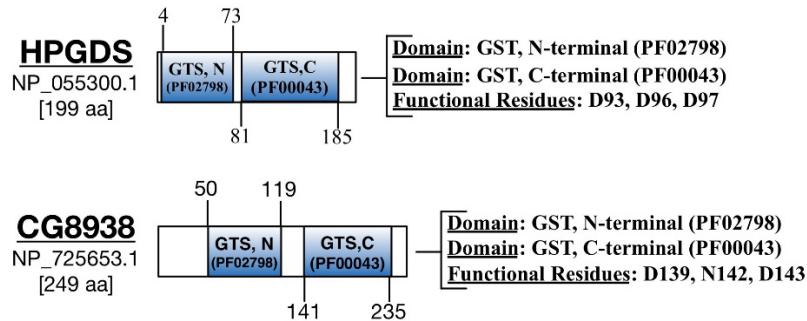
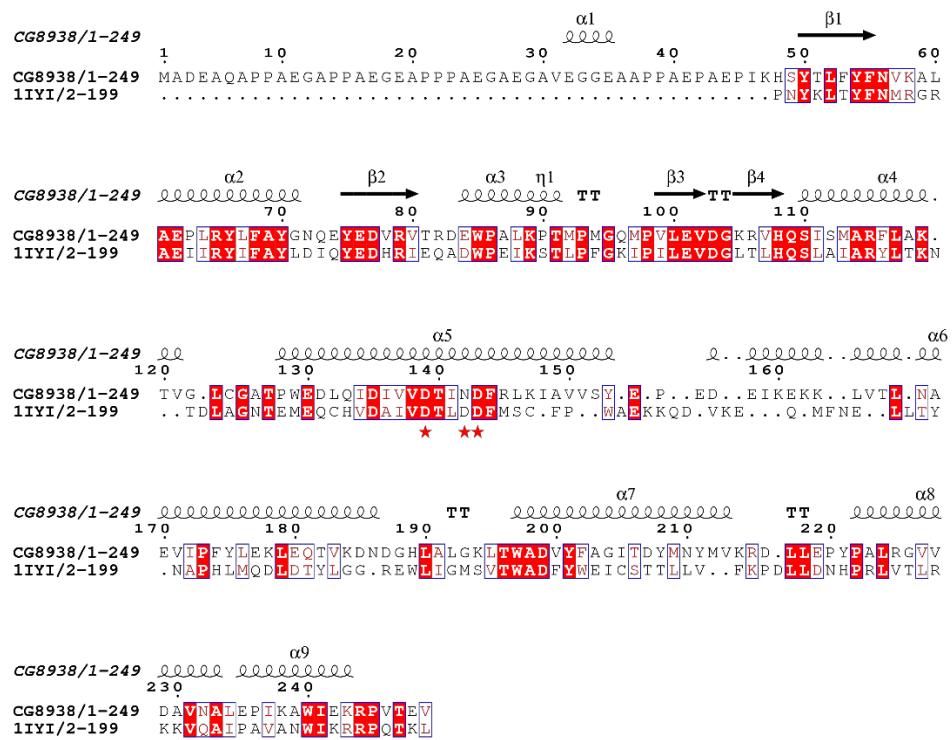


A.

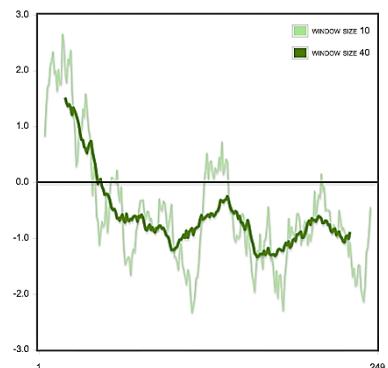
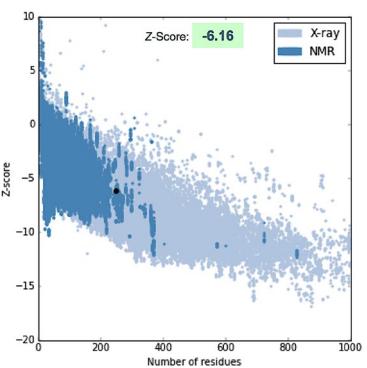
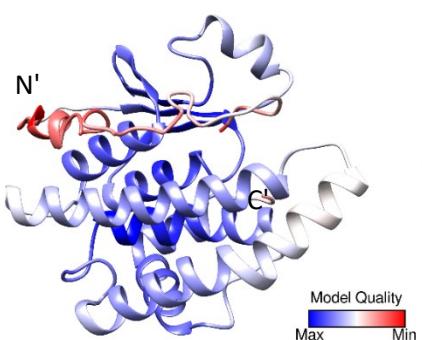


B.

