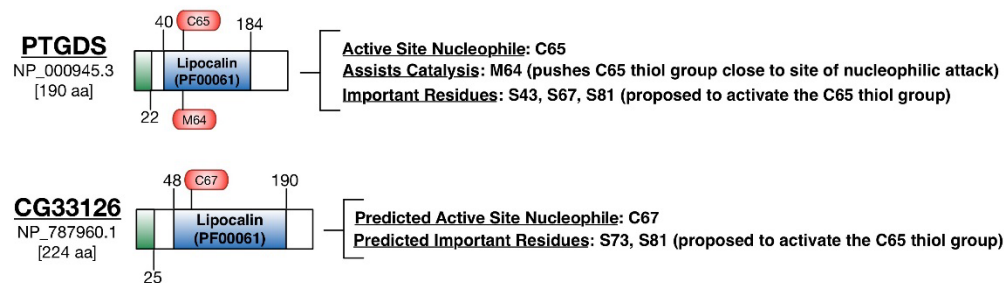
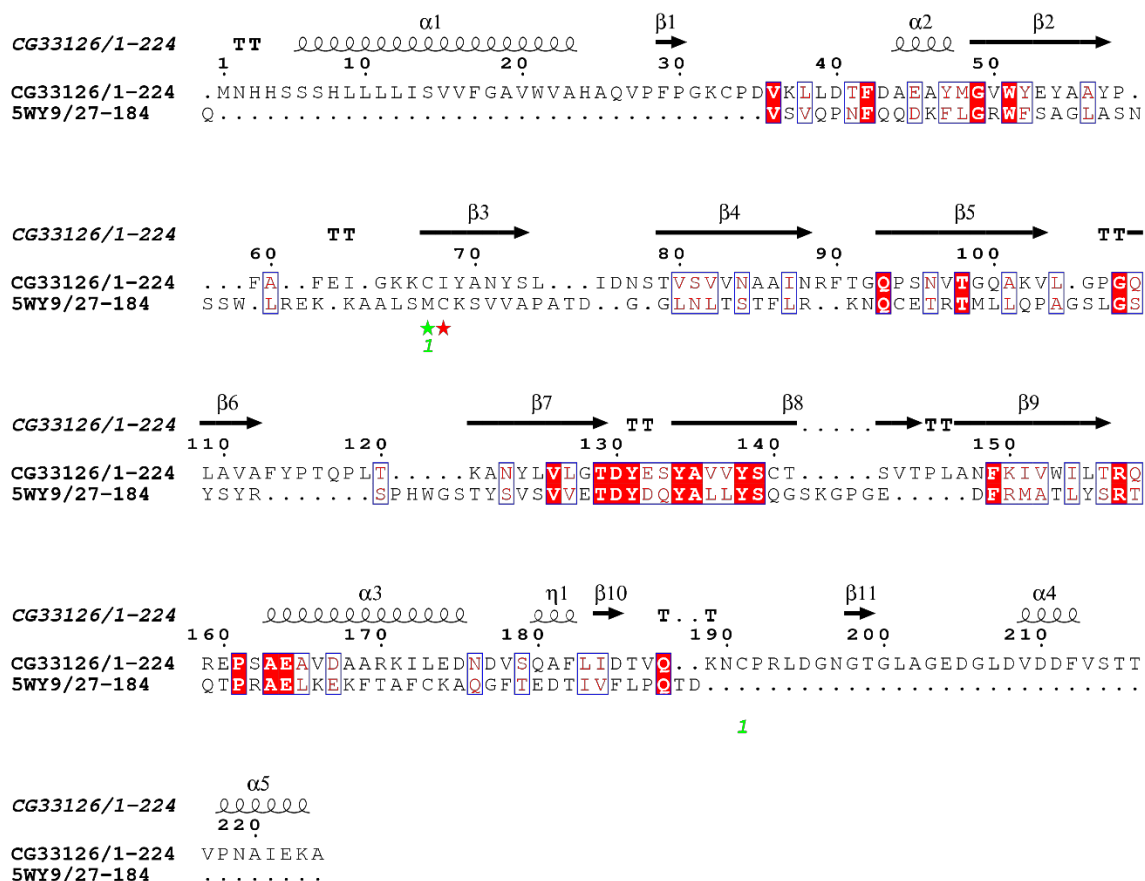


A.



