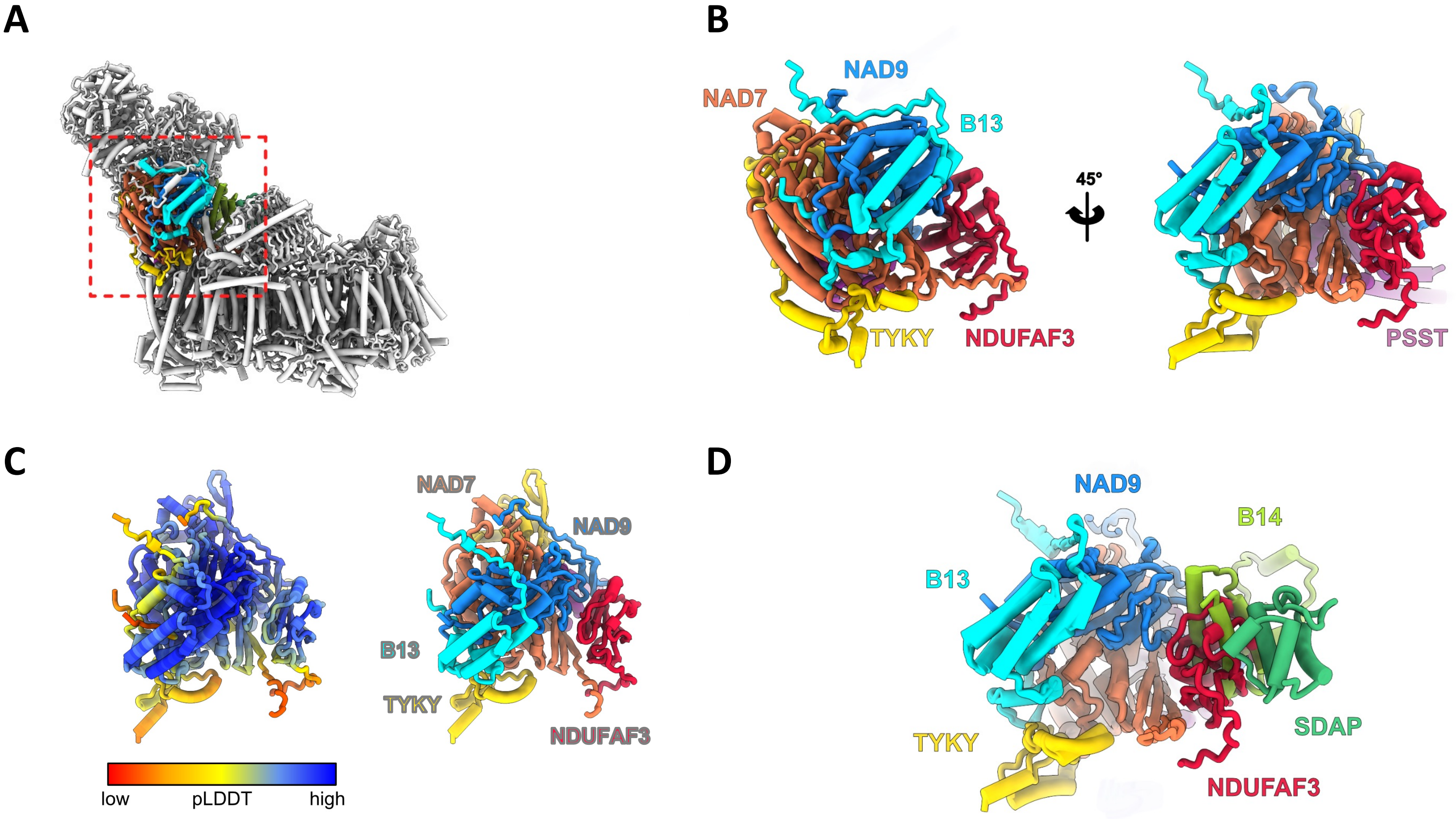

Figure S5. Structure prediction of the Q module of Chlamydomonas in complex with NDUFAF3.

A. Overall view of the mature complex I (Chlamydomonas model PDB: 9FRY). The subunits of the Q module are colored, and the dashed square indicates the zoomed-in view shown in B. **B.** The predicted model of the Chlamydomonas Q module subunits and NDUFAF3, generated by AlphaFold2 Multimer. **C.** pLDDT score for the AlphaFold2 Multimer prediction. Amino acid residues in the predicted model are colored according to their pLDDT score; the higher the score, the more confident the prediction is. Most of the model is predicted with high confidence, except for the C and N terminal parts of the proteins, which is expected. **D.** Chlamydomonas AlphaFold prediction overlaid with the Chlamydomonas model. NDUFAF3 clashes with subunits B14 and SDAP, which connect the matrix and membrane arms via the ferredoxin bridge.