

Analyzing the Effects of Mutations on the Binding Abilities of Drugs in Multidrug-Resistant Tuberculosis (MDR-TB) Using Computational Simulations

Supporting Information

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Table S1: Active Site Frequency Analysis for katG – Active Residues Derived Through Polar Contacts to Isoniazid

Residue Number – Doesn't perfectly align with katG TB as TB katG-Isoniazid structures were unavailable. Frequency analysis remains unchanged.	Amino Acid(s)	Final Count of Each Amino Acid
77-78	2 Tryptophans	Asparagine: 6 Tryptophan: 3 Proline: 3 Threonine: 2 Leucine: 2 Glutamate: 2 Glycine: 2 Isoleucine: 2 Arginine: 2 Aspartate: 1 Lysine: 1 Valine: 1 Serine: 1
123-124	Proline and Aspartate	
126-127	Threonine and Asparagine	
130	Lysine	
183	Valine	
220	Leucine	
224-226	Asparagine, Proline, Glutamate	
271	Asparagine	
291-295	Leucine, Glycine, Tryptophan, Isoleucine, Asparagine	
300-301	Glycine, Isoleucine	
303-304	Arginine, Asparagine	
307-308	Threonine, Serine	
311	Glutamate	
340	Proline	
367-368	Arginine, Asparagine	

Table S2: Full HADDOCK Results for MDR-TB Variants/Mutations

Mutation/ Variant	HADDOCK K Score	Cluster Size	RMSD	Van der Waals Energy	Electrostatic Energy	Desolvation Energy	Restrains Violation Energy	Buried Surface Area	Z-Score
Wild Type, AlphaFold	289.5 +- 5.2	9	0.2 +- 0.0	-8.1 +- 0.6	-7.7 +- 4.2	0.3 +- 0	2981.1 +- 50.6	298 +- 0.8	-1.6
Wild Type, RCSB PDB	292.8 +- 7.9	62	0.5 +- 0.1	-9.9 +- 1	-3.5 +- 3.7	-0.7 +- 0.1	3037.8 +- 80.9	296.7 +- 3.7	-1.7
S315T, AlphaFold	291 +- 4.3	55	0.5 +- 0.0	-11.0 +- 1.0	13.3 +- 2.6	-0.7 +- 0.5	3014.0 +- 40.5	352.1 +- 7.3	-0.9
S315T, RCSB PDB	285.6 +- 28.8	12	0.1 +- 0.1	-7.8 +- 2.4	-18.4 +- 4.0	0.8 +- 0.5	2944.4 +- 268	301.6 +- 2.0	-1.5
Variant 1: T314S, AlphaFold	287.3 +- 35.3	5	0.1 +- 0.1	-9.0 +- 2.0	-6.5 +- 3.8	0.7 +- 0.2	2962.2 +- 343.5	296.2 +- 2.0	-1.5
Variant 2: N323Q, AlphaFold	282.7 +- 26.6	17	0.1 +- 0.1	-10.6 +- 1.9	-29.3 +- 5.4	1.1 +- 0.3	2951.3 +- 281.6	297.5 +- 0.6	-1.8
Variant 3: N323S, AlphaFold	295.1 +- 5.0	18	0.2 +- 0	-8.8 +- 1.9	-11.7 +- 1.4	0.6 +- 0.3	3044.5 +- 49.7	296 +- 3.7	-1.1
Variant 4: N330Q, AlphaFold	298.0 +- 5.0	16	0.3 +- 0.1	-6.9 +- 2.2	-13.3 +- 4.1	0.4 +- 0.2	3057.4 +- 38.9	293 +- 2.1	-1.1
Variant 5: N330S, AlphaFold	284.2 +- 28.9	10	0.2 +- 0.1	-11.3 +- 1.5	-27.2 +- 2.3	1.1 +- 0	2971 +- 283.7	298.8 +- 2.2	-2