STRUCTURAL
BIOLOGY

Volume 78 (2022)

Supporting information for article:

Structural analysis of LpqY, a substrate-binding protein of SugABC transporter from *Mycobacterium tuberculosis* provides insights into the trehalose specificity

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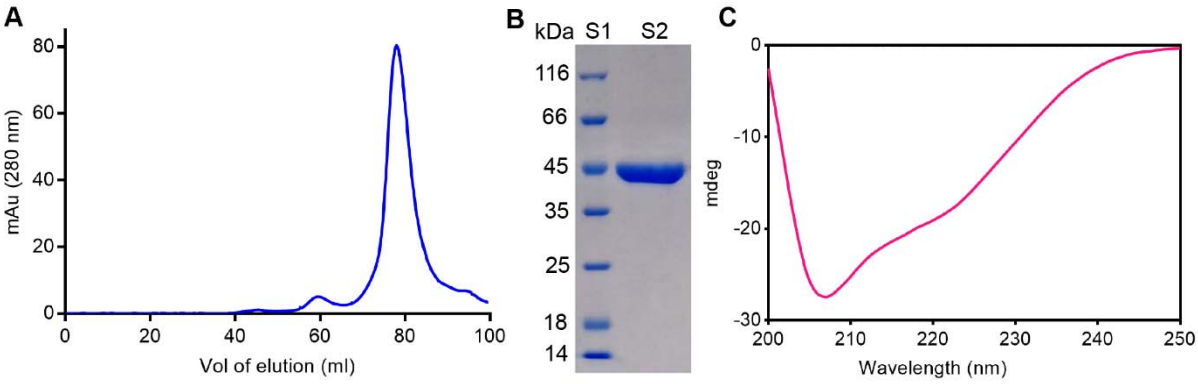

Figure S1 Purification and Circular dichroism spectra of Mtb-LpqY. **A,** The gel filtration profile shows the elution peak of purified Mtb-LpqY. **B**, The SDS-PAGE analysis of the gel filtration peak showing protein ladder at lane S1 and the purified protein in lane S2. The protein ladder is represented along with the S1 lane in kDa. **C**, Circular dichroism spectra of purified Mtb-LpqY represented by a pink curve.

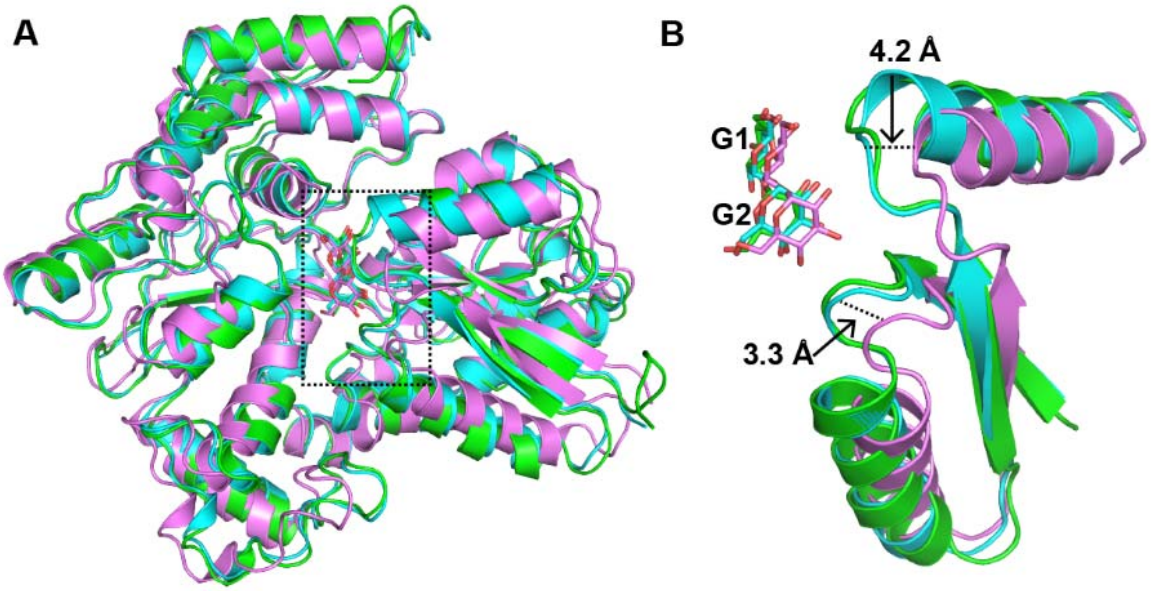

Figure S2 Structural superimposition of LpqY homologues from *Mycobacterium sp*. **A**, Cartoon representation of the superimposition of LpqY from *M.tuberculosis* (purple), *M.thermoresistibile* (cyan), and *M.smegmatis* (green). The trehalose binding site is represented as a dotted rectangle. **B**, The magnified view of the helix-loop region shows their difference in an open and closed conformation. The loops of LpqY in *M.thermoresistibile* and *M.smegmatis* are closer to trehalose giving an overall closed conformation in contrast to *M. tuberculosis.* The trehalose is shown as a stick with the respective color of the cartoon.

