

# **Mutations in the F<sub>420</sub> biosynthetic pathway and a nitroreductase enzyme are the primary resistance determinants in spontaneous *in vitro* selected PA-824 mutants of *Mycobacterium tuberculosis***

## **SUPPLEMENTARY ELECTRONIC MATERIAL**

Hana Haver<sup>1,2</sup>, Adeline Chua<sup>1±</sup>, Pramila Ghode<sup>1,3±</sup>, Suresh B. Lakshminarayana<sup>1</sup>, Amit Singhal<sup>4</sup>, Barun Mathema<sup>5</sup>, René Wintjens<sup>6</sup>, Pablo Bifani<sup>1\*</sup>

<sup>1</sup>Novartis Institute for Tropical Diseases, Singapore.

<sup>2</sup>Department of Microbiology and Immunology Program, Yong Loo Lin School of Medicine, Life Sciences Institute, National University of Singapore, Singapore.

<sup>3</sup>Department of Biological Sciences, Faculty of Science, National University of Singapore, Singapore.

<sup>4</sup>Singapore Immunology Network (SIgN), A\*Star, Singapore.

<sup>5</sup>Department of Epidemiology, Mailman School of Public Health, Columbia University, New York, NY.

<sup>6</sup>Laboratory of Biopolymers and Supramolecular Nanomaterials (CP206/04), Université Libre de Bruxelles, B-1050 Brussels, Belgium.

\*Correspondence: [pablo.bifani@novartis.com](mailto:pablo.bifani@novartis.com)

±These two authors have contributed equally.

1 **Supplementary Table S1: Target genes and primers.**

Gene	Protein	Length (aa)	Function	Pathway	Primers
Rv3547	DDN	151	F <sub>420</sub> -dependent nitroreductase	F <sub>420</sub>	sRV3527F- 5' gcaccgaccagagcctcgectg 3' sRv3527R- 5' cgcctggctcacgtcg 3'
Rv0407	FGD1	336	F <sub>420</sub> -dependent glucose-6-phosphate dehydrogenase	Pentose phosphate pathway (oxidative branch)	sRv0407AF- 5' gcggttcgcgtttatggc 3' sRv0407AR- 5' cggcacgtcgtagatcg 3'  sRv0407BF- 5' gttggggctaattgcggcage 3' sRv0407BR- 5' gcagagagccgcgttaatcgcc 3'
Rv3261	FBIA	331	Catalyzes the transfer of the 2-phospholactate moiety from lactyl (2) diphospho-(5')guanosine (LPPG) to 7,8-didemethyl-8-hydroxy-5-deazariboflavin (FO) with the formation of the L-lactyl phosphodiester of 7,8-didemethyl-8-hydroxy-5-deazariboflavin (F <sub>420</sub> -0) and GMP	Cofactor biosynthesis; coenzyme F <sub>420</sub> biosynthesis	sRv3261F1: 5' gcggttcttgttggttggg 3' sRv3261R1-1: 5' gcatgatgatgtcgccgtcg 3'  sRv3261F1-1: 5' gccaccegacgaccgttgeaaaccc 3' sRv3261R1: 5' ccgtacggccaggatctcgatgg 3'
Rv3562	FBIB	448	Catalyzes the GTP-dependent successive addition of multiple gamma-linked L-glutamates to the L-lactyl phosphodiester of 7,8-didemethyl-8-hydroxy-5-deazariboflavin (F <sub>420</sub> -0) to form polyglutamated F <sub>420</sub> derivatives	Cofactor biosynthesis; coenzyme F <sub>420</sub> biosynthesis	sFBiBF3: 5' ggtgccgtctgtatggaccgacc 3' sFBiBR1: 5' cgaccacgtcgccgttcgg 3'  sRv3262F1-1: 5' gccggccacttggtaaaggc 3' sRv3262R1: 5' cgccgtgaattgtatccgtcggg 3'
Rv1173	FBIC	856	Catalyzes the radical-mediated transfer of the hydroxybenzyl group from 4-hydroxyphenylpyruvate (HPP) to 5-amino-6-ribitylamino-2,4(1H,3H)-pyrimidinedione to form 7,8-didemethyl-8-hydroxy-5-deazariboflavin (FO)	Cofactor biosynthesis; coenzyme F <sub>420</sub> biosynthesis	sRv1173FP1- 5' ccttcacggatggtatcgc 3' sRv1173RP1- 5' cgtcgaggatctegtcgggttcc 3'  sRv1173FP2- 5' ggttttatcccggtcacccgg 3' sRv1173RP2- 5' cttggcgccggaaagtctgcacg 3'  sRv1173FP3- 5' cgcggccatacgttacatcg 3' sRv1173RP3- 5' ccgtacgcaggcggcaagc 3'  sRv1173FP4- 5' ggaaatcgatccgcgaggcagg 3' sRv1173RP4- 5' ccagcgaacctcgctcggcagg 3'  sRv1173FP5- 5' gcgtcaccaagagccggc 3' sRv1173RP5- 5' cgtcgccgggttaggcagattgc 3'

