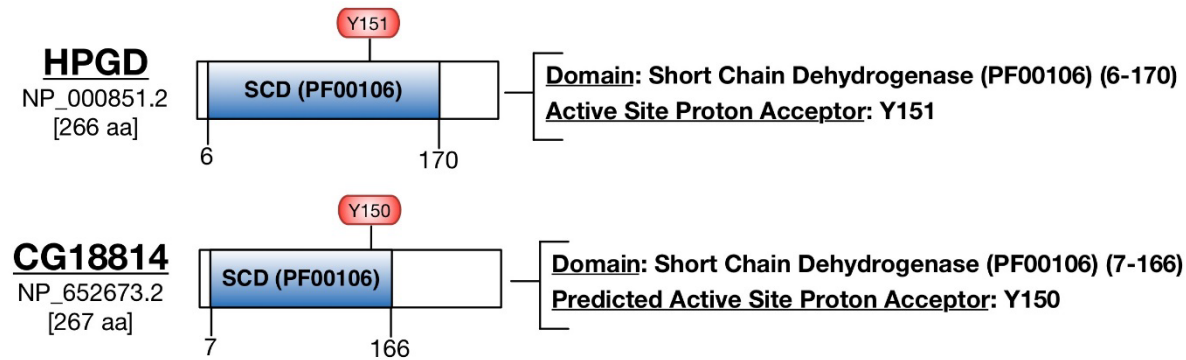
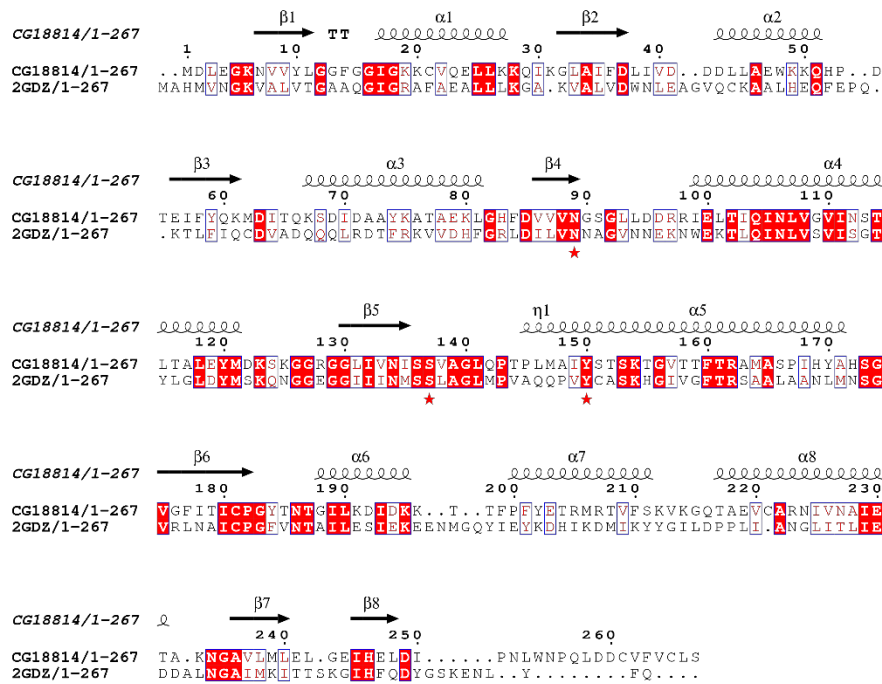


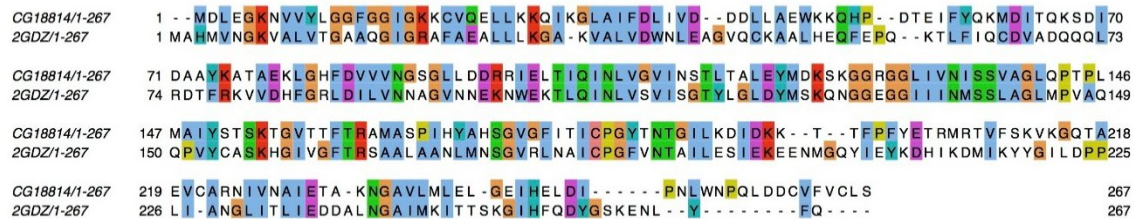
A.



