (NADPH:quinone reductase) (zeta-crystallin)                                                                            |
| 164 | <a href="#">MytuD.01193.a</a> | Probable serine/threonine-protein kinase pknH                                                                                                                      |
| 165 | <a href="#">MytuD.01204.a</a> | Short chain dehydrogenase                                                                                                                                          |
| 166 | <a href="#">MytuD.01212.a</a> | Malate dehydrogenase                                                                                                                                               |
| 167 | <a href="#">MytuD.01241.a</a> | Probable thiosulfate sulfurtransferase SSEA (rhodanese) (thiosulfate cyanide transsulfurase) (thiosulfate thiotransferase)                                         |
| 168 | <a href="#">MytuD.01244.a</a> | 6-phosphogluconolactonase                                                                                                                                          |
| 169 | <a href="#">MytuD.01249.a</a> | Short chain dehydrogenase                                                                                                                                          |
| 170 | <a href="#">MytuD.01254.a</a> | Bifunctional phosphopantothienoylcysteine decarboxylase/phosphopantothenate synthase                                                                               |
| 171 | <a href="#">MytuD.01263.a</a> | Possible acyl-CoA dehydrogenase FadE19 (MMGC)                                                                                                                      |
| 172 | <a href="#">MytuD.01263.b</a> | Probable acyl-CoA dehydrogenase fadE28 (Rv3544c)                                                                                                                   |
| 173 | <a href="#">MytuD.01279.a</a> | 30S ribosomal protein S9                                                                                                                                           |
| 174 | <a href="#">MytuD.01285.a</a> | 5'-methylthioadenosine phosphorylase                                                                                                                               |
| 175 | <a href="#">MytuD.01319.a</a> | Probable fatty-acid-CoA ligase FadD18 (fragment) (fatty-acid-CoA synthetase) (fatty-acid-CoA synthase)                                                             |
| 176 | <a href="#">MytuD.01322.a</a> | 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) |
| 177 | <a href="#">MytuD.01326.a</a> | 3-ketoacyl-(acyl-carrier-protein) reductase                                                                                                                        |
| 178 | <a href="#">MytuD.01331.a</a> | Phosphoglycerate kinase                                                                                                                                            |
| 179 | <a href="#">MytuD.01347.a</a> | Probable adhesion component transport ATP-binding protein ABC transporter                                                                                          |
| 180 | <a href="#">MytuD.01353.a</a> | O-succinylhomoserine sulfhydrylase                                                                                                                                 |
| 181 | <a href="#">MytuD.01356.a</a> | Probable UDP-glucose 6-dehydrogenase UdgA (UDP-glc dehydrogenase) (UDP-GlcDH) (UDPGDH)                                                                             |
| 182 | <a href="#">MytuD.01365.a</a> | Short chain dehydrogenase                                                                                                                                          |
| 183 | <a href="#">MytuD.01370.a</a> | Phosphomannomutase/phosphoglucomutase                                                                                                                              |
| 184 | <a href="#">MytuD.01379.a</a> | Probable dehydrogenase/reductase                                                                                                                                   |
| 185 | <a href="#">MytuD.01379.b</a> | Probable 3-hydroxyisobutyrate dehydrogenase (HIBADH) (EC 1.1.1.31) (Rv0751c)                                                                                       |
| 186 | <a href="#">MytuD.01381.a</a> | Enoyl-CoA hydratase                                                                                                                                                |
| 187 | <a href="#">MytuD.01395.a</a> | Probable thiosulfate sulfurtransferase SseB                                                                                                                        |
| 188 | <a href="#">MytuD.01396.a</a> | Acylphosphatase                                                                                                                                                    |
| 189 | <a href="#">MytuD.01407.a</a> | Probable dipeptidase PepE                                                                                                                                          |
| 190 | <a href="#">MytuD.01414.a</a> | Probable sulfate-transport ATP-binding protein ABC transporter cysA1                                                                                               |
| 191 | <a href="#">MytuD.01455.a</a> | Carbamoyl phosphate synthase small subunit                                                                                                                         |
| 192 | <a href="#">MytuD.01464.a</a> | Probable phosphotriesterase PHP (parathion hydrolase) (PTE) (aryldialkylphosphatase) (paraoxonase) (a-esterase) (aryltriphosphatase) (paraoxon hydrolase)          |
| 193 | <a href="#">MytuD.01484.a</a> | 30S ribosomal protein S10                                                                                                                                          |
| 194 | <a href="#">MytuD.01507.a</a> | Fumarate hydratase                                                                                                                                                 |
| 195 | <a href="#">MytuD.01530.a</a> | Enoyl-CoA hydratase                                                                                                                                                |
| 196 | <a href="#">MytuD.01548.a</a> | Methionine aminopeptidase                                                                                                                                          |
| 197 | <a href="#">MytuD.01549.a</a> | Pyruvate phosphate dikinase                                                                                                                                        |
| 198 | <a href="#">MytuD.01557.a</a> | Possible acetyl-CoA acetyltransferase (acetoacetyl-CoA thiolase)                                                                                                   |
| 199 | <a href="#">MytuD.01566.a</a> | Enoyl-CoA hydratase                                                                                                                                                |
| 200 | <a href="#">MytuD.01568.a</a> | Probable Sn-glycerol-3-phosphate transport ATP-binding protein ABC transporter UgpC                                                                                |
| 201 | <a href="#">MytuD.01570.a</a> | 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase                                                                                               |
| 202 | <a href="#">MytuD.01582.a</a> | 3-ketoacyl-(acyl-carrier-protein) reductase                                                                                                                        |
| 203 | <a href="#">MytuD.01585.a</a> | NADH dehydrogenase subunit E                                                                                                                                       |
| 204 | <a href="#">MytuD.01608.a</a> | Ribonucleotide-diphosphate reductase subunit beta                                                                                                                  |
| 205 | <a href="#">MytuD.01609.a</a> | Possible osmoprotectant (glycine betaine/carnitine/choline/L-proline) transport ATP-binding protein ABC transporter ProV                                           |
| 206 | <a href="#">MytuD.01613.a</a> | Probable acyl-CoA dehydrogenase FadE17                                                                                                                             |
| 207 | <a href="#">MytuD.01625.a</a> | S-adenosylmethionine synthetase                                                                                                                                    |
| 208 | <a href="#">MytuD.01626.a</a> | Hypothetical protein                                                                                                                                               |
| 209 | <a href="#">MytuD.01635.a</a> | Probable rubredoxin RubB                                                                                                                                           |
| 210 | <a href="#">MytuD.01640.a</a> | Acyl-CoA dehydrogenase FadE7                                                                                                                                       |
| 211 | <a href="#">MytuD.01649.a</a> | Putative conserved protein Rv2377c                                                                                                                                 |
| 212 | <a href="#">MytuD.01655.a</a> | Flavin-Dependent Thymidylate synthase Rv2754c                                                                                                                      |
| 213 | <a href="#">MytuD.01657.a</a> | Possible transcriptional regulatory protein (DNA-binding protein, putative) Rv2745c                                                                                |
| 214 | <a href="#">MytuD.01665.a</a> | Exported repetitive protein (Cell surface protein PirG) (EXP53)                                                                                                    |
| 215 | <a href="#">MytuD.07054.a</a> | Probable cytochrome P450 130 Cyp130                                                                                                                                |
| 216 | <a href="#">MytuD.10050.a</a> | Deoxyuridine 5'-triphosphate nucleotidohydrolase                                                                                                                   |
| 217 | <a href="#">MytuD.10520.a</a> | Putative beta-lactamase                                                                                                                                            |
| 218 | <a href="#">MytuD.10520.b</a> | Possible glyoxalase II (hydroxyacylglutathione hydrolase) (Glx II) (putative beta-lactamase)                                                                       |
