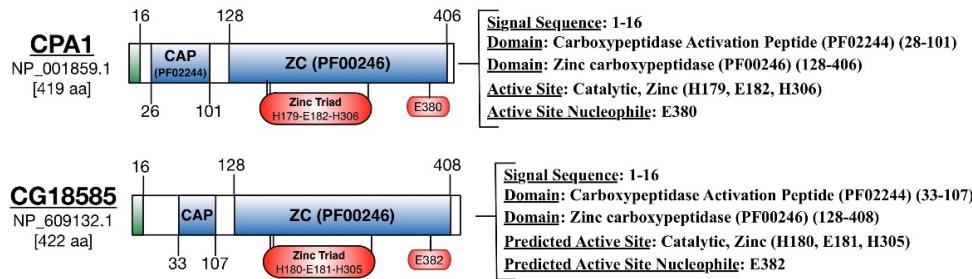
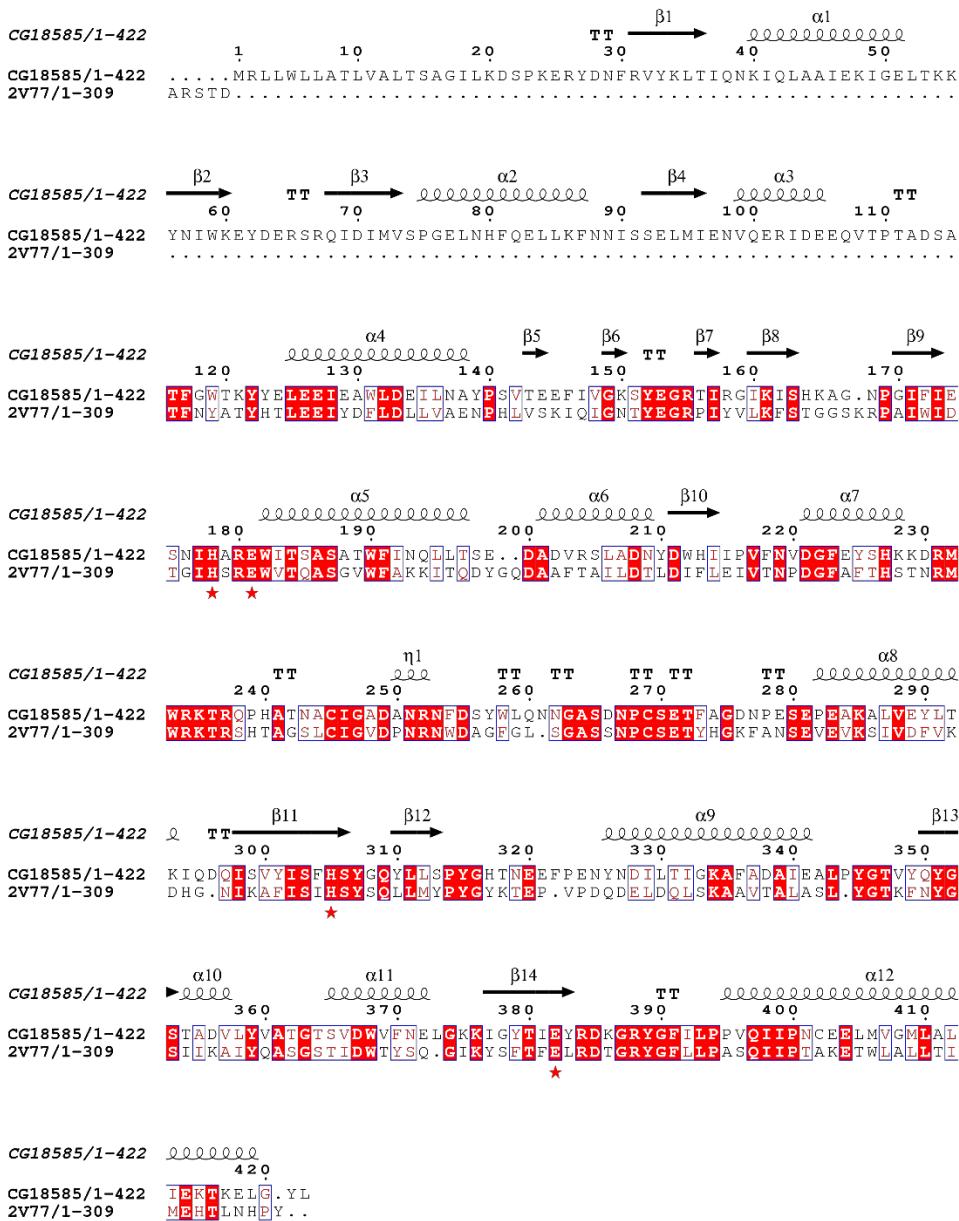