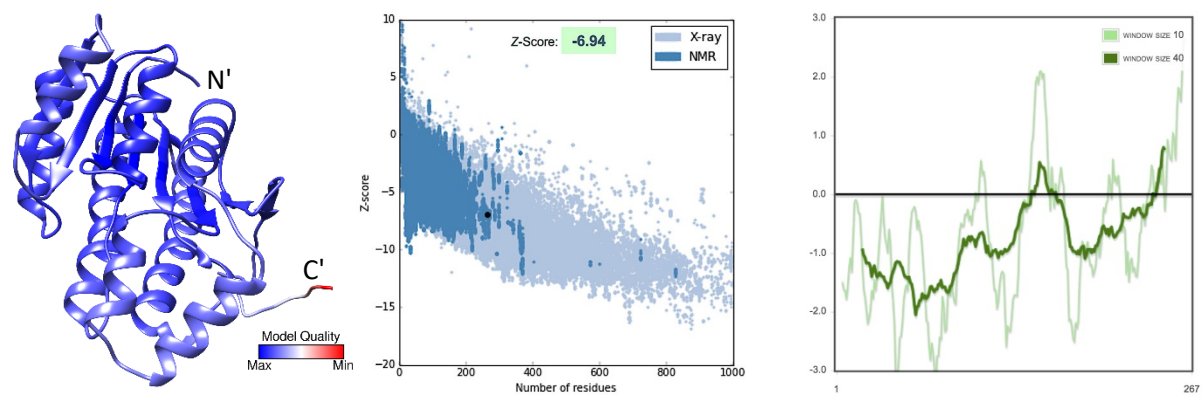
B.



C.



D.



E.

HPGD Structure	<i>D. melanogaster</i> Model	Superimposed
<p>Ribbon diagram of the HPGD protein structure, colored cyan. The N-terminus (N') and C-terminus (C') are labeled. Specific residues are highlighted: Y251, S198, and S148.</p>	<p>Ribbon diagram of the <i>D. melanogaster</i> model, colored green. The N-terminus (N') and C-terminus (C') are labeled. Specific residues are highlighted: S137 and S138.</p>	<p>Superimposed ribbon diagram showing the HPGD structure (cyan) and the <i>D. melanogaster</i> model (green) overlaid. The N-terminus (N') and C-terminus (C') are labeled.</p>

F.	Length (AA)	Domain Architecture (Pfam, range)	Functional Residues (aligned matches in <i>D. melanogaster</i> )	Sequence ID%	Structural Overlap (RMSD)
15-hydroxyprostaglandin dehydrogenase NAD(+) (HPGD, NP_000851.2, PDB: 2GDZ)	266	Short chain dehydrogenase domain (PF00106) 6-170	Y151	26% ID 47% SIM	0.715 Å
Uncharacterized protein (CG18814, NP_652673.2)	267	Short chain dehydrogenase domain (PF00106) 7-166	Y150		

**S12 Fig. Sequence and structural details of the modeled fly HPGD candidate.** A. Domain architecture of HPGD and CG18814 and known/predicted functional residues B. Pairwise alignment of CG18814 and 2GDZ generated from structural superposition showing shared secondary structure elements and known/predicted functional residues ( marked with red asterisks) C. Pairwise alignment of CG18814 and 2GDZ generated from structural superposition with conserved residues highlighted using the physiochemical color scheme (CLUSTALX) D. Validation of the CG18814 model: ProQ2 quality score mapped to a 3D model of CG18814 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. HPGD (2GDZ, cyan-blue) superimposed on the predicted structure of CG18814 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by HPGD and potential *D. melanogaster* ortholog CG18814.