| 219 | <a href="#">MytuD.10611.a</a> | Probable zinc-dependent alcohol dehydrogenase AdhE2                                                                                                                |
| 220 | <a href="#">MytuD.10611.b</a> | Possible zinc-containing alcohol dehydrogenase NAD dependent AdhB                                                                                                  |
| 221 | <a href="#">MytuD.10611.c</a> | Putative alcohol dehydrogenase D                                                                                                                                   |
| 222 | <a href="#">MytuD.11416.a</a> | Chromosome partitioning protein                                                                                                                                    |
| 223 | <a href="#">MytuD.12746.a</a> | Putative beta-lactamase                                                                                                                                            |
| 224 | <a href="#">MytuD.12797.a</a> | Possible transcriptional regulatory protein                                                                                                                        |
| 225 | <a href="#">MytuD.16715.a</a> | Beta lactamase like protein                                                                                                                                        |
| 226 | <a href="#">MytuD.17056.a</a> | Probable conserved membrane protein Rv0347                                                                                                                         |
| 227 | <a href="#">MytuD.17056.b</a> | Hypothetical protein Rv0831c                                                                                                                                       |
| 228 | <a href="#">MytuD.17057.a</a> | Probable lipoprotein LppN Rv2270                                                                                                                                   |
| 229 | <a href="#">MytuD.17058.a</a> | Hypothetical protein Rv0349                                                                                                                                        |

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| 230 | <a href="#">MytuD.17060.a</a> | Hypothetical protein Rv3172c                                                                |
| 231 | <a href="#">MytuD.17065.a</a> | Anti-anti-sigma factor RsfA (anti-sigma factor antagonist) (regulator of sigma F A) Rv1365c |
| 232 | <a href="#">MytuD.17076.a</a> | Hypothetical protein Rv3081                                                                 |
| 233 | <a href="#">MytuD.17078.a</a> | Hypothetical protein Rv1813c                                                                |
| 234 | <a href="#">MytuD.17102.a</a> | Putative uncharacterized protein Rv3683                                                     |
| 235 | <a href="#">MytuD.17112.a</a> | DUF3349 superfamily protein Rv0543c                                                         |
| 236 | <a href="#">MytuD.17208.a</a> | RNA polymerase sigma factor                                                                 |
| 237 | <a href="#">MytuD.17208.b</a> | ECF RNA polymerase sigma factor SigH                                                        |
| 238 | <a href="#">MytuD.17229.a</a> | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase 1 (IspH/LytB) (IspG/H)                   |
| 239 | <a href="#">MytuD.17230.a</a> | 1-deoxy-D-xylulose-5-phosphate synthase (DOXP/dxs/dxp)                                      |
| 240 | <a href="#">MytuD.17230.b</a> | Probable 1-deoxy-D-xylulose-5-phosphate synthase (DXS)                                      |
| 241 | <a href="#">MytuD.17231.a</a> | (E)-4-hydroxy-3-methylbut-2-enyl diphosphate synthase (IspG/GcpE) (IspG/H)                  |
| 242 | <a href="#">MytuD.17233.a</a> | 4-hydroxy-3-methylbut-2-enyl diphosphate reductase 2 (IspH/LytB) (IspG/H)                   |
| 243 | <a href="#">MytuD.17236.a</a> | Uncharacterized protein Rv1354c/MT1397                                                      |
| 244 | <a href="#">MytuD.17257.a</a> | Putative methyltransferase Rv1403c                                                          |
| 245 | <a href="#">MytuD.17258.a</a> | Helicase-nuclease AddA Rv3201c                                                              |
| 246 | <a href="#">MytuD.17259.a</a> | Helicase-nuclease AddB Rv3202c                                                              |
| 247 | <a href="#">MytuD.17260.a</a> | RecC Exodeoxyribonuclease V gamma chain (EC 3.1.11.5) Rv0631c                               |
| 248 | <a href="#">MytuD.17261.a</a> | RecB Exodeoxyribonuclease V beta chain (EC 3.1.11.5) Rv0630c                                |
| 249 | <a href="#">MytuD.17262.a</a> | RecD Exodeoxyribonuclease V alpha chain (EC 3.1.11.5) Rv0629c                               |
| 250 | <a href="#">MytuD.17268.a</a> | ID93 fusion (Rv3619c, Rv2608, Rv3620c, Rv1813c)                                             |
| 251 | <a href="#">MytuD.17268.b</a> | PPE family protein                                                                          |
| 252 | <a href="#">MytuD.17268.c</a> | PPE family protein                                                                          |
| 253 | <a href="#">MytuD.17268.d</a> | PE family protein. Possible lipase.                                                         |
| 254 | <a href="#">MytuD.17269.a</a> | Rv0577                                                                                      |
| 255 | <a href="#">MytuD.17274.a</a> | DNA-directed RNA polymerase subunit beta' Rv0668                                            |
| 256 | <a href="#">MytuD.17285.a</a> | Amino acid ABC transporter, amino acid-binding protein                                      |
| 257 | <a href="#">MytuD.17287.a</a> | Probable thioesterase tesA                                                                  |
| 258 | <a href="#">MytuD.17291.a</a> | Luciferase-related protein                                                                  |
| 259 | <a href="#">MytuD.17291.b</a> | Luciferase-related protein                                                                  |
| 260 | <a href="#">MytuD.17302.a</a> | Possible transposase                                                                        |
| 261 | <a href="#">MytuD.17303.a</a> | Putative uncharacterized protein                                                            |
| 262 | <a href="#">MytuD.17304.a</a> | IS1536, resolvase                                                                           |
| 263 | <a href="#">MytuD.17304.b</a> | IS1537, resolvase                                                                           |
| 264 | <a href="#">MytuD.17304.c</a> | Uncharacterized protein Rv2886c/MT2954                                                      |
| 265 | <a href="#">MytuD.17304.d</a> | IS1538, resolvase                                                                           |
| 266 | <a href="#">MytuD.17310.a</a> | Conserved hypothetical protein TB31.7                                                       |
| 267 | <a href="#">MytuD.17324.a</a> | Magnesium chelatase, putative                                                               |
| 268 | <a href="#">MytuD.17324.b</a> | Magnesium chelatase, putative                                                               |
| 269 | <a href="#">MytuD.17328.a</a> | IS1560, transposase                                                                         |
| 270 | <a href="#">MytuD.17328.b</a> | IS1560, transposase                                                                         |
| 271 | <a href="#">MytuD.17328.c</a> | Possible transposase                                                                        |
| 272 | <a href="#">MytuD.17366.a</a> | Chaperone protein DnaJ2 (Rv2373c)                                                           |
| 273 | <a href="#">MytuD.17369.a</a> | Probable ATP synthase beta chain atpD                                                       |
| 274 | <a href="#">MytuD.17369.b</a> | Transcription termination factor Rho (Rv1297)                                               |
| 275 | <a href="#">MytuD.17387.a</a> | Citrate lyase, beta subunit, putative                                                       |
| 276 | <a href="#">MytuD.17388.a</a> | UPF0039 protein Rv2851c/MT2917                                                              |
| 277 | <a href="#">MytuD.17389.a</a> | Uncharacterized protein Rv3404c/MT3512                                                      |
| 278 | <a href="#">MytuD.17392.a</a> | IS1558', transposase                                                                        |
| 279 | <a href="#">MytuD.17392.b</a> | IS1607, transposase                                                                         |
| 280 | <a href="#">MytuD.17393.a</a> | Probable PhoH -like protein PhoH2 (phosphate starvation-inducible protein PsiH)             |
| 281 | <a href="#">MytuD.17394.a</a> | Putative uncharacterized protein                                                            |
| 282 | <a href="#">MytuD.17396.a</a> | Possible alternative RNA polymerase sigma factor SigI                                       |
| 283 | <a href="#">MytuD.17397.a</a> | Putative uncharacterized protein                                                            |
| 284 | <a href="#">MytuD.17398.a</a> | Putative uncharacterized protein                                                            |
| 285 | <a href="#">MytuD.17399.a</a> | Stearoyl-CoA 9-desaturase electron transfer partner                                         |
| 286 | <a href="#">MytuD.17417.a</a> | Putative uncharacterized protein                                                            |
| 287 | <a href="#">MytuD.17442.a</a> | RNA polymerase sigma factor SigK                                                            |
| 288 | <a href="#">MytuD.17446.a</a> | Putative uncharacterized protein                                                            |
| 289 | <a href="#">MytuD.17459.a</a> | Possible transposase                                                                        |
| 290 | <a href="#">MytuD.17461.a</a> | Uncharacterized protein Rv0030/MT0034                                                       |
| 291 | <a href="#">MytuD.17464.a</a> | Possible transposase                                                                        |
| 292 | <a href="#">MytuD.17470.a</a> | Putative NAD(P)H nitroreductase RV3131/MT3217                                               |
| 293 | <a href="#">MytuD.17470.b</a> | Putative NAD(P)H nitroreductase acg (EC 1.-.-.-)                                            |
| 294 | <a href="#">MytuD.17471.a</a> | Probable cutinase [second part] Cut5b                                                       |
| 295 | <a href="#">MytuD.17479.a</a> | Putative uncharacterized protein                                                            |
| 296 | <a href="#">MytuD.17486.a</a> | Putative uncharacterized protein                                                            |
