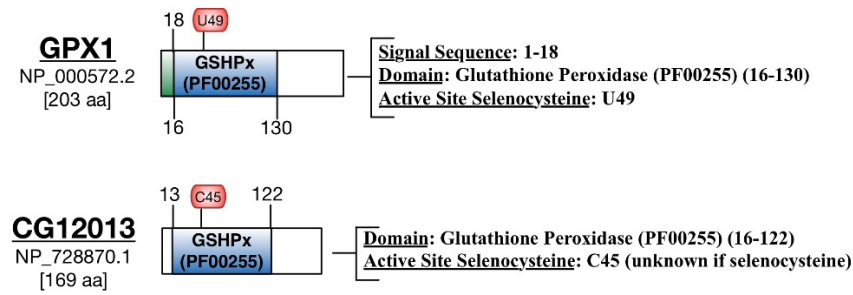
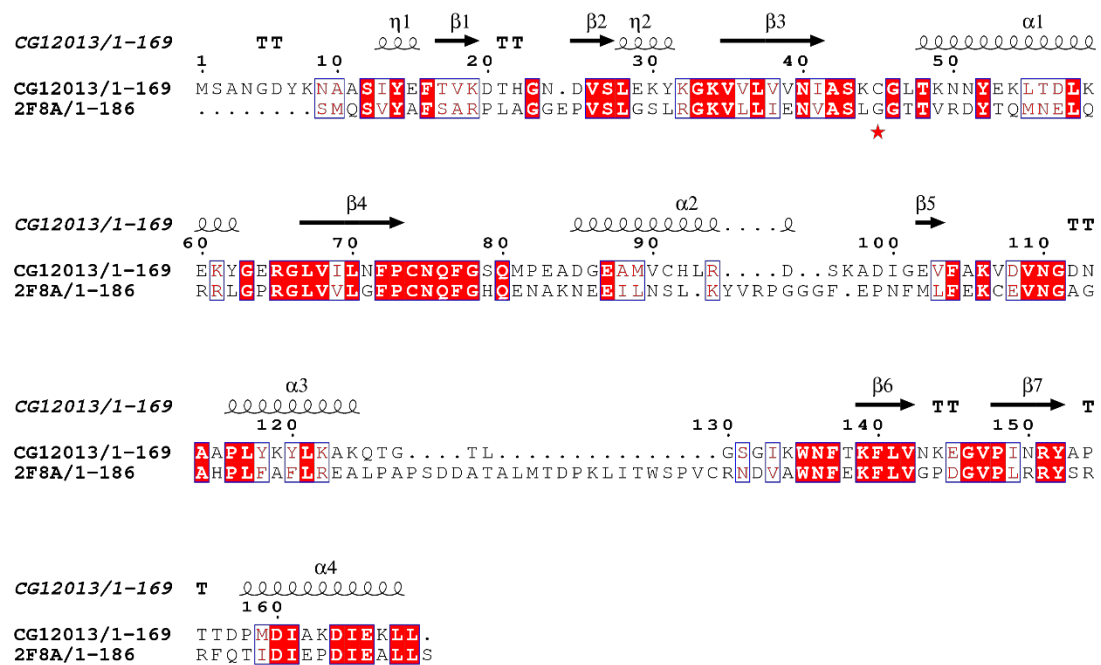


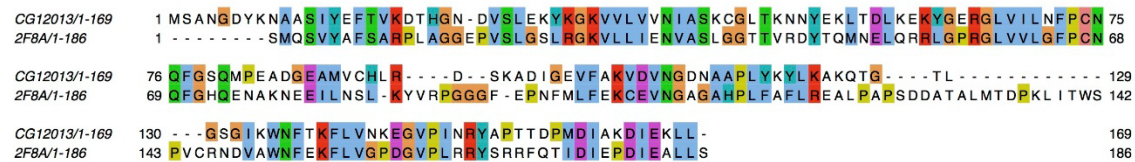
A.



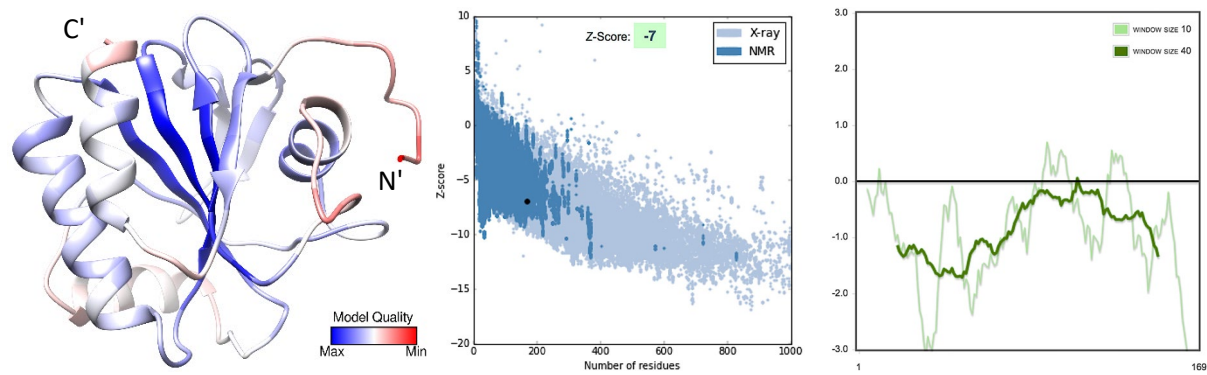
B.



C.



D.



E.

GPX1 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)
Glutathione peroxidase 1 (GPX1, NP_000572.2, PDB: 2F8A)	203	GSHPx (PF00255) 16-130	C49	32% ID 44% SIM	0.699Å
Glutathione peroxidase (CG12013, NP_728870.1)	169	GSHPx (PF00255) 13-122	C45		

**S7 Fig. Sequence and structural details of the modeled fly GPX1 candidate.** A. Domain architecture of GPX1 and CG12013 and known/predicted functional residues B. Pairwise alignment of CG12013 and 2F8A generated from structural superposition showing shared secondary structure elements and known/predicted functional residues (marked with red asterisk; in the GPX1 crystal structure, the selenocysteine is mutated to a glycine) C. Pairwise alignment of CG12013 and 2F8A generated from structural superposition with conserved residues highlighted using the physiochemical color scheme (CLUSTALX) D. Validation of the CG12013 model: ProQ2 quality score mapped to a 3D model of CG12013 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. GPX1 (2F8A, cyan-blue) superimposed on the predicted structure of CG12013 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by GPX1 and potential *D. melanogaster* ortholog CG12013.

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