STRUCTURAL BIOLOGY
COMMUNICATIONS

Volume 78 (2022)

Supporting information for article:

Crystallization and crystallographic studies of a novel chickpea 11S globulin

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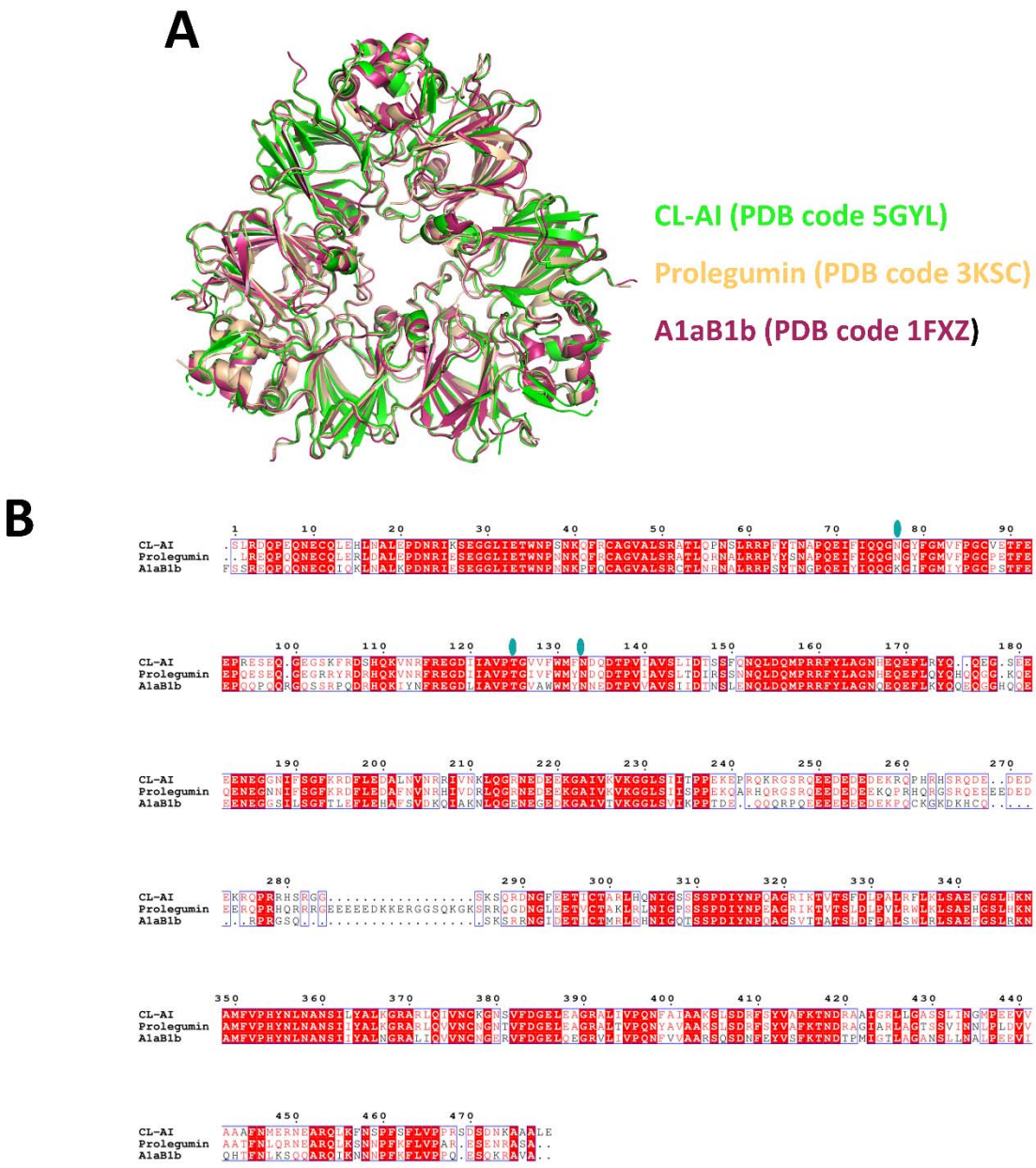

Figure S1 Structure superposition and sequence alignment among CL-AI (PDB code 5GYL). (a) Prolegumin (PDB code 3KSC), and A1aB1b (PDB code 1FXZ).CL-AI, Prolegumin, and A1aB1b colored with green, wheat, and warmpink. (b) Strictly conserved amino acid residues are highlighted in red background and moderately conserved amino acid residues are colored in red. cyan ovals represent the key residues for CL-AI inhibitory activity.

