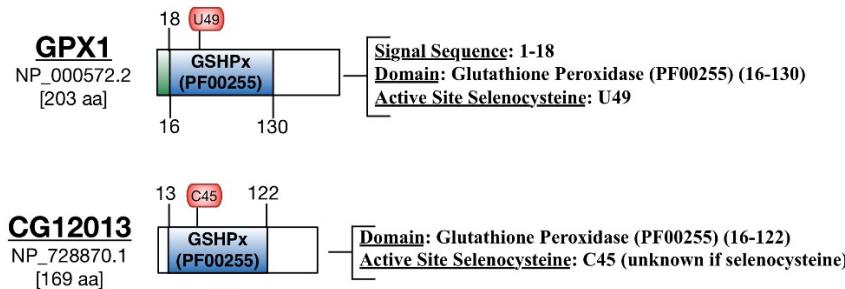
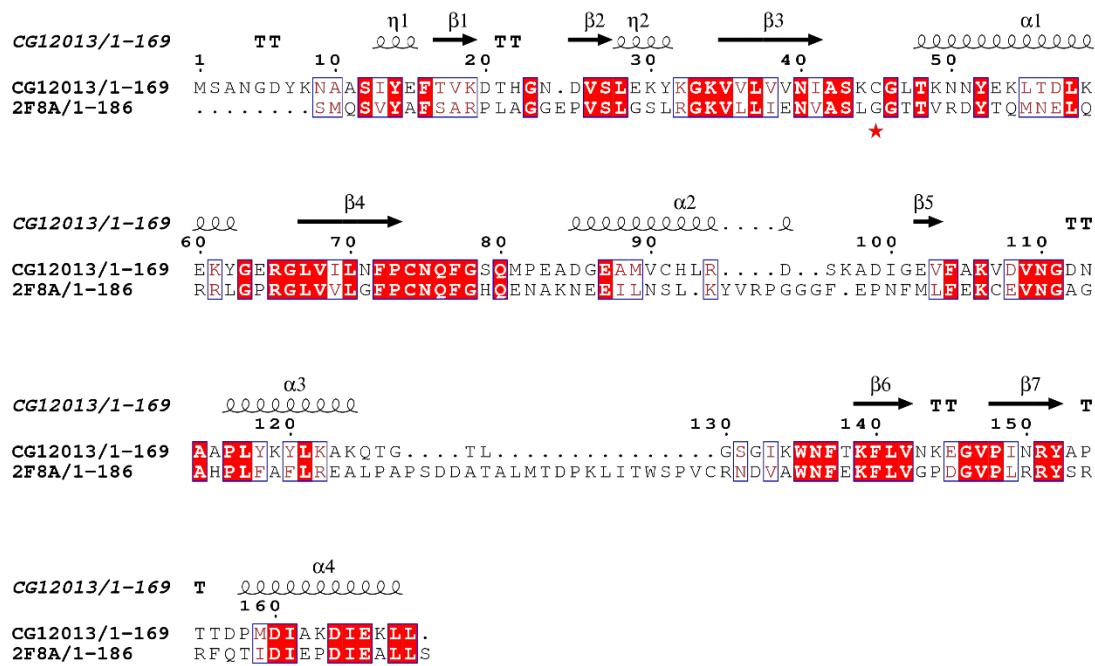
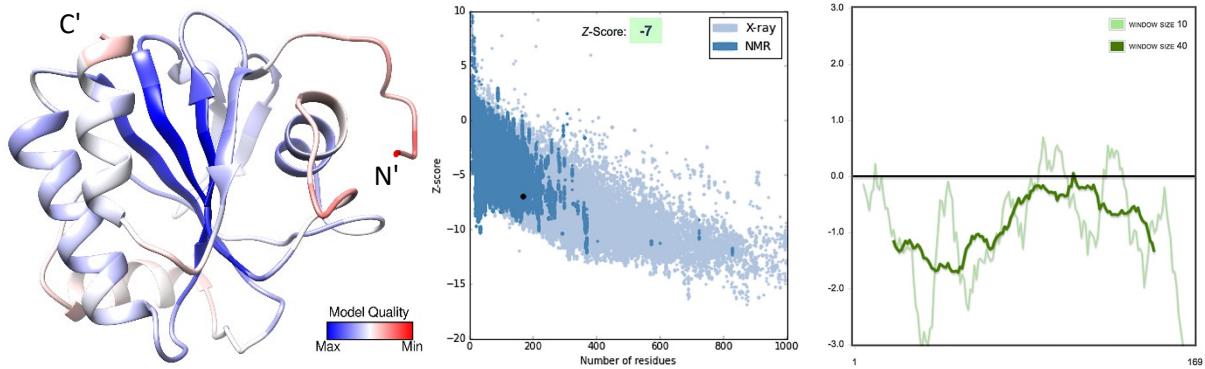
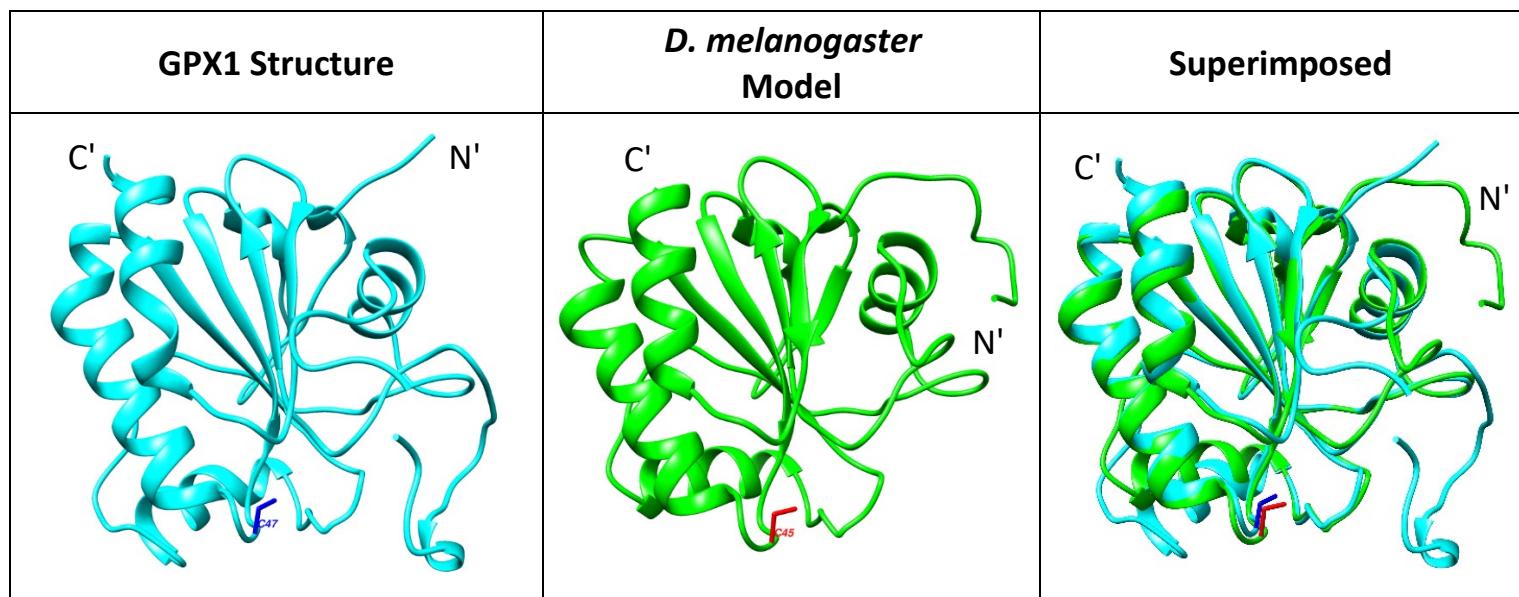


**A.****B.****C.**

<b>CG12013/1-169</b>	1 MSANGDYKNAAS <sub>10</sub> SIYEFTVKDTHGN.DVSLEKYKGKVVLVNVNIASKCGLTKNNYEKLTDLK 2F8A/1-186 1 . . . . . SMQSVYAFSARPLAGGEPVSLGSLRGKVLLIENVASLGGTTVRDYTQMNELQFRRLGPRGLVVLGFPN	75
<b>CG12013/1-169</b>	76 QFGSDMP <sub>69</sub> EADGEAMVCHLR...D...SKADIGEVFAKVDVNGDNAAAPLYKYLKA <sub>142</sub> KQTG...TL... 2F8A/1-186 69 QFGHDENAKNEEILNSL-KYVRPGGGF-EPNFMLFECEVNGAGAHPLFAFLREALPAPSDDATAALMTDPKLITWS	129
<b>CG12013/1-169</b>	130 - - GSGIKWNFTKFLVNKEGVPINRYAPTTDPMDIAKDIKEKL. 2F8A/1-186 143 PVCRNDVAWNFEXFLVGPDG <sub>169</sub> VPLRRYSRRQTDIEPDIEALLS	169
		186

**D.****E.****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	0.699 Å
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.