**Supplementary Table S2: Mutations on *fbiABC* genes**

**Gene Rv1173/ *fbiC***

Nucleotide Change	Amino acid (aa) Change	Freq.	*Conc	Comments
<sup>148</sup> G>C	<sup>50</sup> Ala→Pro	1	1	Single nucleotide substitution
<sup>155</sup> ΔG	<sup>52</sup> Gly→Val	1	1	Single nucleotide deletion → Frame-shift
<sup>160/161</sup> GA>AT	<sup>54</sup> Glu→Met	1	5	Dinucleotide substitution.
<sup>258</sup> T>G	<sup>86</sup> Tyr→STOP	1	1	Single nucleotide substitution → Early termination codon
<sup>271</sup> T>G	<sup>91</sup> Phe→Val	1	1	Single nucleotide substitution
<sup>313</sup> T>C	<sup>105</sup> Cys→Arg	1	5	Single nucleotide substitution
<sup>569</sup> A>G	<sup>190</sup> His→Arg	1	5	Single nucleotide substitution
<sup>604</sup> T>C	<sup>202</sup> Ser→Pro	1	1	Single nucleotide substitution
<sup>611</sup> T>C	<sup>204</sup> Leu→Pro	1	1	Single nucleotide substitution
<sup>628</sup> T>C	<sup>210</sup> Ser→Pro	1	1	Single nucleotide substitution
<sup>647</sup> A>C	<sup>216</sup> Glu→Ala	1	1	Single nucleotide substitution
<sup>818</sup> C>G	<sup>273</sup> Thr→Arg	1	1	Single nucleotide substitution
<sup>830</sup> △A	<sup>277</sup> Ile→Asn,	1	1	Single nucleotide insertion → Frame-shift
<sup>847</sup> △G	<sup>283</sup> Glu→Gly	1	5	Single nucleotide insertion → Frame-shift
<sup>1008</sup> C>G	<sup>336</sup> Asn→Lys	1	5	Single nucleotide substitution
<sup>1066</sup> G>T	<sup>356</sup> Gly→Cys	1	1	Single nucleotide substitution
<sup>1072</sup> T>G	<sup>358</sup> Ser→Ala	1	1	Single nucleotide substitution
<sup>1114</sup> C>T	<sup>372</sup> Pro→Ser	3	5	Single nucleotide substitution
<sup>1154</sup> G>T	<sup>385</sup> Gly→Val	1	1	Single nucleotide substitution
<sup>1159</sup> G>T	<sup>387</sup> Asp→Tyr	2	1/5	Single nucleotide substitution
<sup>1891</sup> C>T	<sup>631</sup> His→Tyr	1	1	Single nucleotide substitution
<sup>2124</sup> G>A	<sup>708</sup> Met→Ile	2	5	Single nucleotide substitution
<sup>2127/28</sup> △GT	<sup>709</sup> Met→Ile	1	5	Dinucleotide deletion → Frame-shift
<sup>2131</sup> G>T	<sup>711</sup> Gly→Trp	1	5	Single nucleotide substitution
<sup>2133</sup> △G	<sup>711</sup> Gly→Gly	1	1	Single nucleotide deletion → Frame-shift
<sup>2143</sup> A>C	<sup>715</sup> Ser→Arg	1	1	Single nucleotide substitution
<sup>2156</sup> G>T	<sup>719</sup> Trp→Leu	1	5	Single nucleotide substitution
<sup>2159</sup> T>G	<sup>720</sup> Val→Gly	1	1	Single nucleotide substitution
<sup>2158</sup> G>A	<sup>720</sup> Val→Ile	3	1	Single nucleotide substitution
<sup>2165</sup> A>G	<sup>722</sup> His→Arg	1	5	Single nucleotide substitution
<sup>2158</sup> G>A	<sup>720</sup> Val→Ile	1	1	Single nucleotide substitution
<sup>2274</sup> △G	<sup>758</sup> Arg→Arg	1	5	Single nucleotide insertion → Frame-shift
<sup>2374</sup> △CAGACC	<sup>△792</sup> QTSWVKL	1	5	Repeat of preceding 7 aa, in-frame insertions
AGCTGGGTG AAACTT				
<sup>2399</sup> T>G	<sup>800</sup> Leu→Arg	1	5	Single nucleotide substitution
<sup>2549</sup> △C	<sup>843</sup> Thr→Thr	4	5	Single nucleotide insertion → Frame-shift
<sup>2734</sup> △AACTT	<sup>912</sup> △AACTT	1	1	Five nucleotide insertion → Frame-shift
<sup>491</sup> △AACGGG	<sup>164</sup> Glu→Ala	1	5	Seven nucleotide deletion → Frame-shift
G				
<sup>2158</sup> G>A	<sup>720</sup> Val→Ile	1	5	Single nucleotide substitution