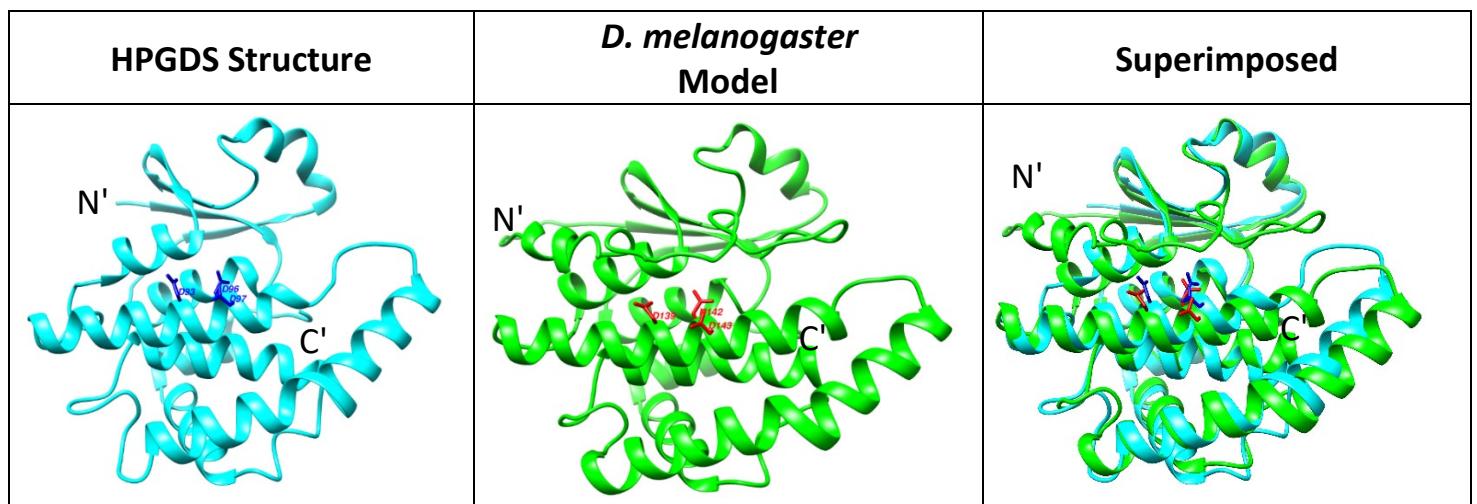


C.

D.



E.



F.	Length (AA)	Domain Architecture (Pfam, range)	Functional Residues (aligned matches in <i>D. melanogaster</i> )	Sequence ID%	Structural Overlap (RMSD)
Hematopoietic Prostaglandin D synthase (HPGDS, NP_055300.1, PDB: 1IYI)	160	GST-N domain (PF02798) 4-73 GST-C domain (PF00043) 81-185	D93, D96, D97	27% ID	1.045 Å
Glutathione S transferase S1 (CG8938, NP_725653.1)	184	GST-N domain (PF02798) 50-119 GST-C domain (PF00043) 141-235	D139, D143, N142	43% SIM	

**S9 Fig. Sequence and structural details of the modeled fly HPGDS candidate.** A. Domain architecture of HPGDS and CG8938 and known/predicted functional residues B. Pairwise alignment of CG8938 and 1IYI generated from structural superposition showing shared secondary structure elements and known/predicted functional residues ( marked with red asterisks) C. Pairwise alignment of CG8938 and 1IYI generated from structural superposition with conserved residues highlighted using the physicochemical color scheme (CLUSTALX) D. Validation of the CG8938 model: ProQ2 quality score mapped to a 3D model of CG8938 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. CPA1 (1IYI, cyan-blue) superimposed on the predicted structure of CG8938 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by HPGDS and potential *D. melanogaster* ortholog CG8938.