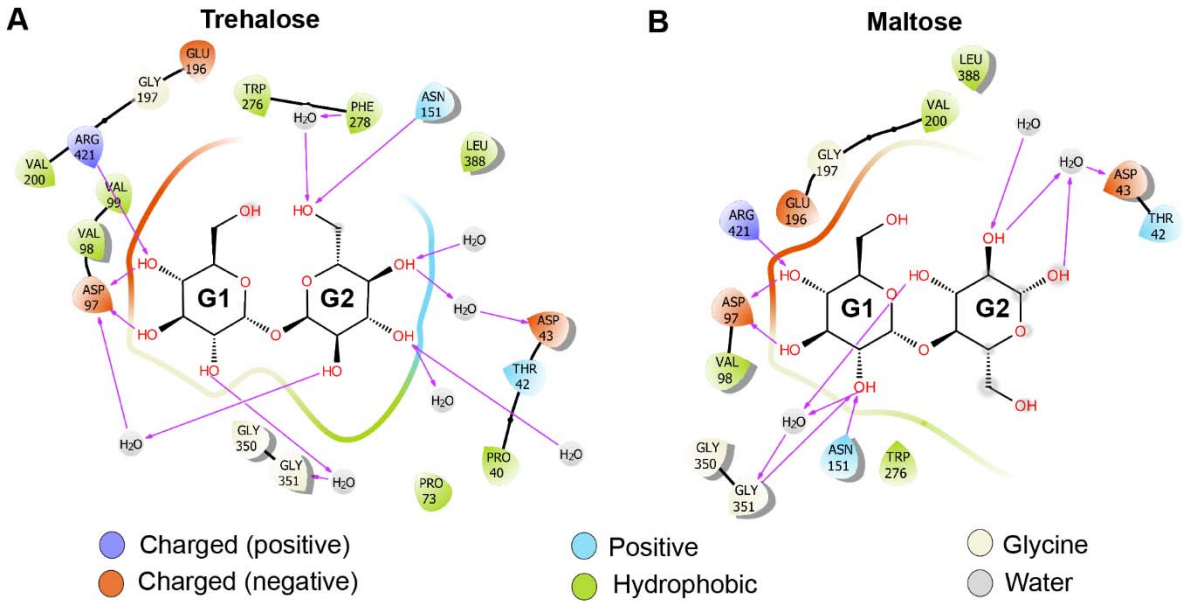

Figure S3 2D diagram of the docking interaction of Mtb-LpqY with trehalose and maltose. **A,** The docked pose of trehalose at the binding cavity of Mtb-LpqY shows various interactions with the binding site residues. **B**, The docked pose of maltose at the binding site, showing the loss of direct or water-mediated interactions between G2 moiety of trehalose and binding site residues. The properties of amino acids are represented by respective color codes as mentioned in the figure. The hydrogen bonds are represented with magenta arrows. The 2D diagrams are generated by Maestro (Schrodinger).