| 297 | <a href="#">MytuD.17507.a</a> | Conserved protein                                                                           |
| 298 | <a href="#">MytuD.17509.a</a> | Putative uncharacterized protein                                                            |
| 299 | <a href="#">MytuD.17510.a</a> | Possible transposase                                                                        |
| 300 | <a href="#">MytuD.17531.a</a> | Putative uncharacterized protein                                                            |
| 301 | <a href="#">MytuD.17532.a</a> | Protease-related protein                                                                    |
| 302 | <a href="#">MytuD.17537.a</a> | Possible transposase                                                                        |
| 303 | <a href="#">MytuD.17559.a</a> | Putative uncharacterized protein                                                            |
| 304 | <a href="#">MytuD.17568.a</a> | Probable lipase LipD                                                                        |

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| 305 | <a href="#">MytuD.17576.a</a> | Putative uncharacterized protein                                                                    |
| 306 | <a href="#">MytuD.17590.a</a> | Putative uncharacterized protein                                                                    |
| 307 | <a href="#">MytuD.17600.a</a> | Possible transposase                                                                                |
| 308 | <a href="#">MytuD.17602.a</a> | Conserved protein                                                                                   |
| 309 | <a href="#">MytuD.17614.a</a> | ClpP protease chaperone protein ClpC2; uncharacterized protein Rv2667/MT2741                        |
| 310 | <a href="#">MytuD.17614.b</a> | ClpP protease chaperone protein ClpC2; uncharacterized protein Rv2667/MT2741                        |
| 311 | <a href="#">MytuD.17616.a</a> | Uncharacterized protein Rv0948c/MT0975                                                              |
| 312 | <a href="#">MytuD.17627.a</a> | IS1557', transposase                                                                                |
| 313 | <a href="#">MytuD.17634.a</a> | Possible transposase                                                                                |
| 314 | <a href="#">MytuD.17642.a</a> | D-tyrosyl-tRNA(Tyr) deacylase                                                                       |
| 315 | <a href="#">MytuD.17649.a</a> | Probable phiRv1 phage protein                                                                       |
| 316 | <a href="#">MytuD.17655.a</a> | Possible hydrolase                                                                                  |
| 317 | <a href="#">MytuD.17671.a</a> | Putative uncharacterized protein                                                                    |
| 318 | <a href="#">MytuD.17673.a</a> | Putative esterase Rv1847/MT1895                                                                     |
| 319 | <a href="#">MytuD.17674.a</a> | Putative diacylglycerol O-acyltransferase Rv0221/MT0231                                             |
| 320 | <a href="#">MytuD.17674.b</a> | Conserved hypothetical protein. Possible triacylglycerol synthase (diacylglycerol acyltransferase). |
| 321 | <a href="#">MytuD.17675.a</a> | Probable monoacyl phosphatidylinositol tetramannoside-binding protein LpqW                          |
| 322 | <a href="#">MytuD.17682.a</a> | Universal stress protein Rv2319c/MT2382                                                             |
| 323 | <a href="#">MytuD.17686.a</a> | Probable phiRv1 integrase                                                                           |
| 324 | <a href="#">MytuD.17705.a</a> | Possible transposase for insertion sequence element IS1533                                          |
| 325 | <a href="#">MytuD.17706.a</a> | Putative uncharacterized protein                                                                    |
| 326 | <a href="#">MytuD.17711.a</a> | Putative uncharacterized protein                                                                    |
| 327 | <a href="#">MytuD.17716.a</a> | Urease subunit alpha                                                                                |
| 328 | <a href="#">MytuD.17718.a</a> | Putative uncharacterized protein                                                                    |
| 329 | <a href="#">MytuD.17724.a</a> | Putative uncharacterized protein                                                                    |
| 330 | <a href="#">MytuD.17729.a</a> | Putative uncharacterized protein                                                                    |
| 331 | <a href="#">MytuD.17733.a</a> | IS1603, transposase                                                                                 |
| 332 | <a href="#">MytuD.17752.a</a> | Putative uncharacterized protein                                                                    |
| 333 | <a href="#">MytuD.17758.a</a> | Putative Rieske 2Fe-2S iron-sulfur protein Rv3818/MT3926                                            |
| 334 | <a href="#">MytuD.17758.b</a> | Putative Rieske 2Fe-2S iron-sulfur protein Rv3818/MT3926 (EC 1.-.-.-)                               |
| 335 | <a href="#">MytuD.17760.a</a> | Putative uncharacterized protein                                                                    |
| 336 | <a href="#">MytuD.17770.a</a> | Hypothetical glycine rich protein                                                                   |
| 337 | <a href="#">MytuD.17777.a</a> | Uncharacterized protein Rv2850c/MT2916                                                              |
| 338 | <a href="#">MytuD.17778.a</a> | Uncharacterized protein Rv2085/MT2147                                                               |
| 339 | <a href="#">MytuD.17779.a</a> | Probable RNA polymerase sigma-D factor                                                              |
| 340 | <a href="#">MytuD.17782.a</a> | Probable conserved lipoprotein                                                                      |
| 341 | <a href="#">MytuD.17784.a</a> | Membrane-anchored mycosin MYCP1 (serine protease) (Rv3883c)                                         |
| 342 | <a href="#">MytuD.17784.b</a> | Probable alanine- and proline-rich membrane-anchored mycosin MYCP2 (serine protease) (Rv3886c)      |
| 343 | <a href="#">MytuD.17784.c</a> | Probable membrane-anchored mycosin MYCP3 (serine protease) (Rv0291)                                 |
| 344 | <a href="#">MytuD.17784.d</a> | Probable membrane-anchored mycosin MYCP4 (serine protease) (Rv3449)                                 |
| 345 | <a href="#">MytuD.17784.e</a> | Probable proline-rich membrane-anchored mycosin MYCP5 (serine protease) (Rv1796)                    |
| 346 | <a href="#">MytuD.17792.a</a> | Nonspecific lipid-transfer protein (ltp2) (Rv3540c)                                                 |
| 347 | <a href="#">MytuD.17796.a</a> | Putative uncharacterized protein (Rv3541c)                                                          |
| 348 | <a href="#">MytuD.17797.a</a> | Probable exported protease Rv2224c/MT2282                                                           |
| 349 | <a href="#">MytuD.17801.a</a> | Peptidase, M23/M37 family (Rv0950c)                                                                 |
| 350 | <a href="#">MytuD.17804.a</a> | Putative uncharacterized protein (Rv3542c)                                                          |
| 351 | <a href="#">MytuD.17817.a</a> | Putative uncharacterized protein TB39.8                                                             |
| 352 | <a href="#">MytuD.17817.b</a> | Probable regulatory protein embR                                                                    |
| 353 | <a href="#">MytuD.17818.a</a> | Serine/threonine-protein kinase pknB                                                                |
| 354 | <a href="#">MytuD.17818.b</a> | Serine/threonine-protein kinase pknD                                                                |
| 355 | <a href="#">MytuD.17819.a</a> | Possible phiRv2 prophage protein                                                                    |
| 356 | <a href="#">MytuD.17820.a</a> | Putative uncharacterized protein                                                                    |
| 357 | <a href="#">MytuD.17821.a</a> | Toxin                                                                                               |
| 358 | <a href="#">MytuD.17822.a</a> | Putative uncharacterized protein                                                                    |
| 359 | <a href="#">MytuD.17823.a</a> | Putative uncharacterized protein                                                                    |
| 360 | <a href="#">MytuD.17824.a</a> | Possible phiRv2 prophage protein                                                                    |
| 361 | <a href="#">MytuD.17825.a</a> | Putative uncharacterized protein                                                                    |
| 362 | <a href="#">MytuD.17826.a</a> | Putative uncharacterized protein                                                                    |
| 363 | <a href="#">MytuD.17827.a</a> | possible transcriptional regulatory protein                                                         |
| 364 | <a href="#">MytuD.17830.a</a> | Putative uncharacterized protein                                                                    |
| 365 | <a href="#">MytuD.17831.a</a> | Putative uncharacterized protein                                                                    |
| 366 | <a href="#">MytuD.17861.a</a> | DNA-directed RNA polymerase subunit beta Rv0667                                                     |
| 367 | <a href="#">MytuD.17868.a</a> | 30S ribosomal protein S1                                                                            |
| 368 | <a href="#">MytuD.17869.a</a> | Protein Rv2204c/MT2260                                                                              |
| 369 | <a href="#">MytuD.17943.a</a> | Leucine--tRNA ligase                                                                                |
| 370 | <a href="#">MytuD.17946.a</a> | DNA ligase A (Rv3014c)                                                                              |
| 371 | <a href="#">MytuD.17961.a</a> | PROBABLE FERREDOXIN FDXA                                                                            |
| 372 | <a href="#">MytuD.17987.a</a> | Beta sliding clamp (DnaN) (Rv0002)                                                                  |
| 373 | <a href="#">MytuD.18013.a</a> | Elongation factor G                                                                                 |
| 374 | <a href="#">MytuD.18032.a</a> | Chaperone protein ClpB                                                                              |
| 375 | <a href="#">MytuD.18032.b</a> | Probable ATP-dependent Clp protease ATP-binding subunit                                             |
| 376 | <a href="#">MytuD.18062.a</a> | DNA topoisomerase 1                                                                                 |
