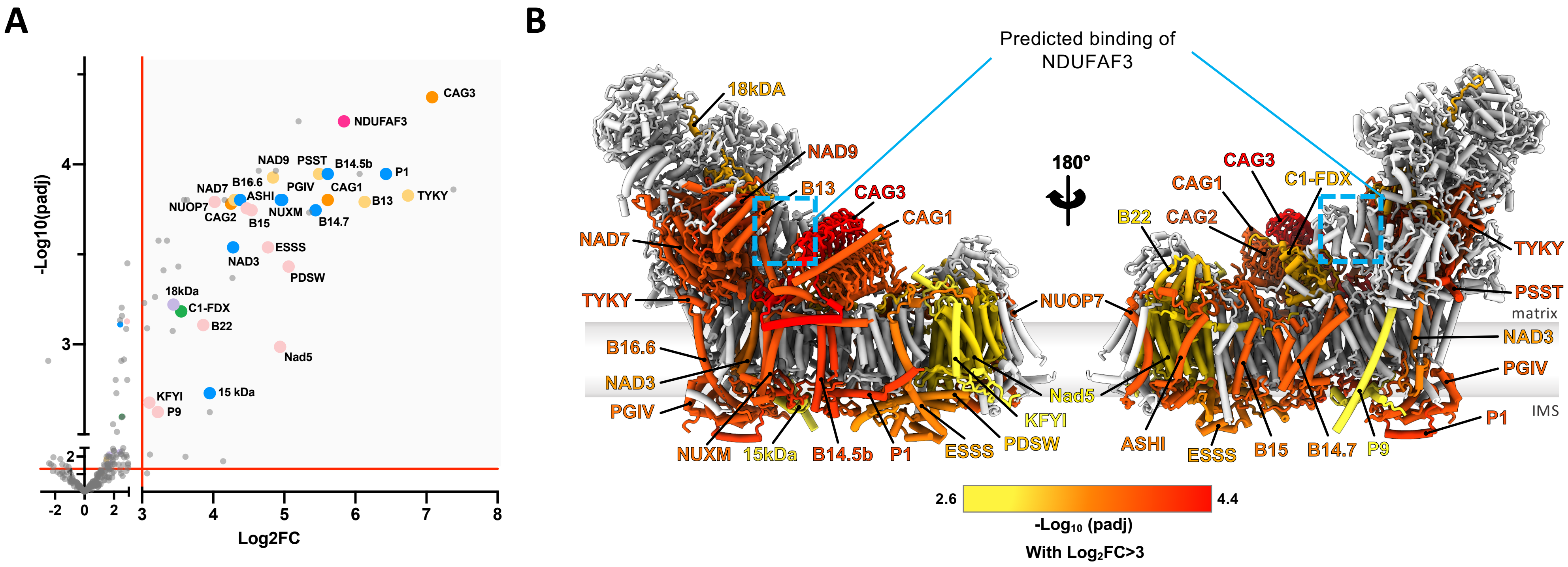

Figure 3. **NDUFAF3 is associated with subunits of the Q and P modules, including plant-specific proteins.**
A. Volcano plot illustrating the global enrichment of proteins in the immunoprecipitation of NDUFAF3-3xFLAG-tagged versus the control strain (n=3). The x-axis represents the $\log_2$ fold change (log2FC), while the y-axis displays $-\text{Log}_{10}$ of the adjusted *p*-value (-Log_{10}(adj)), obtained using the IPinquiry4 R software package. Significantly enriched proteins are defined by a $\text{Log}_2\text{FC}>3$ and a -$\text{Log}_{10}(\text{padj})>1.3$ (corresponding to an adjusted *p*-value<0.05), as indicated by the red axes. NDUFAF3 is marked by a red dot; the N module subunits are shown in violet, the Q module subunits in yellow, the P_p module subunits in blue, the P_d module subunits in pink, the ferredoxin bridge subunits in green, and the γ carbonic anhydrase subunits in orange. The complete datasets and analyses are available in the supplemental (**Table S1**). **B.** Structural model of mitochondrial complex I from Chlamydomonas (Waltz *et al.*, 2025). IMS: intermembrane space. The subunits with a $\text{Log}_2\text{FC}>3$ are colored according to -Log_{10}(padj). The predicted binding region from the Alphafold2 multimer is shown by dashed blue squares. The Alphafold prediction is available in the supplemental materials (**Fig. S5**).