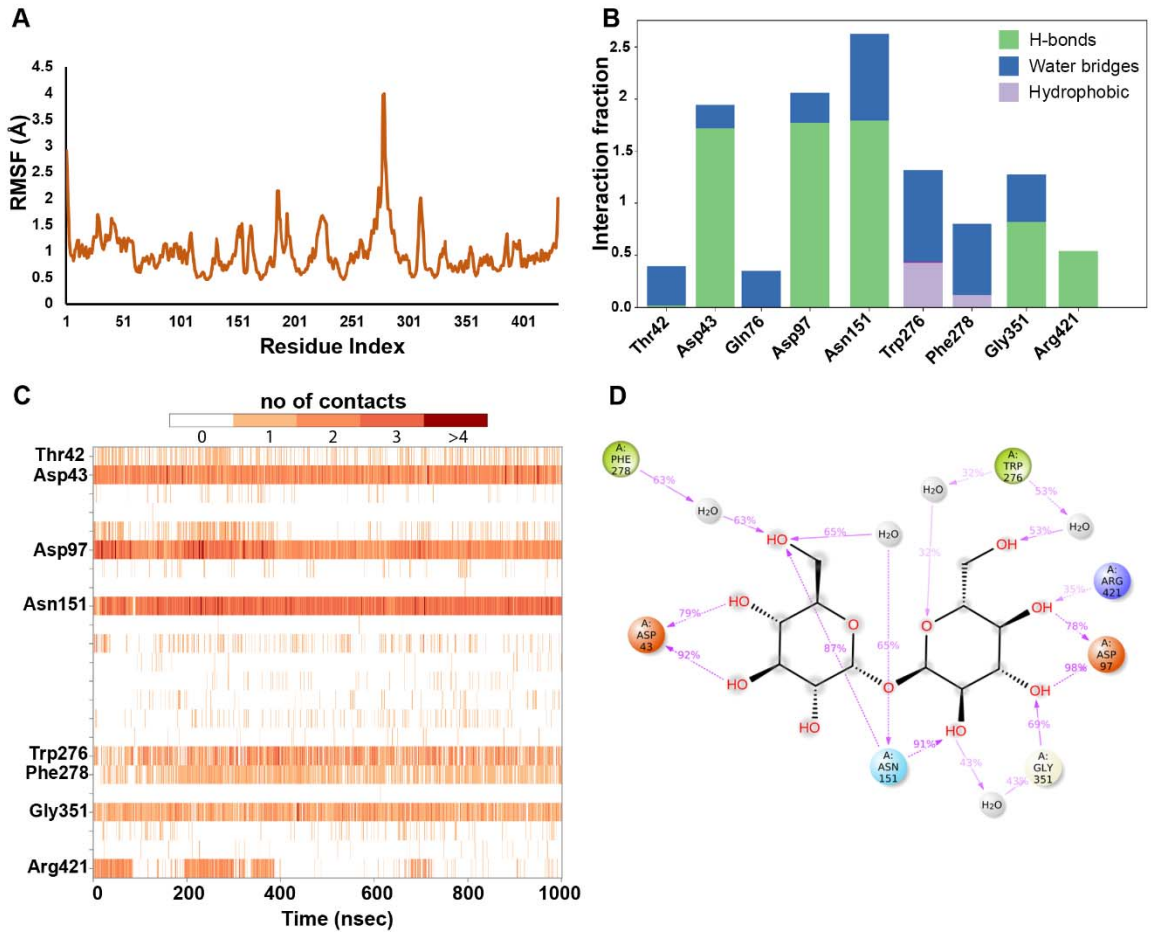

Figure S4 Simulation trajectory and interactional analysis of Mtb-LpqY with trehalose. **A,** RMSF plot of backbone atoms of LpqY amino acid residues. **B,** Histogram showing key residue of binding site of LpqY and their mode of interaction with trehalose. **C**, Timeline representation of the interactions and contacts of the simulated complex of LpqY with trehalose. The graph explains represents the interactions for binding site residues in contact with the trehalose as a function of time. **D**, Diagrammatic representation of average % interactions of the binding site residues of LpqY with trehalose as recorded throughout the simulation. The figures are generated by Desmond simulation event analysis (Schrodinger).

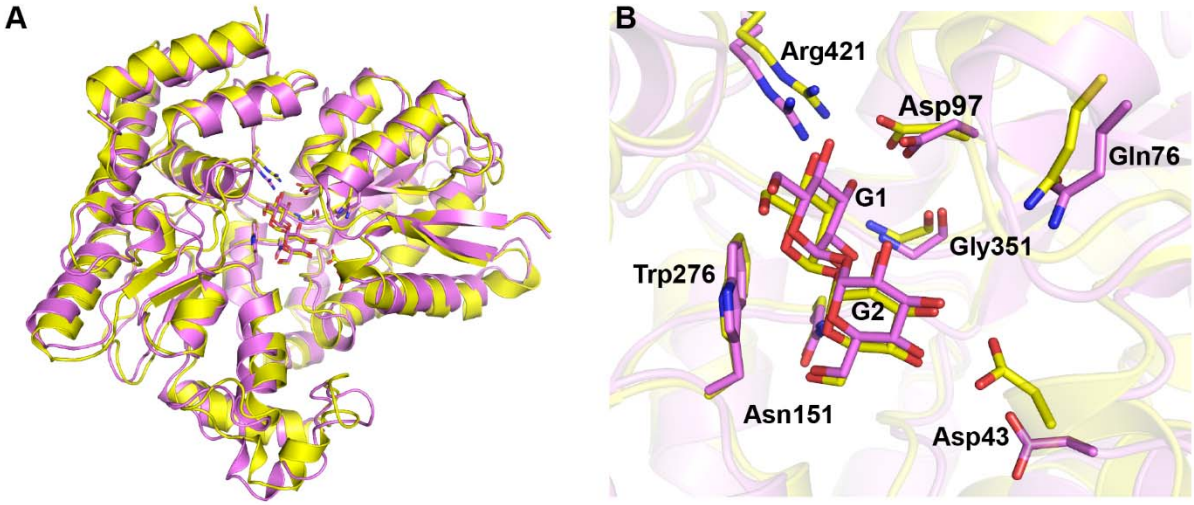

Figure S5 Superimposition of crystal structure of Mtb-LpqY bound trehalose with MD simulation output structure. **A,** The cartoon representation showing the superimposition of the crystal structure of LpqY bound trehalose (pink) with the structure from the last frame from 1 µs molecular dynamics simulation run (yellow) resulting an RMSD of 1.6 Å. **B**, The snapshot of the binding cleft showing the displacement of residues during the simulation run. The Asp43 is seen to come closer to trehalose after the molecular dynamics simulation run thereby constricting the binding cavity and making direct hydrogen bonding interaction.