| 377 | <a href="#">MytuD.18166.a</a> | UPF0051 protein Rv1462/MT1509                                                                       |
| 378 | <a href="#">MytuD.18189.a</a> | Bifunctional (p)ppGpp synthase/hydrolase RelA (Rv2583c)                                             |

|     |                                |                                                                                                |
|-----|--------------------------------|------------------------------------------------------------------------------------------------|
| 379 | <a href="#">MytuD.18213.a</a>  | PE family protein. Possible lipase.                                                            |
| 380 | <a href="#">MytuD.18213.aa</a> | PE family protein. Possible lipase.                                                            |
| 381 | <a href="#">MytuD.18213.ab</a> | PE-PGRS family protein                                                                         |
| 382 | <a href="#">MytuD.18213.ac</a> | PE-PGRS family protein                                                                         |
| 383 | <a href="#">MytuD.18213.ad</a> | PE-PGRS family protein                                                                         |
| 384 | <a href="#">MytuD.18213.ae</a> | PE-PGRS family protein                                                                         |
| 385 | <a href="#">MytuD.18213.af</a> | PE-PGRS family protein                                                                         |
| 386 | <a href="#">MytuD.18213.ag</a> | PE family protein. Possible lipase.                                                            |
| 387 | <a href="#">MytuD.18213.b</a>  | PE-PGRS family protein                                                                         |
| 388 | <a href="#">MytuD.18213.c</a>  | PE family protein. Possible lipase.                                                            |
| 389 | <a href="#">MytuD.18213.d</a>  | PE-PGRS family protein                                                                         |
| 390 | <a href="#">MytuD.18213.e</a>  | PE-PGRS family protein                                                                         |
| 391 | <a href="#">MytuD.18213.f</a>  | PE family protein. Possible lipase.                                                            |
| 392 | <a href="#">MytuD.18213.g</a>  | PE-PGRS family protein                                                                         |
| 393 | <a href="#">MytuD.18213.h</a>  | PE-PGRS family protein (Rv1068c)                                                               |
| 394 | <a href="#">MytuD.18213.i</a>  | PE family protein. Possible lipase.                                                            |
| 395 | <a href="#">MytuD.18213.j</a>  | PE family protein. Possible lipase.                                                            |
| 396 | <a href="#">MytuD.18213.k</a>  | PE-PGRS family protein                                                                         |
| 397 | <a href="#">MytuD.18213.l</a>  | PE-PGRS family protein (Rv1325c)                                                               |
| 398 | <a href="#">MytuD.18213.m</a>  | PE-PGRS family protein                                                                         |
| 399 | <a href="#">MytuD.18213.n</a>  | PE-PGRS family protein                                                                         |
| 400 | <a href="#">MytuD.18213.o</a>  | PE family protein. Possible lipase.                                                            |
| 401 | <a href="#">MytuD.18213.p</a>  | PE-PGRS family protein                                                                         |
| 402 | <a href="#">MytuD.18213.q</a>  | PE-PGRS family protein                                                                         |
| 403 | <a href="#">MytuD.18213.r</a>  | PE-PGRS family protein (Rv1818c)                                                               |
| 404 | <a href="#">MytuD.18213.s</a>  | PE-PGRS family protein                                                                         |
| 405 | <a href="#">MytuD.18213.t</a>  | PE-PGRS family protein                                                                         |
| 406 | <a href="#">MytuD.18213.u</a>  | PE-PGRS family protein                                                                         |
| 407 | <a href="#">MytuD.18213.v</a>  | PE family protein. Possible lipase.                                                            |
| 408 | <a href="#">MytuD.18213.w</a>  | PE-PGRS family protein                                                                         |
| 409 | <a href="#">MytuD.18213.x</a>  | PE family protein. Possible lipase.                                                            |
| 410 | <a href="#">MytuD.18213.y</a>  | PE-PGRS family protein (Rv2591)                                                                |
| 411 | <a href="#">MytuD.18213.z</a>  | PE-PGRS family protein                                                                         |
| 412 | <a href="#">MytuD.18214.a</a>  | PPE family protein                                                                             |
| 413 | <a href="#">MytuD.18214.b</a>  | PPE family protein                                                                             |
| 414 | <a href="#">MytuD.18214.c</a>  | PPE family protein                                                                             |
| 415 | <a href="#">MytuD.18214.d</a>  | PPE family protein                                                                             |
| 416 | <a href="#">MytuD.18214.e</a>  | PPE family protein (Rv1808)                                                                    |
| 417 | <a href="#">MytuD.18214.f</a>  | PPE family protein (Rv1809)                                                                    |
| 418 | <a href="#">MytuD.18214.g</a>  | PPE family protein                                                                             |
| 419 | <a href="#">MytuD.18214.h</a>  | PPE family protein                                                                             |
| 420 | <a href="#">MytuD.18214.i</a>  | PPE family protein                                                                             |
| 421 | <a href="#">MytuD.18223.a</a>  | PPE family protein                                                                             |
| 422 | <a href="#">MytuD.18223.b</a>  | PPE family protein                                                                             |
| 423 | <a href="#">MytuD.18249.a</a>  | Probable cytochrome P450 130 CYP130                                                            |
| 424 | <a href="#">MytuD.18251.a</a>  | Conserved hypothetical protein                                                                 |
| 425 | <a href="#">MytuD.18252.a</a>  | Conserved hypothetical protein                                                                 |
| 426 | <a href="#">MytuD.18253.a</a>  | Probable transcriptional regulatory protein                                                    |
| 427 | <a href="#">MytuD.18254.a</a>  | Probable transaldolase TAL                                                                     |
| 428 | <a href="#">MytuD.18255.a</a>  | L,D-transpeptidase                                                                             |
| 429 | <a href="#">MytuD.18256.a</a>  | Possible conserved membrane protein                                                            |
| 430 | <a href="#">MytuD.18256.b</a>  | Putative L,D-transpeptidase Rv0483/MT0501 (EC 2.-.-.-)                                         |
| 431 | <a href="#">MytuD.18258.a</a>  | ESX-1 secretion-associated protein EspD                                                        |
| 432 | <a href="#">MytuD.18273.a</a>  | Conserved hypothetical protein TB31.7                                                          |
| 433 | <a href="#">MytuD.18273.b</a>  | Universal stress protein Rv2624c/MT2699 (USP Rv2624c)                                          |
| 434 | <a href="#">MytuD.18275.a</a>  | Probable cytochrome P450 130 CYP130                                                            |
| 435 | <a href="#">MytuD.18277.a</a>  | PE-PGRS family protein                                                                         |
| 436 | <a href="#">MytuD.18287.a</a>  | PE-PGRS family protein                                                                         |
| 437 | <a href="#">MytuD.18289.a</a>  | Hypothetical protein                                                                           |
| 438 | <a href="#">MytuD.18304.a</a>  | Probable cytochrome P450 130 CYP130                                                            |
| 439 | <a href="#">MytuD.18310.a</a>  | Hypothetical protein                                                                           |
| 440 | <a href="#">MytuD.18311.a</a>  | PE-PGRS family protein                                                                         |
| 441 | <a href="#">MytuD.18320.a</a>  | Adenylyl cyclase (ATP pyrophosphate-lyase) (adenylate cyclase)                                 |
| 442 | <a href="#">MytuD.18321.a</a>  | Conserved protein                                                                              |
| 443 | <a href="#">MytuD.18324.a</a>  | Conserved hypothetical protein                                                                 |
| 444 | <a href="#">MytuD.18327.a</a>  | PE family protein. Possible lipase.                                                            |
| 445 | <a href="#">MytuD.18328.a</a>  | PPE family protein (Rv3021c)                                                                   |
| 446 | <a href="#">MytuD.18329.a</a>  | PE-PGRS family protein                                                                         |
| 447 | <a href="#">MytuD.18332.a</a>  | Probable cytochrome P450 130 CYP130                                                            |
| 448 | <a href="#">MytuD.18337.a</a>  | ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit) (F-ATPase epsilon subunit) |
| 449 | <a href="#">MytuD.18350.a</a>  | Probable cytochrome P450 130 CYP130                                                            |
| 450 | <a href="#">MytuD.18359.a</a>  | PE-PGRS family protein                                                                         |
| 451 | <a href="#">MytuD.18363.a</a>  | Probable transcriptional regulatory protein (probably MerR-family)                             |
| 452 | <a href="#">MytuD.18367.a</a>  | ESX-1 secretion-associated protein EspA                                                        |
| 453 | <a href="#">MytuD.18368.a</a>  | PE-PGRS family protein                                                                         |

|     |                               |                                                                                                                                      |
|-----|-------------------------------|--------------------------------------------------------------------------------------------------------------------------------------|
