



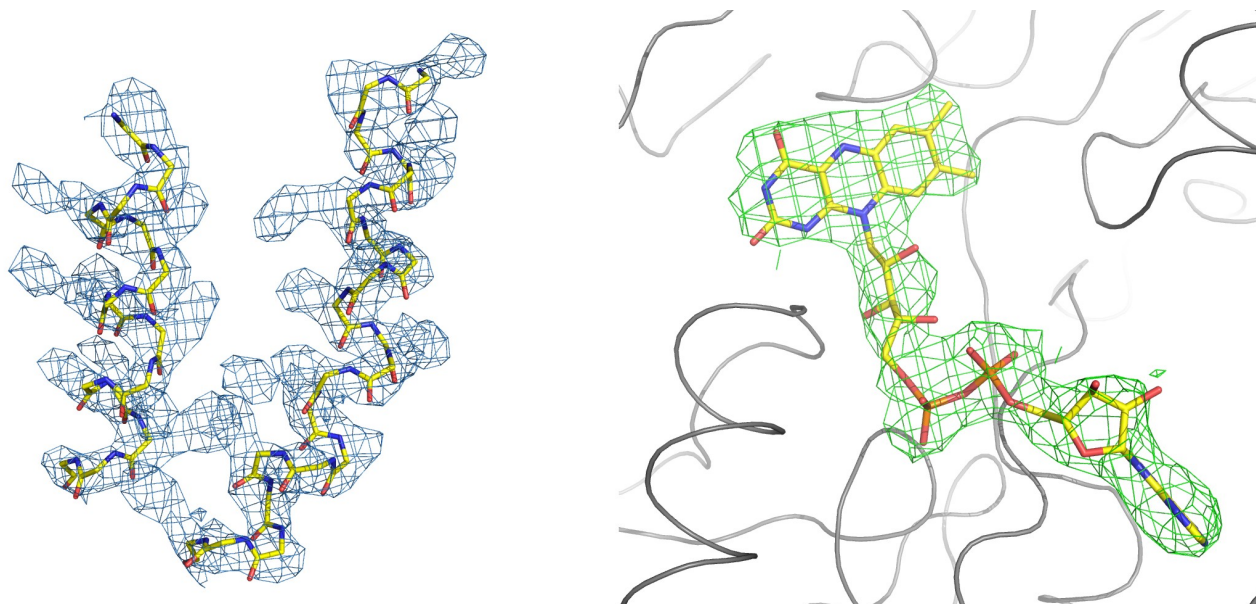
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**Supporting information for article:**

**Expression, purification, crystallization and preliminary X-ray diffraction analysis of a type II NADH:quinone oxidoreductase from the human pathogen *Staphylococcus aureus***

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**Figure S1** – (a)  $2mF_o - Df_c$  electron density map contoured at  $1.5\sigma$  level of one particular region of the *Staphylococcus aureus* NDH-II crystal structure (under iterative model building and refinement at the moment). After a molecular replacement solution was found, the resulting MTZ file was subjected to one round of automated model building after which secondary structure elements were clearly visible. (b) Simulated annealing omit map rendering clear electron density for the FAD cofactor. The map was generated with the program *PHENIX* using the molecular replacement solution MTZ file and the most recent model built. The map is contoured at  $1.5\sigma$  level. The figure was prepared with *PyMol* (Schrödinger, New York, USA).