**Total number of *fbiC* mutants** **47**

\*Conc: concentration used to select mutant.

**Gene Rv3261/ *fbiA***

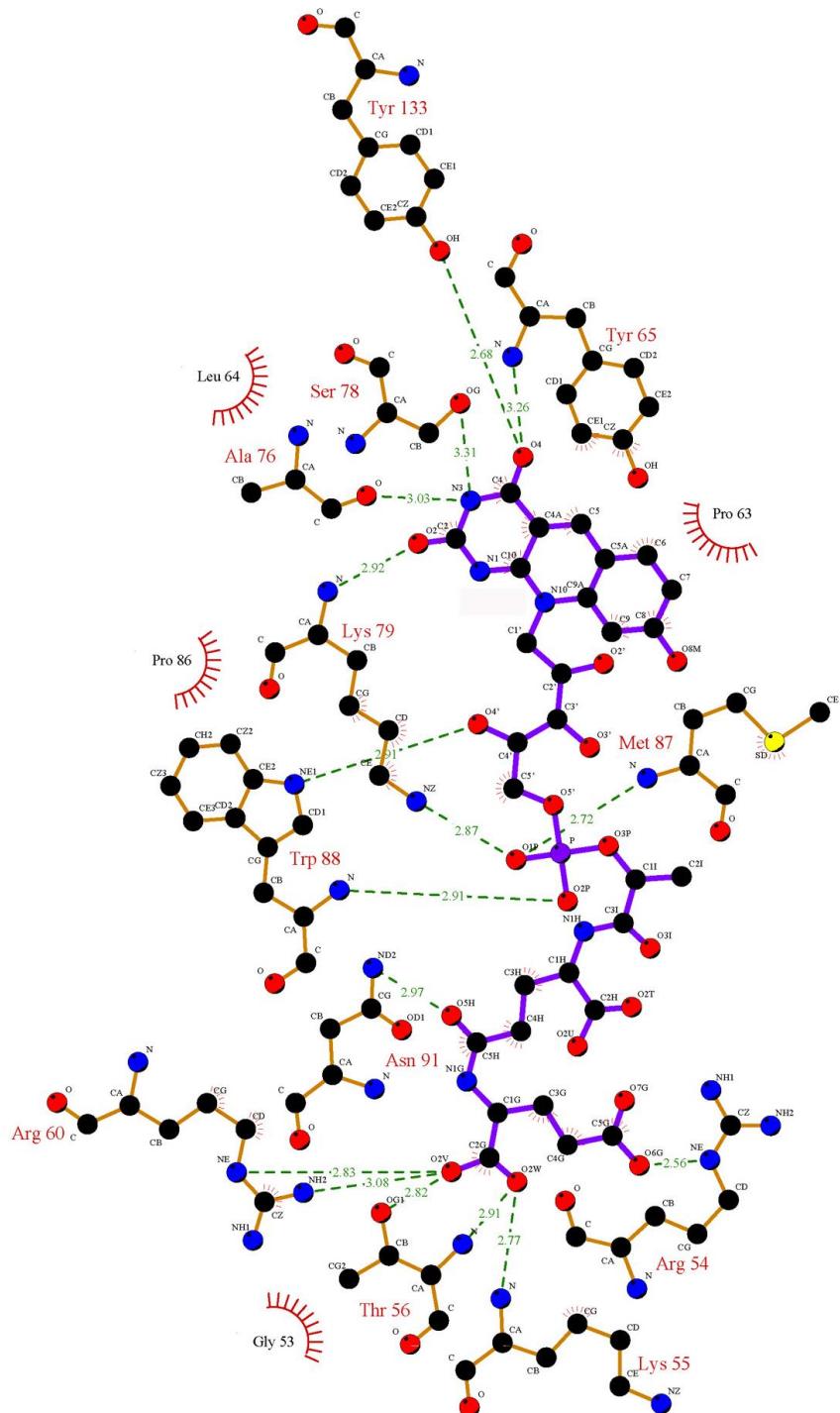
Nucleotide Change	Amino acid Change	Freq.	*Con (μM)	Comments
<sup>62</sup> A>C	<sup>21</sup> Gln→Pro	1	1	Single nucleotide substitution
<sup>145</sup> G>T	<sup>43</sup> Asp→Tyr	1	1	Single nucleotide substitution
<sup>167</sup> T>C	<sup>56</sup> Leu→Pro	1	1	Single nucleotide substitution
<sup>188</sup> A>G	<sup>63</sup> Asp→Gly	2	1/5	Single nucleotide substitution
<sup>195</sup> C>G	<sup>65</sup> Cys→Trp	1	5	Single nucleotide substitution
<sup>211<sup>Δ</sup></sup> G	<sup>71</sup> Gly→Ala	2	5	Single nucleotide deletion → Frame-shift
<sup>222<sup>Δ</sup></sup> C	<sup>74</sup> Asp→Asp	1	5	Single nucleotide deletion → Frame-shift
<sup>227<sup>Δ</sup></sup> C	<sup>76</sup> Gln→Pro	1	5	Single nucleotide insertion → Frame-shift
<sup>237</sup> G>A	<sup>79</sup> Trp→STOP	2	5	Single nucleotide substitution → Early termination codon
<sup>242<sup>Δ</sup></sup> C	<sup>81</sup> Gln→Pro	1	5	Single nucleotide insertion → Frame-shift
<sup>263</sup> C>A	<sup>88</sup> Ala→Asp	1	5	Single nucleotide substitution
<sup>337<sup>Δ</sup></sup> T	<sup>113</sup> Leu→Ser	1	1	Single nucleotide insertion → Frame-shift
<sup>349<sup>Δ</sup></sup> C	<sup>117</sup> Gln→Pro	1	1	Single nucleotide deletion → Frame-shift