B.



C.

**CG33126/1-224** 1 - MNHSSSHLLLLISVVFQAVVVAHAQVPFPQKCPDVKLLDFAEAYMGVWYEAAYP- - - FA- - FEI- GKCCIYA 70  
**5WY9/27-184** 27 Q- - - - - VSVQPNFQQKFLGRWFSAGLASNSW- LREK- KAALSMCKSV 67

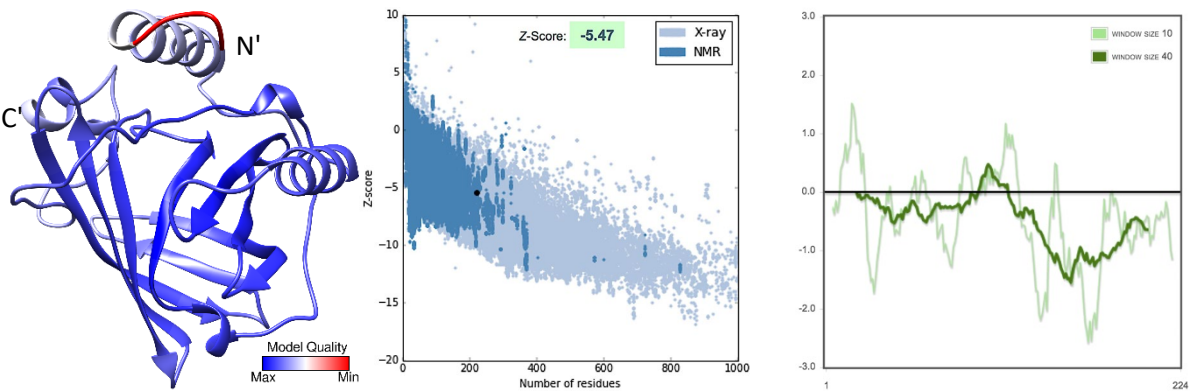
**CG33126/1-224** 71 NYSL- - - IDNSTVSVVNAAINRFTGQPSNVTGQAKVL- GPGQLAVAFYPTQPLT- - - - KANYLVLTGTDYESYAVVYS 139  
**5WY9/27-184** 68 VVAEATD- - G- GLNLTSTFLR- - KNQCETRMMLLQPAAGSLGSYSYR- - - - SPHWGSTYSVSVVETDQYALLYYS 133

**CG33126/1-224** 140 CT- - - - SVTFLANFKIIVWILTRQREPAAEAVDAARKILEDNVSCAFLIDTVQ- - KNCPRLDGNGTGLAGEDGLDVDDFVSTT 210  
**5WY9/27-184** 134 QGSKGPGE- - - - DFRMATLYSRTQTTPRAELKEKFTAFCKAQGFTEDTIVFLPQTD- - - - - 184

**CG33126/1-224** 211 DFVSTTVNNAIEKA  
**5WY9/27-184** .....

224

D.



E.

PTGDS 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)
Prostaglandin-D-synthase (PTGDS, NP_000945.3, PDB: 5WY9)	190	Lipocalin domain (PF00061) 40-184	C65	12% ID	2.084 Å
Neural Lazarillo (CG33126, NP_787960.1)	224	Lipocalin domain (PF00061) 48-190	C67	31% SIM	

**S15 Fig. Sequence and structural details of the modeled fly PTGDS candidate.** A. Domain architecture of PTGDS and CG33126 and known/predicted functional residues B. Pairwise alignment of CG33126 and 5WY9 generated from structural superposition showing shared secondary structure elements and known/predicted functional residues (marked with a red asterisk; the green asterisk denotes the putative analog for C65) C. Pairwise alignment of CG33126 and 5WY9 generated from structural superposition with conserved residues highlighted using the physiochemical color scheme (CLUSTALX) D. Validation of the CG33126 model: ProQ2 quality score mapped to a 3D model of CG33126 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. PTGDS (5WY9, cyan-blue) superimposed on the predicted structure of CG33126 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by PTGDS and potential *D. melanogaster* ortholog CG33126.