A.

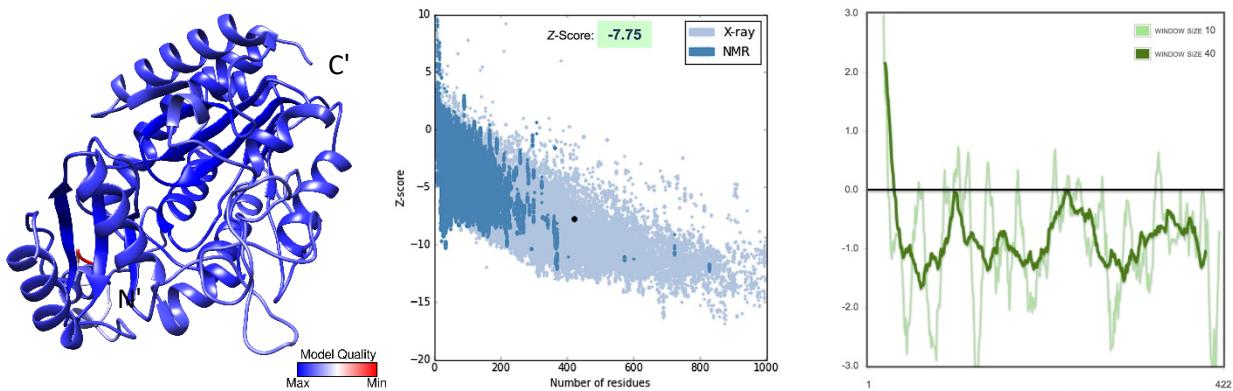


B.



C.

D.



E.

CPA1 Structure	<i>D. melanogaster</i> Model	Superimposed

F.	Length (AA)	Domain Architecture (Pfam, range)	Functional Residues (aligned matches in <i>D. melanogaster</i> )	Sequence ID%	Structural Overlap (RMSD)
Carboxypeptidase A1 (CPA1, NP_001859.1, PDB: 3FJU)	419	Carboxypeptidase activation peptide (PF02244) 26-100  Zinc carboxypeptidase (PF00246) 128-406	H179, E182, H306 and E380		
CPA (CG18585, NP_609132.1)	422	Carboxypeptidase activation peptide (PF02244) 33-106  Zinc carboxypeptidase (PF00246) 128-408	H178, E181, H305 and E382	34% ID 54% SIM	0.753 Å

**S8 Fig. Sequence and structural details of the modeled fly CPA1 candidate.** A. Domain architecture of CPA1 and CG18585 and known/predicted functional residues B. Pairwise alignment of CG18585 and 3FJU generated from structural superposition showing shared secondary structure elements and known/predicted functional residues ( marked with red asterisks) C. Pairwise alignment of CG18585 and 3FJU generated from structural superposition with conserved residues highlighted using the physicochemical color scheme (CLUSTALX) D. Validation of the CG18585 model: ProQ2 quality score mapped to a 3D model of CG18585 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. CPA1 (3FJU, cyan-blue) superimposed on the predicted structure of CG18585 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by CPA1 and potential *D. melanogaster* ortholog CG18585.