| 454 | <a href="#">MytuD.18383.a</a> | PE family protein. Possible lipase.                                                                                                  |
| 455 | <a href="#">MytuD.18384.a</a> | ESX-1 secretion system protein EccA1 (ESX conserved component A1) (Type VII secretion system protein EccA1) (T7SS protein EccA1)     |
| 456 | <a href="#">MytuD.18384.b</a> | ESX-3 secretion system protein EccA3 (ESX conserved component A3) (Type VII secretion system protein EccA3) (T7SS protein EccA3)     |
| 457 | <a href="#">MytuD.18386.a</a> | Putative uncharacterized protein                                                                                                     |
| 458 | <a href="#">MytuD.18393.a</a> | Maltokinase (MaK) (EC 2.7.1.n8) (Maltose-1-phosphate synthase)                                                                       |
| 459 | <a href="#">MytuD.18395.a</a> | Uncharacterized protein Rv2004c/MT2060                                                                                               |
| 460 | <a href="#">MytuD.18397.a</a> | Putative uncharacterized protein                                                                                                     |
| 461 | <a href="#">MytuD.18399.a</a> | Uncharacterized protein Rv1002c/MT1031                                                                                               |
| 462 | <a href="#">MytuD.18400.a</a> | Putative uncharacterized protein                                                                                                     |
| 463 | <a href="#">MytuD.18401.a</a> | Divalent cation transporter, MgtE family (possible Mg <sup>2+</sup> transport transmembrane protein MgtE)                            |
| 464 | <a href="#">MytuD.18402.a</a> | Uncharacterized protein Rv1738/MT1780                                                                                                |
| 465 | <a href="#">MytuD.18443.a</a> | Protein MraZ                                                                                                                         |
| 466 | <a href="#">MytuD.18452.a</a> | DNA-directed RNA polymerase subunit omega                                                                                            |
| 467 | <a href="#">MytuD.18523.a</a> | Protein tyrosine kinase (PtkA)                                                                                                       |
| 468 | <a href="#">MytuD.18528.a</a> | Penicillin-binding protein 1                                                                                                         |
| 469 | <a href="#">MytuD.18529.a</a> | Uncharacterized protein Rv2927c/MT2997                                                                                               |
| 470 | <a href="#">MytuD.18530.a</a> | Putative asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)                                                                  |
| 471 | <a href="#">MytuD.18532.a</a> | Putative uncharacterized protein                                                                                                     |
| 472 | <a href="#">MytuD.18661.a</a> | Antitoxin VapB28                                                                                                                     |
| 473 | <a href="#">MytuD.18662.a</a> | Probable ribonuclease VapC28                                                                                                         |
| 474 | <a href="#">MytuD.18665.b</a> | Hypothetical protein Rv0647c                                                                                                         |
| 475 | <a href="#">MytuD.18666.a</a> | Putative Holliday junction resolvase (EC 3.1.-.-)                                                                                    |
| 476 | <a href="#">MytuD.18667.a</a> | Uncharacterized glycosyltransferase Rv1514c/MT1564 (EC 2.4.-.-)                                                                      |
| 477 | <a href="#">MytuD.18668.a</a> | HNH endonuclease family protein                                                                                                      |
| 478 | <a href="#">MytuD.18669.a</a> | Putative uncharacterized protein                                                                                                     |
| 479 | <a href="#">MytuD.18670.a</a> | ESX-1 secretion-associated protein EspC                                                                                              |
| 480 | <a href="#">MytuD.18672.a</a> | Putative uncharacterized protein                                                                                                     |
| 481 | <a href="#">MytuD.18673.a</a> | Possible conserved membrane or secreted protein                                                                                      |
| 482 | <a href="#">MytuD.18674.a</a> | Conserved hypothetical alanine rich protein (Ribonuclease D, putative)                                                               |
| 483 | <a href="#">MytuD.18675.a</a> | CRISPR type III-associated RAMP protein Csm5 (CRISPR type III-A/Mtube-associated RAMP protein Csm5)                                  |
| 484 | <a href="#">MytuD.18676.a</a> | UPF0109 protein Rv2908c/MT2976                                                                                                       |
| 485 | <a href="#">MytuD.18677.a</a> | Putative uncharacterized protein                                                                                                     |
| 486 | <a href="#">MytuD.18678.a</a> | Putative 2-dehydropantoate 2-reductase                                                                                               |
| 487 | <a href="#">MytuD.18679.a</a> | Nucleoside triphosphate pyrophosphohydrolase (NTP-PPase) (EC 3.6.1.8)                                                                |
| 488 | <a href="#">MytuD.18680.a</a> | Uncharacterized protein Rv2411c/MT2484                                                                                               |
| 489 | <a href="#">MytuD.18682.a</a> | PP2C-family Ser/Thr phosphatase (EC 3.1.3.16) (Mycobacterial Ser/Thr phosphatase) (Mstp) (Possible serine/threonine phosphatase Ppp) |
| 490 | <a href="#">MytuD.18683.a</a> | Uncharacterized protein Rv2229c/MT2288                                                                                               |
| 491 | <a href="#">MytuD.18684.a</a> | Pup deamidase/depupylase (EC 3.4.-.-) (EC 3.5.1.-) (Deamidase of protein Pup)                                                        |
| 492 | <a href="#">MytuD.18685.a</a> | Uncharacterized protein Rv2030c/MT2089                                                                                               |
| 493 | <a href="#">MytuD.18686.a</a> | Putative uncharacterized protein                                                                                                     |
| 494 | <a href="#">MytuD.18687.a</a> | DNA-binding protein, putative                                                                                                        |
| 495 | <a href="#">MytuD.18688.a</a> | Putative uncharacterized protein                                                                                                     |
| 496 | <a href="#">MytuD.18689.a</a> | Uncharacterized protein Rv1278/MT1315                                                                                                |
| 497 | <a href="#">MytuD.18690.a</a> | Putative uncharacterized protein                                                                                                     |
| 498 | <a href="#">MytuD.18691.a</a> | Uncharacterized protein Rv1339/MT1380                                                                                                |
| 499 | <a href="#">MytuD.18692.a</a> | Putative uncharacterized protein                                                                                                     |
| 500 | <a href="#">MytuD.18693.a</a> | CRISPR-associated endonuclease Cas1 (EC 3.1.-.-)                                                                                     |
| 501 | <a href="#">MytuD.18703.a</a> | Toxin RelE                                                                                                                           |
| 502 | <a href="#">MytuD.18708.a</a> | Isoleucine--tRNA ligase                                                                                                              |
| 503 | <a href="#">MytuD.18738.a</a> | Putative mycofactocin system protein (MftB)                                                                                          |
| 504 | <a href="#">MytuD.18758.a</a> | Uncharacterized protein Rv0036c/MT0041                                                                                               |
| 505 | <a href="#">MytuD.18758.b</a> | Conserved protein                                                                                                                    |
| 506 | <a href="#">MytuD.18760.a</a> | Conserved protein                                                                                                                    |
| 507 | <a href="#">MytuD.18761.a</a> | Uncharacterized protein Rv2226/MT2285                                                                                                |
| 508 | <a href="#">MytuD.18763.a</a> | Uncharacterized HTH-type transcriptional regulator Rv1830/MT1879                                                                     |
| 509 | <a href="#">MytuD.18764.a</a> | Conserved protein                                                                                                                    |
| 510 | <a href="#">MytuD.18765.a</a> | Conserved protein                                                                                                                    |
| 511 | <a href="#">MytuD.18767.a</a> | Uncharacterized protein Rv1480/MT1527                                                                                                |
| 512 | <a href="#">MytuD.18768.a</a> | Conserved protein                                                                                                                    |
| 513 | <a href="#">MytuD.18769.a</a> | Uncharacterized protein Rv2629/MT2704                                                                                                |
| 514 | <a href="#">MytuD.18772.a</a> | Uncharacterized protein                                                                                                              |
| 515 | <a href="#">MytuD.18773.a</a> | Conserved protein                                                                                                                    |
| 516 | <a href="#">MytuD.18775.a</a> | Uncharacterized protein                                                                                                              |
| 517 | <a href="#">MytuD.18776.a</a> | Uncharacterized protein Rv2000/MT2056                                                                                                |
