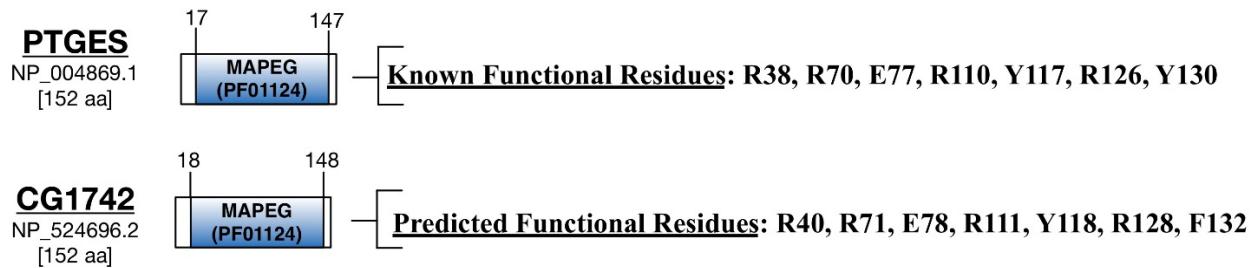
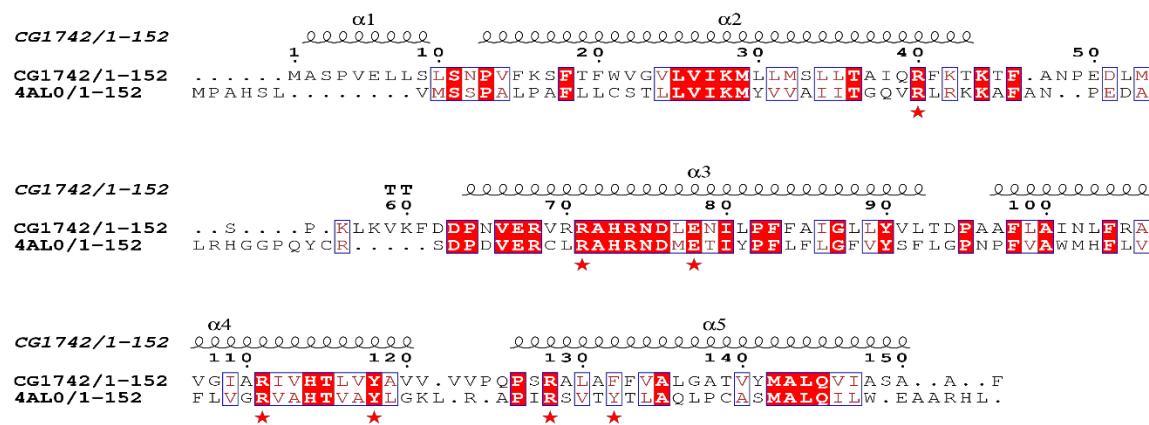


A.

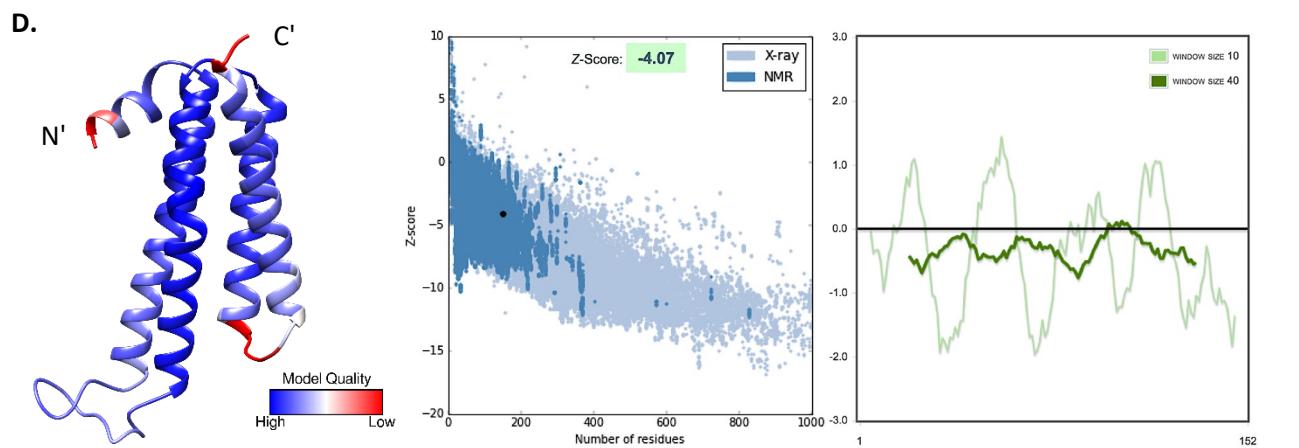


B.

