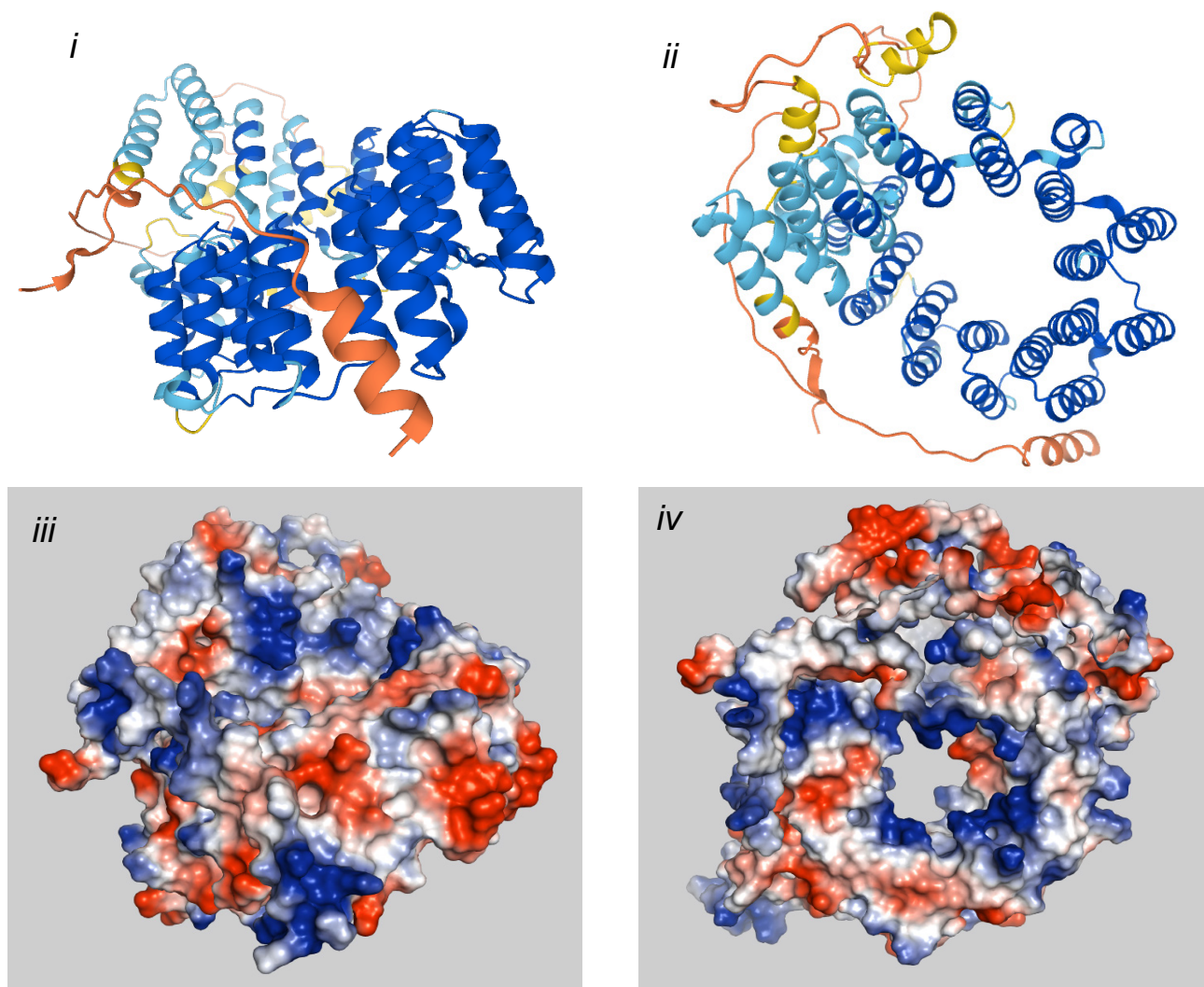


**a**

MPP/ICP55 cleavage site

MLTKLRISKLVSYTLPRRIFQRRFLVTNNTAEESPIVAAESPESLP<sub>SWIKDFLSNKPSSSS</sub>  
SSVSKDDEDFVIPS<sub>LANWVESQKFSRQQVSEGNVVKKPVEDIDKVCDFLNKKDTS</sub>HEDVV  
KELSKCDVVVTESLVLQVLRRFSNGWNQAYGFFIWANSQTGYVHS | GHTYNAMVDVLGKC  
RNFDLMWELVNEMNKNEESKL | VT I | LDTMSKVMRRLAKSGKYNKAVDAFLEMEKSYGVK  
TD | TIAMNSLMDALVKENSIEHAHEVFLKLFDTIKPD | ARTFNILIHGFCKARKFDDARA  
MMDLMKVTEFTPD | VVTYTSFVEAYCKEGDFRRVNEMLEEMRENGCNPN | VVTYTIVMHS  
LGKSKQVAEALGVYEKMKEDGCVPD | AKFYSSLIHILSKTGRFKDAAEIFEDMTNQGVRR  
D | VLVYNTMISAALHHSRDEMALRLLKRMEDDEEGESCPN | VETYAPLLKMCCHKKKMKL  
LGILLHHMVKNDVSID | VSTYILLIRGLCMSGKVEEACLFFEEAVRKGMVPR | DSTCKML  
VDELEKKNMAEAKLKIQSLVQSKTMIDSHSPLSVS

**b**

**Figure S1.** The topology and structure of MISF2 protein. (a) Amino acid sequence of the MISF2 protein (At3g22670). The region corresponding to the predicted mitochondrial targeting sequence is underlined and highlighted in red. The predicted cleavage sites of the Mitochondrial Processing Peptidase (MPP) or Intermediate Cleavage Peptidase 55 (ICP55) is indicated with a red arrow. The 10 PPR motifs (highlighted in blue letters) were predicted with the PPRfinder (Gutmann et al. 2020), PPRCODE (Shen et al. 2019), SMART (Letunic et al. 2012) and CDD (Marchler-Bauer et al. 2003) web-servers. Underlined letters indicate the 5 and 35 positions within each PPR repeat. (b) Atomic structural model of MISF2 predicted by the AlphaFold server (Jumper et al. 2021). Ribbon structures (i and ii) were generated by the PyMol software suite. Panels “iii” and “iv” represent charges on the surface of MISF2 from two different angles, with red, white, and blue for negatively, neutral, and positively charged residues, respectively.