| 518 | <a href="#">MytuD.18777.a</a> | Uncharacterized protein Rv2574/MT2650                                                                                                |
| 519 | <a href="#">MytuD.18778.a</a> | Conserved protein                                                                                                                    |
| 520 | <a href="#">MytuD.18779.a</a> | Uncharacterized protein Rv1507c/MT1555                                                                                               |
| 521 | <a href="#">MytuD.18781.a</a> | Uncharacterized protein                                                                                                              |
| 522 | <a href="#">MytuD.18782.a</a> | Uncharacterized protein                                                                                                              |
| 523 | <a href="#">MytuD.18783.a</a> | Conserved protein                                                                                                                    |
| 524 | <a href="#">MytuD.18784.a</a> | Uncharacterized protein                                                                                                              |

|     |                               |                                                                                                       |
|-----|-------------------------------|-------------------------------------------------------------------------------------------------------|
| 525 | <a href="#">MytuD.18785.a</a> | Uncharacterized protein                                                                               |
| 526 | <a href="#">MytuD.18786.a</a> | Conserved protein                                                                                     |
| 527 | <a href="#">MytuD.18787.a</a> | Uncharacterized protein Rv2305/MT2362                                                                 |
| 528 | <a href="#">MytuD.18788.a</a> | 10 kDa iron regulated protein Irp10 (Conserved protein)                                               |
| 529 | <a href="#">MytuD.18789.a</a> | Conserved protein                                                                                     |
| 530 | <a href="#">MytuD.18791.a</a> | Uncharacterized protein Rv2067c/MT2127                                                                |
| 531 | <a href="#">MytuD.18792.a</a> | Conserved protein                                                                                     |
| 532 | <a href="#">MytuD.18793.a</a> | Conserved protein                                                                                     |
| 533 | <a href="#">MytuD.18795.a</a> | Carboxymethylenebutenolidase, putative (Conserved protein)                                            |
| 534 | <a href="#">MytuD.18796.a</a> | Conserved protein                                                                                     |
| 535 | <a href="#">MytuD.18797.a</a> | Conserved protein                                                                                     |
| 536 | <a href="#">MytuD.18798.a</a> | Putative trans-acting enoyl reductase Rv2449c (EC 1.3.1.-)                                            |
| 537 | <a href="#">MytuD.18799.a</a> | Conserved protein                                                                                     |
| 538 | <a href="#">MytuD.18800.a</a> | Uncharacterized protein                                                                               |
| 539 | <a href="#">MytuD.18801.a</a> | Uncharacterized protein                                                                               |
| 540 | <a href="#">MytuD.18802.a</a> | Uncharacterized protein                                                                               |
| 541 | <a href="#">MytuD.18803.a</a> | Conserved protein                                                                                     |
| 542 | <a href="#">MytuD.18804.a</a> | Conserved protein (U0002kb)                                                                           |
| 543 | <a href="#">MytuD.18805.a</a> | CRISPR-associated endoribonuclease Cas6 (EC 3.1.-.-)                                                  |
| 544 | <a href="#">MytuD.18807.a</a> | Uncharacterized protein                                                                               |
| 545 | <a href="#">MytuD.18808.a</a> | Uncharacterized protein Rv3633/MT3735                                                                 |
| 546 | <a href="#">MytuD.18811.a</a> | Uncharacterized protein Rv3292/MT3391                                                                 |
| 547 | <a href="#">MytuD.18813.a</a> | Uncharacterized glycosyl hydrolase Rv3401/MT3509 (EC 3.2.1.-)                                         |
| 548 | <a href="#">MytuD.18817.a</a> | Conserved protein                                                                                     |
| 549 | <a href="#">MytuD.18818.a</a> | Uncharacterized protein                                                                               |
| 550 | <a href="#">MytuD.18819.a</a> | Conserved protein                                                                                     |
| 551 | <a href="#">MytuD.18820.a</a> | Conserved protein                                                                                     |
| 552 | <a href="#">MytuD.18821.a</a> | Conserved protein                                                                                     |
| 553 | <a href="#">MytuD.18822.a</a> | Putative gluconeogenesis factor                                                                       |
| 554 | <a href="#">MytuD.18823.a</a> | UPF0051 protein Rv1461/MT1508 [Cleaved into: Endonuclease PI-MtuHIIP (EC 3.1.-.-) (Mtu pps1 intein)]  |
| 555 | <a href="#">MytuD.18964.a</a> | Bifunctional oligoribonuclease and PAP phosphatase NrnA                                               |
| 556 | <a href="#">MytuD.19035.a</a> | hypothetical hydrolase; uncharacterized protein                                                       |
| 557 | <a href="#">MytuD.19056.a</a> | hypothetical hydrolase; membrane protein                                                              |
| 558 | <a href="#">MytuD.19095.a</a> | hypothetical hydrolase; conserved protein                                                             |
| 559 | <a href="#">MytuD.19126.a</a> | hypothetical hydrolase; conserved protein                                                             |
| 560 | <a href="#">MytuD.19140.a</a> | hypothetical hydrolase; membrane protein                                                              |
| 561 | <a href="#">MytuD.19154.a</a> | Uncharacterized HTH-type transcriptional regulator Rv0023                                             |
| 562 | <a href="#">MytuD.19163.a</a> | Uncharacterized protein Rv0863                                                                        |
| 563 | <a href="#">MytuD.19264.a</a> | Possible conserved secreted alanine rich protein (Rv2700)                                             |
| 564 | <a href="#">MytuD.19273.a</a> | Polyphosphate kinase (EC 2.7.4.1) (ATP-polyphosphate phosphotransferase) (Polyphosphoric acid kinase) |
| 565 | <a href="#">MytuD.19287.a</a> | Ubiquinol-cytochrome c reductase iron-sulfur subunit (Rieske iron-sulfur protein)                     |
| 566 | <a href="#">MytuD.19296.a</a> | Ubiquinol-cytochrome c reductase cytochrome c subunit                                                 |
| 567 | <a href="#">MytuD.19316.a</a> | Lysylphosphatidylglycerol biosynthesis bifunctional protein (LysX) (LysS2) (Rv1640c)                  |
| 568 | <a href="#">MytuD.19483.a</a> | Dephospho-CoA kinase CoaE (Rv1631)                                                                    |
| 569 | <a href="#">MytuD.19534.a</a> | Acetyltransferase (Rv0133)                                                                            |
| 570 | <a href="#">MytuD.20209.a</a> | Uncharacterized protein (Rv2633c)                                                                     |
| 571 | <a href="#">MytuD.20304.a</a> | Possible bifunctional enzyme long-chain acyl-CoA synthase and lipase (Rv1683)                         |
| 572 | <a href="#">MytuD.20373.a</a> | ESX-3 secretion system protein EccE3 (Rv0292)                                                         |
| 573 | <a href="#">MytuD.20375.a</a> | Uncharacterized protein (Rv1376)                                                                      |
| 574 | <a href="#">MytuD.20386.a</a> | Uncharacterized protein; EspM                                                                         |
| 575 | <a href="#">MytuD.20406.a</a> | Polyketide synthase Pks13 (Rv3800c)                                                                   |
| 576 | <a href="#">MytuD.20412.a</a> | Probable fatty acid synthase/synthetase Fas (Rv2524c)                                                 |

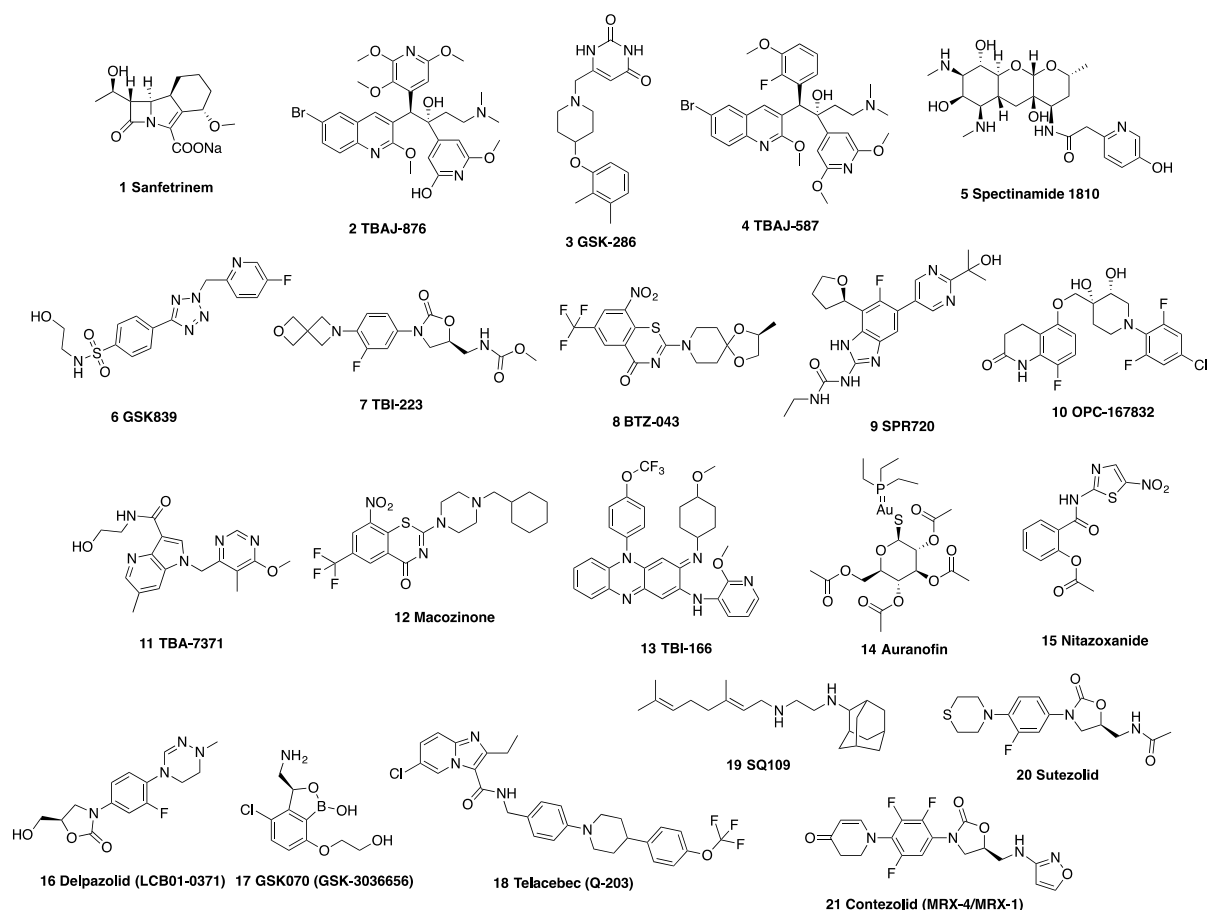
Data retrieved from SSGCID (<https://www.ssgcid.org/>)

**Table S3 NP inhibitors of mycobacterial enzymes**

| No. | Compound          | Species                             | Target | Ref. |
|-----|-------------------|-------------------------------------|--------|------|
| 1   | Rufomycin NBZ1    | <i>Streptomyces atratus</i> MJM3502 | ClpC1  | 17   |
| 2   | Rufomycin NBZ2    | <i>Streptomyces atratus</i> MJM3502 | ClpC1  | 17   |
| 3   | Rufomycin NBZ3    | <i>Streptomyces atratus</i> MJM3502 | ClpC1  | 17   |
| 4   | Rufomycin NBZ4    | <i>Streptomyces atratus</i> MJM3502 | ClpC1  | 17   |
| 5   | Rufomycin NBZ5    | <i>Streptomyces atratus</i> MJM3502 | ClpC1  | 17   |
| 6   | Rufomycin NBZ6    | <i>Streptomyces atratus</i> MJM3502 | ClpC1  | 17   |
| 7   | Rufomycin NBZ7    | <i>Streptomyces atratus</i> MJM3502 | ClpC1  | 17   |
| 8   | Rufomycin NBZ8    | <i>Streptomyces atratus</i> MJM3502 | ClpC1  | 17   |
| 9   | Fiscpropionate A  | <i>Aspergillus fischeri</i> FS452   | MptpB  | 18   |
| 10  | Fiscpropionate B  | <i>Aspergillus fischeri</i> FS452   | MptpB  | 18   |
| 11  | Fiscpropionate C  | <i>Aspergillus fischeri</i> FS452   | MptpB  | 18   |
| 12  | Fiscpropionate D  | <i>Aspergillus fischeri</i> FS452   | MptpB  | 18   |
| 13  | Asperophiobolin B | <i>Aspergillus</i> sp. ZJ-68        | MptpB  | 19   |

|    |                                                                                      |                                          |                    |       |
|----|--------------------------------------------------------------------------------------|------------------------------------------|--------------------|-------|
| 14 | Asperophiobolin D                                                                    | <i>Aspergillus</i> sp. ZJ-68             | MptpB              | 19    |
| 15 | Asperophiobolin E                                                                    | <i>Aspergillus</i> sp. ZJ-68             | MptpB              | 19    |
| 16 | Asperophiobolin H                                                                    | <i>Aspergillus</i> sp. ZJ-68             | MptpB              | 19    |
| 17 | Asperophiobolin I                                                                    | <i>Aspergillus</i> sp. ZJ-68             | MptpB              | 19    |