<sup>356</sup> T>C	<sup>119</sup> Leu→Pro	1	1	Single nucleotide substitution
<sup>376</sup> T>C	<sup>126</sup> Ser→Pro	1	1	Single nucleotide substitution
<sup>406</sup> T>C	<sup>136</sup> Trp→Arg	2	5	Single nucleotide substitution
<sup>436</sup> A>G	<sup>146</sup> Thr→Ala	1	1	Single nucleotide substitution
<sup>899<sup>Δ</sup></sup> GGGTGA CG	<sup>164</sup> Gly→Gly	1	5	Single nucleotide deletion → Frame-shift
<sup>899<sup>Δ</sup></sup> G	<sup>164</sup> Gly→Gly	1	5	Single nucleotide deletion → Frame-shift
<sup>514</sup> T>C	<sup>172</sup> Trp→Arg	1	1	Single nucleotide substitution
<sup>563<sup>Δ</sup></sup> T	<sup>188</sup> Val→Val	2	1	Single nucleotide insertion → Frame-shift
<sup>575<sup>Δ</sup></sup> A	<sup>192</sup> Lys→Lys	1	1	Single nucleotide insertion → Frame-shift
<sup>575<sup>Δ</sup></sup> A	<sup>192</sup> Lys→Ser	1	1	Single nucleotide deletion → Frame-shift
<sup>713</sup> C>A	<sup>238</sup> Ala→Glu	1	1	Single nucleotide substitution
<sup>747</sup> AA>GT	<sup>249</sup> Glu→Glu	1	1	Dinucleotide substitution → Frame-shift
<sup>775</sup> T>C	<sup>259</sup> Cys→Arg	2	1	Single nucleotide substitution
<sup>847</sup> G>A	<sup>283</sup> Gly→Arg	2	1	Single nucleotide substitution
<sup>968</sup> G>T	<sup>323</sup> Gly→Val	1	1	Single nucleotide substitution
<b>Total number of <i>fbiA</i> mutants</b>		<b>35</b>		

