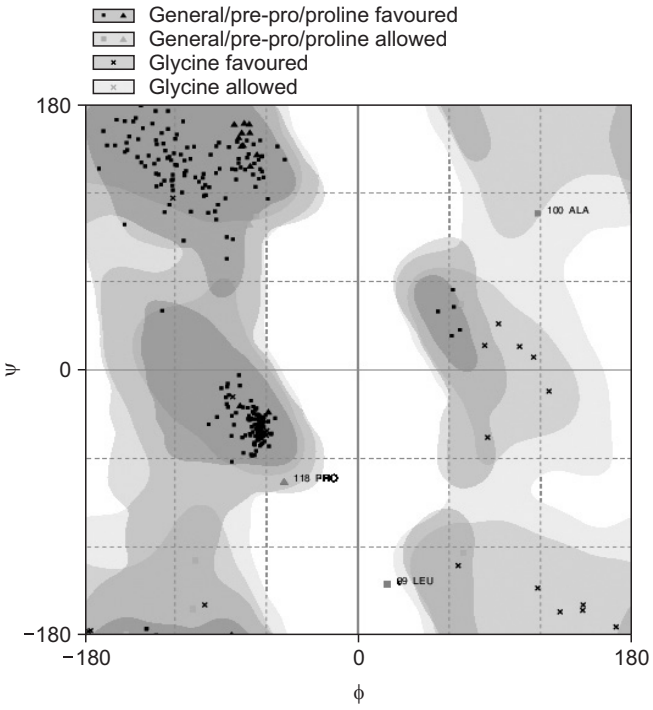

Residue [2: ALA] (−66.53, 104.35) in allowed region
Residue [20: PRO] (−71.31, 99.00) in allowed region
Residue [65: ARG] (67.89, 44.44) in allowed region
Residue [69: TYR] (−108.24, −162.10) in allowed region
Residue [117: PHE] (−152.07, −178.72) in allowed region
Residue [120: SER] (69.17, −123.77) in allowed region
Residue [151: HIS] (−106.54, −129.10) in allowed region
Residue [99: LEU] (19.39, −145.06) in outlier region
Residue [100: ALA] (118.09, 106.12) in outlier region
Residue [118: PRO] (−48.32, −75.53) in outlier region
Number of residues in favoured region (~98.0% expected: 271 (96.4%)
Number of residues in allowed region (~2.0% expected): 7 (2.5%)
Number of residues in outlier region: 3 (1.1%)

Supplementary Figure S3. Ramachandran plot and evaluation of residues for MT model of NAT in MTB. MT: mutant; NAT: *N*-acetyl transferase; MTB: *Mycobacterium tuberculosis*.