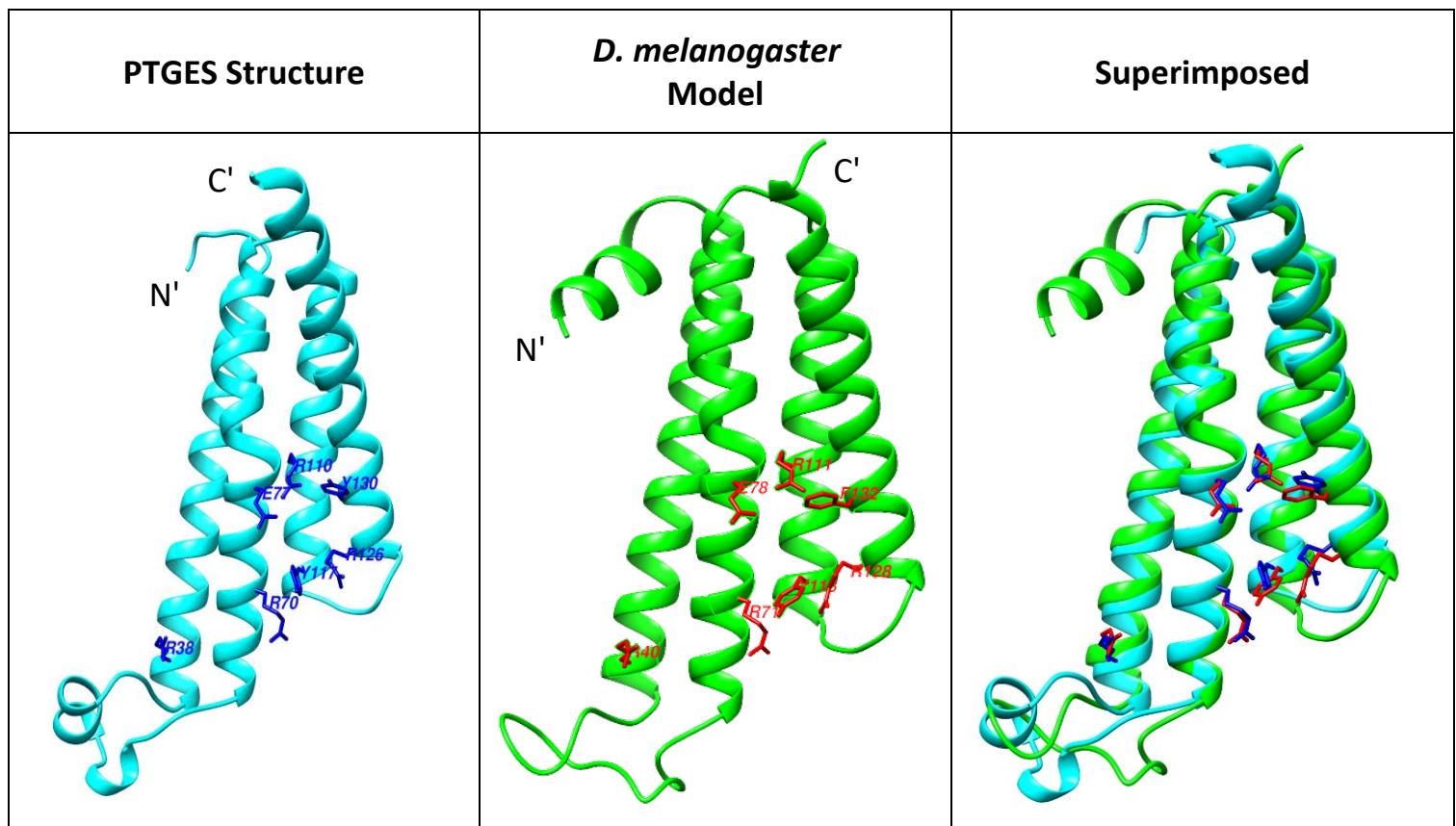


C.

CG1742/1-152	1 - - - - - M A S P V E L L S L S N P V F K S F T F W V G V L V I K M L L M S S L L T A I Q R F K T K T F - A N P E D L M - - S - - - P - K L K V 59
4AL0/1-152	1 M P A H S L - - - - - V M S S P A L P A F L L C S T L L V I K M Y V V A I I T G Q V R L R K K A F A N - - P E D A L R H G G P Q Y C R - - - 60
CG1742/1-152	60 K F D D P N V E R V R R A H R N D L E N I L P F F A I G L L Y V L T D P A A F L A I N L F R A V G I A R I V H T L V Y A V V - V V P Q P S R A L A 131
4AL0/1-152	61 - - S D P D V E R C L R A H R N D M E T I Y P F L F L G F V Y S F L G P N P F V A W M H F L V F L V G R V A H T V A Y L G K L - R - A P I R S V T 129
CG1742/1-152	132 F F V A L G A T V Y M A L O V I A S A - - A - - F 152
4AL0/1-152	130 Y T L A Q L P C A S M A L O I L W - E A A R H L - 152



E.



F.	Length (AA)	Domain Architecture (Pfam, range)	Functional Residues (aligned matches in <i>D. melanogaster</i>)	Sequence ID%	Structural Overlap (RMSD)
Prostaglandin-E-synthase (PTGES, NP_004869.1, PDB: 4AL0)	152	MAPEG (PF01124) 16-146	R38, E77, R70, R110, Y117, R126, Y130	34% ID 53% SIM	1.015 Å
MGST-like (CG1742, NP_524696.1)	152	MAPEG (PF01124) 18-148	R40, E78, R71, R111, Y118, R128, F132		

S1 Fig. Sequence and structural details of the modeled fly PTGES candidate. A. Domain architecture of PTGES and CG1742 and known/predicted functional residues B. Pairwise alignment of CG1742 and 4AL0 generated from structural superposition showing shared secondary structure elements and known/predicted functional residues (marked with a red asterisk) C. Pairwise alignment of CG1742 and 4AL0 generated from structural superposition with conserved residues highlighted using the physicochemical color scheme (CLUSTALX) D. Validation of the CG1742 model: ProQ2 quality score mapped to a 3D model of CG1742 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. PTGES (4AL0, cyan-blue) superimposed on the predicted structure of CG1742 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by PTGES and potential *D. melanogaster* ortholog CG1742.