| 18 | ophiobolin G                                                                         | <i>Aspergillus</i> sp. ZJ-68             | MptpB              | 19    |
| 19 | 21-deoxo-21- hydroxy-6-epi-ophiobolin G                                              | <i>Aspergillus</i> sp. ZJ-68             | MptpB              | 19    |
| 20 | Ophiobolin P                                                                         | <i>Aspergillus</i> sp. ZJ-68             | MptpB              | 19    |
| 21 | Peniisocoumarin G                                                                    | <i>Penicillium commune</i> QQF-3         | MptpB              | 20    |
| 22 | Eupractenoid B                                                                       | <i>Euphorbia ebracteolata</i>            | GlmU               | 21    |
| 23 | Ecumicin                                                                             | <i>Nonomuraea</i> sp. MJM5123            | ClpC1              | 22    |
| 24 | Agelasine D                                                                          | <i>Agelas nakamura</i>                   | BCG3185c           | 23    |
| 25 | Sansanmycin analogues                                                                | <i>Streptomyces</i> sp.                  | MurX               | 24    |
| 26 | Caprazamycin Derivative CPZEN-45                                                     | <i>Streptomyces</i> sp.                  | WecA               | 25    |
| 27 | Peniphenone B                                                                        | <i>Penicillium dipodomycicola</i> HN4-3A | MptpB              | 26    |
| 28 | Peniphenone C                                                                        | <i>Penicillium dipodomycicola</i> HN4-3A | MptpB              | 26    |
| 29 | Diaporisoidole A                                                                     | <i>Diaporthe</i> sp. SYSU-HQ3            | MptpB              | 27    |
| 30 | Tenellone C                                                                          | <i>Diaporthe</i> sp. SYSU-HQ3            | MptpB              | 27    |
| 31 | Asperterpenoid A                                                                     | <i>Aspergillus</i> sp. 16-5c             | MptpB              | 28    |
| 32 | Asperterpenoid B                                                                     | <i>A. oryzae</i>                         | MptpB              | 29    |
| 33 | Trichoderin A                                                                        | <i>Trichoderma</i> sp.                   | ATP synthase       | 30    |
| 34 | Melophlin A                                                                          | <i>Melophlus</i> sp.                     | BCG1083, BCG1321c  | 31    |
| 35 | Teixobactin                                                                          | <i>Eleftheria terrae</i>                 | lipid II lipid III | 32    |
| 36 | Lassomycin                                                                           | <i>Lentzea kentuckyensis</i> sp.         | ClpC1              | 33    |
| 37 | Brunsvicamide A                                                                      | <i>Tychonema</i> sp.                     | MptpB              | 34    |
| 38 | Brunsvicamide B                                                                      | <i>Tychonema</i> sp.                     | MptpB              | 34    |
| 39 | Brunsvicamide C                                                                      | <i>Tychonema</i> sp.                     | MptpB              | 34    |
| 40 | Kuwanol E                                                                            |                                          | MptpB              | 35    |
| 41 | 1,3,8-trihydroxy-6- methyl-4,5,7-triprenylanthrone                                   |                                          | MptpB              | 35    |
| 42 | Trachypone                                                                           |                                          |                    | 35    |
| 43 | 1,3,8-trihydroxy-6- methyl-5,7-diprenyl-4- $\gamma,\gamma'$ dihydroxyprenyl-anthrone |                                          | MptpB              | 35    |
| 44 | tetra-acetyl-trachypone                                                              |                                          | MptpB              | 35    |
| 45 | 4,2',4',6'- tetrahydroxy-3'-prenyl-3-geranyldihydrochalcone                          |                                          | MptpB              | 35    |
| 46 | Cyclomarin A                                                                         | <i>Streptomyces</i> CNB-982              | ClpC1              | 36    |
| 47 | Liparmycin A3                                                                        | <i>Catellatospora</i> sp. Bp3323-81      | RNAP               | 37    |
| 49 | Pyridomycin                                                                          | <i>Dactylosporangium fulvum</i>          | InhA               | 38    |
| 50 | Ascolactone B                                                                        | <i>Ascochyta salicorniae</i>             | MptpB              | 39    |
| 51 | Hyalopyrone                                                                          | <i>Ascochyta salicorniae</i>             | MptpB              | 39    |
| 52 | Ascochitine                                                                          | <i>Ascochyta salicorniae</i>             | MptpB              | 39    |
| 53 | Ascochital                                                                           | <i>Ascochyta salicorniae</i>             | MptpB              | 39    |
| 54 | Platensimycin                                                                        | <i>Streptomyces platensis</i>            | KasA, KasB         | 40    |
| 55 | Butein                                                                               | <i>Rhus verniciflua</i>                  | Dehydratase        | 41    |
| 56 | Isoliquirtigenin                                                                     | <i>Dalbergia odorifera</i>               | Dehydratase        | 41    |
| 57 | 2,2',4'-Trihydroxychalcone                                                           | <i>Dalbergia odorifera</i>               | Dehydratase        | 41    |
| 58 | Fisetin                                                                              | <i>Rhus cotinus</i>                      | Dehydratase        | 41    |
| 59 | Manzamine A                                                                          | <i>Acanthostrongylophora</i> sp.         | MtSK               | 42    |
| 60 | Hydroxymanzamine A                                                                   | <i>Acanthostrongylophora</i> sp.         | MtSK               | 42    |
| 61 | Manzamine E                                                                          | <i>Acanthostrongylophora</i> sp.         | MtSK               | 42    |
| 62 | Manzamine F                                                                          | <i>Acanthostrongylophora</i> sp.         | MtSK               | 42    |
| 63 | 6-deoxymanzamine X                                                                   | <i>Acanthostrongylophora</i> sp.         | MtSK               | 42    |
| 64 | Alkaloid 1                                                                           | <i>Oceanapia</i> sp.                     | MCA                | 43    |
| 65 | Pseudoceratine                                                                       | <i>Oceanapia</i> sp.                     | MCA                | 43    |
| 66 | Alkaloid 4                                                                           | <i>Oceanapia</i> sp.                     | MCA                | 43    |
| 67 | Alkaloid 5                                                                           | <i>Oceanapia</i> sp.                     | MCA                | 43    |
| 68 | Psammaplysin A                                                                       | <i>Pseudoceratina</i> sp.                | MCA                | 44    |
| 69 | Psammaplysin B                                                                       | <i>Pseudoceratina</i> sp.                | MCA                | 44    |
| 70 | Oceanapiside                                                                         | <i>Oceanapia</i> sp.                     | MCA                | 44    |
| 71 | Oceanapiside aglycon                                                                 | <i>Oceanapia</i> sp.                     | MCA                | 44    |
| 72 | Suvanine                                                                             | <i>Coscinoderma matthewsi</i>            | MCA                | 44    |
| 73 | Halisulfate 1                                                                        | <i>Coscinoderma matthewsi</i>            | MCA                | 44    |
| 74 | 1,3-pyridinium polymers                                                              | <i>Amphimedon</i> sp.                    | MCA                | 44    |
| 75 | Gliotoxin                                                                            | <i>Mycena</i> sp.                        | MCA                | 44    |
| 76 | S,S-Dimethyl gliotoxin                                                               | <i>Aspergillus</i> sp.                   | MCA                | 44    |
| 77 | Physcion                                                                             | <i>Aspergillus</i> sp.                   | MCA                | 44    |
| 78 | Psammaplin A                                                                         | <i>Psammaplysilla</i> sp.                | MCA                | 45    |
| 79 | (S)-(-)-Acidomycin                                                                   | <i>Streptomyces</i> sp.                  | BioB               | 46    |
| 80 | Aurachin RE                                                                          | <i>Rhodococcus erythropolis</i> JCM 6824 | MenA               | 47    |
| 81 | Griselimycin                                                                         | <i>Streptomyces</i> sp.                  | DnaN               | 48    |
| 82 | Gladiolin                                                                            | <i>Burkholderia gladioli</i> BCC0238     | RNAP               | 49    |
| 83 | Novobiocin                                                                           | <i>Streptomyces niveus</i>               | GyrB               | 50,51 |
| 84 | Cyclothialidine (GR122222X)                                                          | <i>Streptomyces filipinensis</i> NR0484  | GyrB               | 52    |
| 85 | Anziaic acid                                                                         | <i>Hypotrachyna</i> sp.                  | Topoisomerases     | 53    |
| 86 | Doxorubicin                                                                          | <i>Streptomyces</i>                      | DnaG               | 54    |