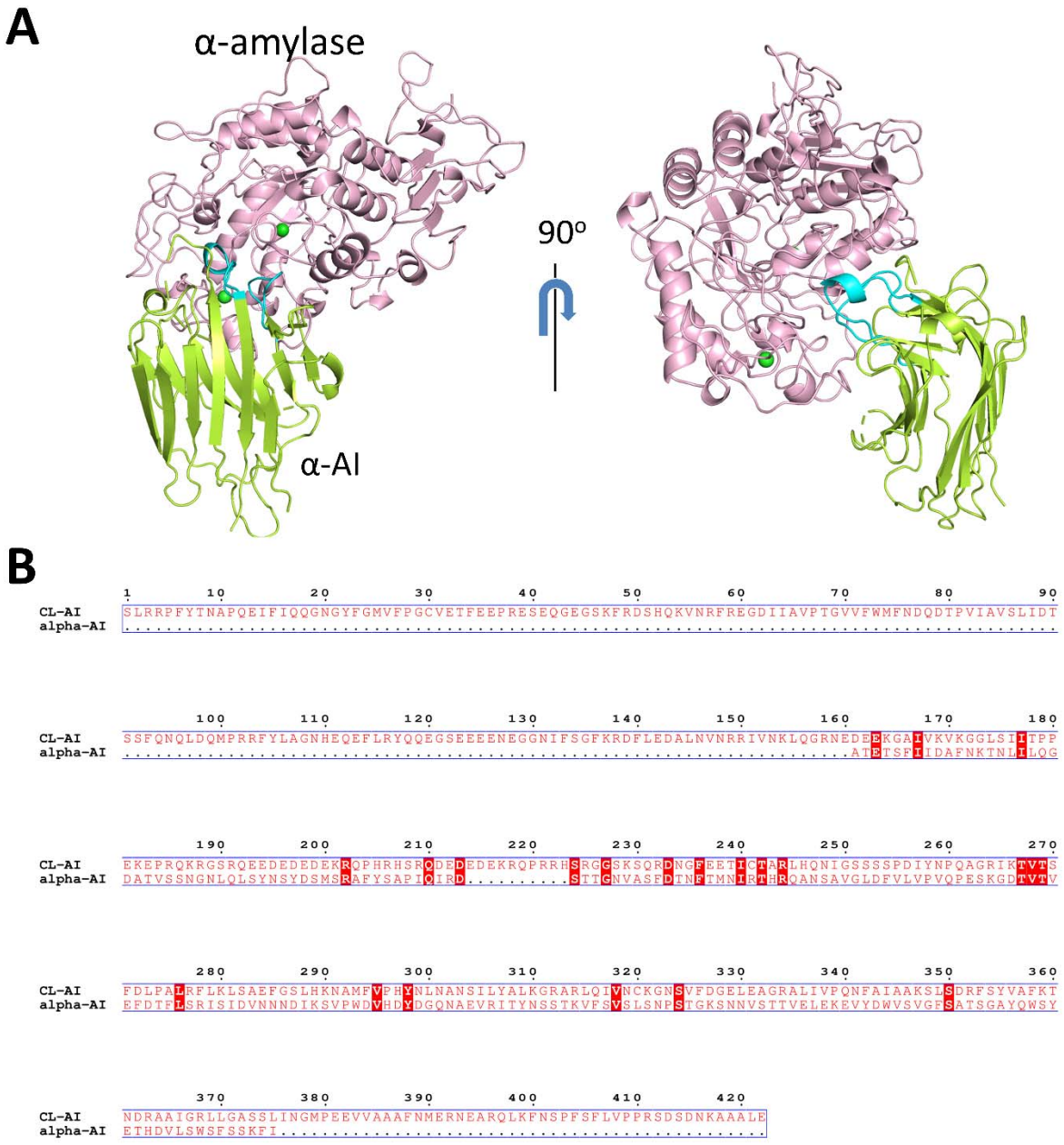

Figure S2 Structural and sequence analysis of α-AI isolated from *Phaseolus vulgaris* (PDB code 1VIW). (a) The complex structure of α-amylase from *Tenebrio molitor* larvae (TMA) with α-AI. The two hairpin loops of the α-AI (colored with cyan), which insert into the active site of the α-amylases, play a key role in inhibitory activity. (b) Sequence alignment of α-AI and CL-AI.