**Rv3262/ *fbiB***

Nucleotide Change	Amino acid Change	Freq.	*Con (μM)	Comments
<sup>536</sup> GGCTCCG CCTCGACC AT	Frame-shift	1	5	Seventeen nucleotide insertions → Frame-shift
<sup>117</sup> G>A	<sup>39</sup> Trp→STOP	1	5	Single nucleotide substitution → Early termination codon
<sup>458</sup> G>T	<sup>153</sup> Gly→Val	1	1	Single nucleotide substitution
<sup>108<sup>1</sup></sup> C>G	<sup>361</sup> Pro→Ala	1	5	Single nucleotide substitution
<b>Total number of <i>fbiB</i> mutants</b>		<b>4</b>		

\*Conc: concentration used to select mutant.

**Supplementary Figure S1:** Schematic 2D interacting plot of F<sub>420</sub> cofactor in the crystal structure of Ddn. Hydrogen bonds (green dashed lines) and van der Waals contacts (red semi-circles with radiating spokes). Color scheme: carbon in dark, nitrogen in blue, oxygen in red and sulfur in yellow. The image was obtained with LigPlot program<sup>1</sup>.



<sup>1</sup> Wallace AC, Laskowski RA, Thornton JM. LIGPLOT: a program to generate schematic diagrams of protein-ligand interactions. *Protein engineering* 1995; **8**: 127-34.

**Supplementary Table S3: Minimum Inhibitory Concentration (MIC<sub>99</sub>)**

Gene	Mutation	MIC <sub>99</sub> (μM)
<i>ddn</i> (3547)	<sup>11</sup> Ser > Stop (15 samples) <sup>22</sup> Ser > Leu <sup>25</sup> Asn > Ile <sup>48</sup> Leu > Pro <sup>78</sup> Ser > Pro <sup>88</sup> Trp > Arg <sup>137</sup> Gln > Stop	>10 >1<5 >10 >5<10 >10 >10 >10
<i>fgd1</i> (0407)	<sup>143</sup> Trp > Stop <sup>169</sup> Gly > Ala <sup>230</sup> Glu > Lys	>10 >5<10 >10
<i>fbiC</i> (1173)	<sup>52</sup> C-deletion <sup>86</sup> Tyr > Stop <sup>105</sup> Cys > Arg <sup>164</sup> AACGGG-deletion <sup>336</sup> Asn > Lys <sup>708</sup> Met > Ile <sup>709</sup> GT-deletion <sup>720</sup> Val > Ile	>10 >10 >10 >10 >10 >5<10 >10 >10
<i>fbiA</i> (3261)	<sup>43</sup> Asp > Tyr <sup>56</sup> Leu > Pro <sup>71</sup> G-deletion <sup>74</sup> C-deletion <sup>81</sup> C-insertion <sup>119</sup> Leu > Pro	>10 >10 >10 >10 >10 >10
<i>fbiB</i> (3262)	Nil tested	--
No mutation identified in <i>ddn</i> , <i>fgd1</i> , <i>fibABC</i> .	2 samples	>10
Wild Type H37Rv		<1