| 87 | Daunorubicin                                                                         |                                          | DnaG               | 54    |
| 88 | Aloe emodin                                                                          |                                          | DnaG               | 54    |

|     |                                                                                                    |                                        |                     |    |
|-----|----------------------------------------------------------------------------------------------------|----------------------------------------|---------------------|----|
| 89  | Fosmidomycin                                                                                       | <i>Streptomyces</i>                    | IspC                | 55 |
| 90  | FR900098                                                                                           | <i>Streptomyces lavendulae</i>         | IspC (or DXR)       | 56 |
| 91  | 3-chloro-4-hydroxyphenylacetamide                                                                  | <i>Xylaria</i> sp.                     | Carbonic anhydrases | 57 |
| 92  | 3-chloro-4-hydroxyphenylacetic acid                                                                | <i>Xylaria</i> sp.                     | Carbonic anhydrases | 57 |
| 93  | (-)-xylariamide A                                                                                  | <i>Xylaria</i> sp.                     | Carbonic anhydrases | 57 |
| 94  | 2-hydroxy-6-methyl-8-methoxy-9-oxo-9H-xanthene-1-carboxylic acid                                   | <i>Xylaria</i> sp.                     | Carbonic anhydrases | 57 |
| 95  | 2-hydroxy-6- hydroxymethyl-8-methoxy-9-oxo-9H-xanthene-1-carboxylic acid                           | <i>Xylaria</i> sp.                     | Carbonic anhydrases | 57 |
| 96  | Polyandrocarpamine A                                                                               | <i>Polyandrocarpa</i> sp.              | Carbonic anhydrases | 57 |
| 97  | Polyandrocarpamine B                                                                               | <i>Polyandrocarpa</i> sp.              | Carbonic anhydrases | 57 |
| 98  | Endiandrin A                                                                                       | <i>Endiandra anthropophagorum</i>      | Carbonic anhydrases | 57 |
| 99  | Endiandrin B                                                                                       | <i>Endiandra anthropophagorum</i>      | Carbonic anhydrases | 57 |
| 100 | (-)-Dihydroguaiaretic acid                                                                         | <i>Endiandra anthropophagorum</i>      | Carbonic anhydrases | 57 |
| 101 | Cycloserine                                                                                        | <i>Streptomyces</i> sp.                | Alr and Ddl         | 58 |
| 102 | Rifamycin                                                                                          | <i>Amycolatopsis mediterranei</i>      | RNAP                |    |
| 103 | Kanamycin                                                                                          | <i>Streptomyces kanamyceticus</i>      | Rrs, Eis            |    |
| 104 | Streptomycin                                                                                       | <i>Streptomyces griseus</i>            | RpsL, Rrs, GidB     |    |
| 105 | Erythromycin                                                                                       | <i>Streptomyces erythreus</i>          | MABP-1              | 59 |
| 106 | Thiolactomycin                                                                                     | <i>Nocardia</i> sp.                    | KasA, KasB          | 60 |
| 107 | Cerulenin                                                                                          | <i>Cephalosporium caerulens</i>        | FAS                 | 61 |
| 108 | Agonodepside A                                                                                     | fungal strain F7524                    | InhA                | 62 |
| 109 | Pseudopyronine B                                                                                   | <i>Pseudomonas</i> sp. F92S91          | InhA                | 63 |
| 110 | Fusidic acid                                                                                       | <i>Fusidium coccineum</i>              | FusA1 and FusA2     | 64 |
| 111 | (E)-3-(3,4-dihydroxyphenyl)acrylic acid                                                            |                                        | Carbonic anhydrases | 65 |
| 112 | (E)-3-(4-hydroxy-3-methoxyphenyl)acrylic acid                                                      |                                        | Carbonic anhydrases | 65 |
| 113 | (E)-3-(4-hydroxyphenyl)acrylic acid                                                                |                                        | Carbonic anhydrases | 65 |
| 114 | Cyclophostin                                                                                       |                                        | Serine hydrolases   | 66 |
| 115 | Sclerotiorin                                                                                       | <i>Penicillium</i> sp.                 | PknG                | 67 |
| 116 | Ophiobolin K                                                                                       | <i>Emericella varicolor</i>            | Biofilm             | 68 |
| 117 | Bostrycin                                                                                          | <i>Bostrichonema alpestre</i>          | MptpB               | 69 |
| 118 | Betulinic acid                                                                                     | <i>Betula</i> sp.,                     | Serine protease     | 70 |
| 119 | Butyrolactone I                                                                                    | <i>Aspergillus terreus</i> SCSIO 41008 | MptpB               | 71 |
| 120 | Polycarpine                                                                                        | <i>Polycarpa aurata</i>                | Rv1466              | 72 |
| 121 | Simplicilliumtide B                                                                                | <i>Simplicillium</i> sp. SCSIO41209    | MptpB               | 73 |
| 122 | Cyclo-(Pro-Val)                                                                                    | <i>Simplicillium</i> sp. SCSIO41209    | MptpB               | 73 |
| 123 | (±)-asperlone A                                                                                    | <i>Aspergillus</i> sp. 16-5C           | MptpB               | 74 |
| 124 | (±)-asperlone B                                                                                    | <i>Aspergillus</i> sp. 16-5C           | MptpB               | 74 |
| 125 | (-)-mitorubrin                                                                                     | <i>Aspergillus</i> sp. 16-5C           | MptpB               | 74 |
| 126 | Talaramide A                                                                                       | <i>Talaromyces</i> sp. (HZ-YX1)        | PknG                | 75 |
| 127 | Alterporriol S                                                                                     | <i>Alternaria</i> sp. (SK11)           | MptpB               | 76 |
| 128 | (+)-aS-alterporriol C                                                                              | <i>Alternaria</i> sp. (SK11)           | MptpB               | 76 |
| 129 | Clorobiocin                                                                                        | <i>Streptomyces</i>                    | SerB2               | 77 |
| 130 | Micrococcin P1                                                                                     | <i>Staphylococcus equorum</i> WS 2733  | RplK                | 78 |
| 131 | Plumbagin                                                                                          | <i>Plumbago indica</i>                 | ThyX                | 79 |
| 132 | 3-O-methyl-butylgallate                                                                            | <i>Loranthus micranthus</i>            | DesA3               | 80 |
| 133 | Norlobaric acid                                                                                    | NCI                                    | MtbNei2             | 81 |
| 134 | Chaetochromin                                                                                      | NCI                                    | MtbNei2             | 81 |
| 135 | Gangetin                                                                                           | NCI                                    | MtbNei2             | 81 |
| 136 | Alpha-Linolenic Acid                                                                               | <i>Sutherlandia frutescens</i>         | MtSK                | 82 |
| 137 | I2906                                                                                              | Plant                                  | ICL                 | 83 |
| 138 | (E)-2-(methyl(phenyl) amino) ethyl 2-(2-hydroxyundecanamido)-7, 11-dimethyl-3-oxotetradec-4-enoate | <i>Arisaema sinii</i> Krause           | Bioflim             | 84 |
| 139 | Kanglemycin A                                                                                      | <i>Amycolatopsis</i> DEM3035           | RNAP                | 85 |
| 140 | Ilimaquinone                                                                                       | <i>Hippospongia metachromia</i>        | MtSK                | 86 |
| 141 | 3-methoxynordomesticine                                                                            | <i>Ocotea macrophylla</i> (Lauraceae)  | MurE                | 87 |
| 142 | N-methoxycarbonyl-3-methoxynordomesticine                                                          | <i>Ocotea macrophylla</i> (Lauraceae)  | MurE                | 87 |
| 143 | Ursolic acid                                                                                       | <i>Ocimum sanctum</i>                  |                     | 88 |
| 144 | Ergosterdiacid A                                                                                   |                                        | MptpB               | 89 |
| 145 | Ergosterdiacid B                                                                                   |                                        | MptpB               | 89 |
| 146 | Halicyclamine A                                                                                    | <i>Haliclona</i> sp. 05A08             | DedA                | 90 |
| 147 | Altholactone                                                                                       | <i>Polyalthia</i> sp.                  | Rv1466              | 91 |



**Figure S1 Chemical structure of TB drug candidates in clinical trials**

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