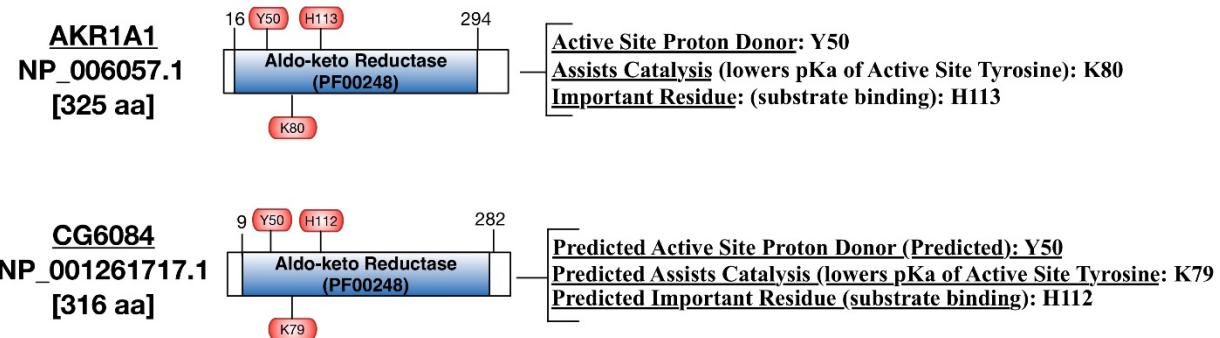
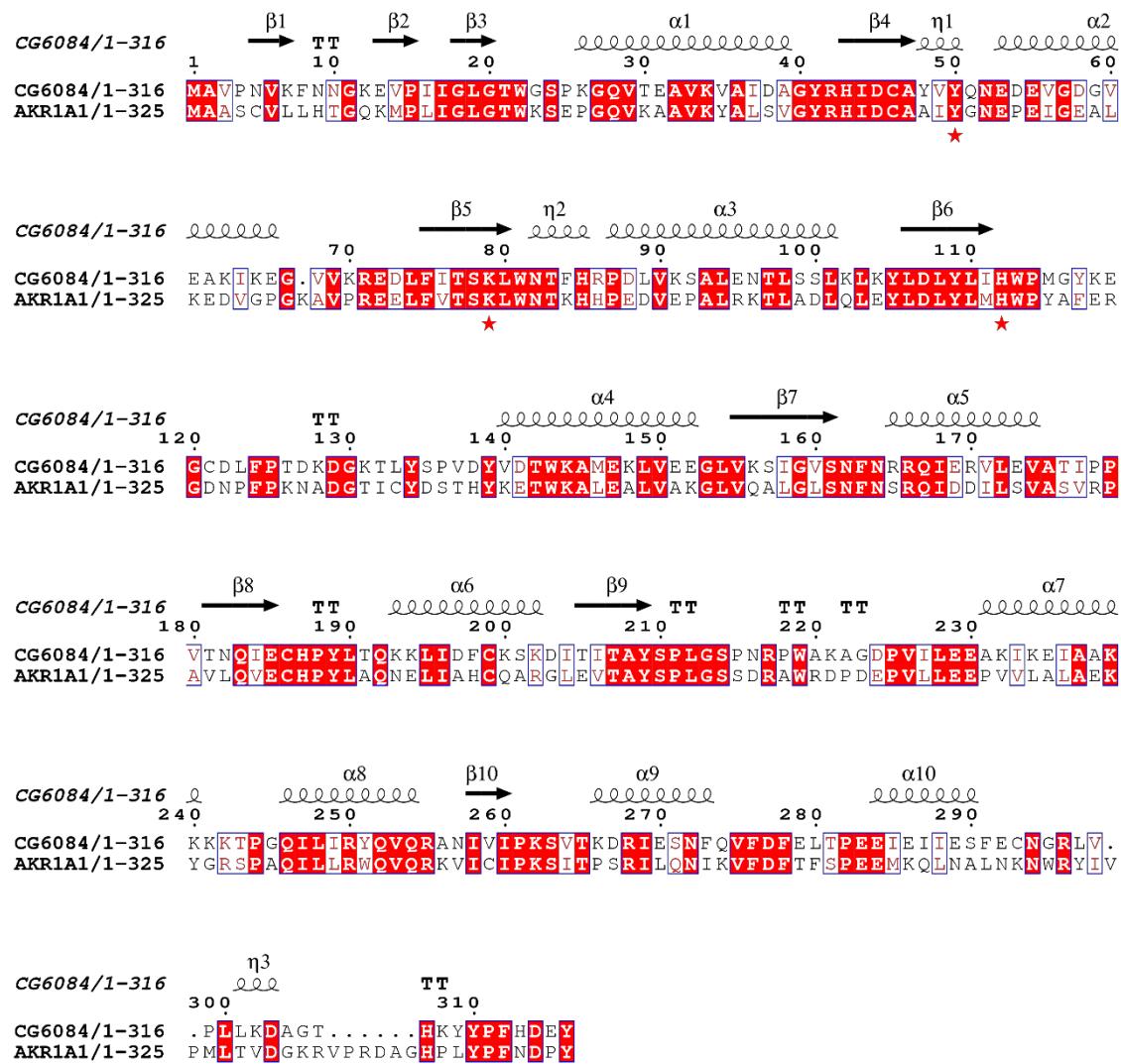


A.



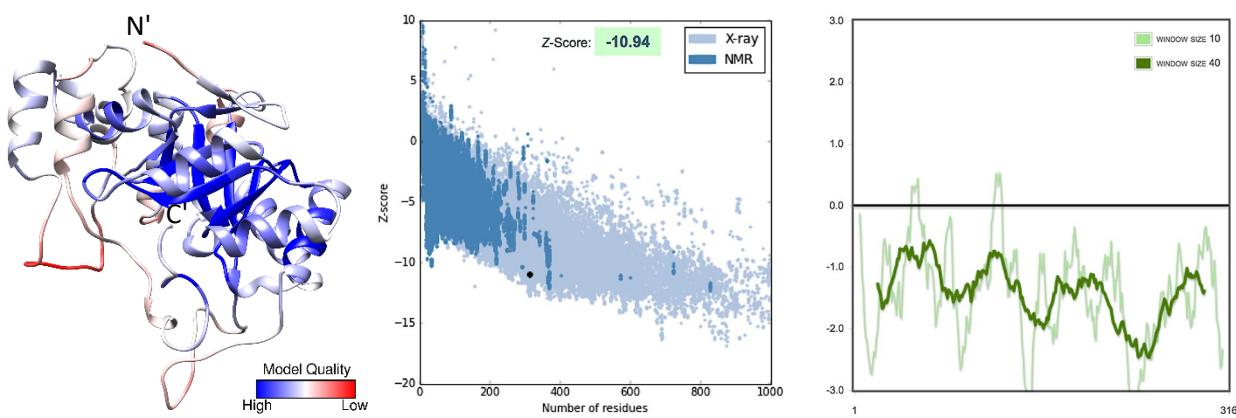
B.



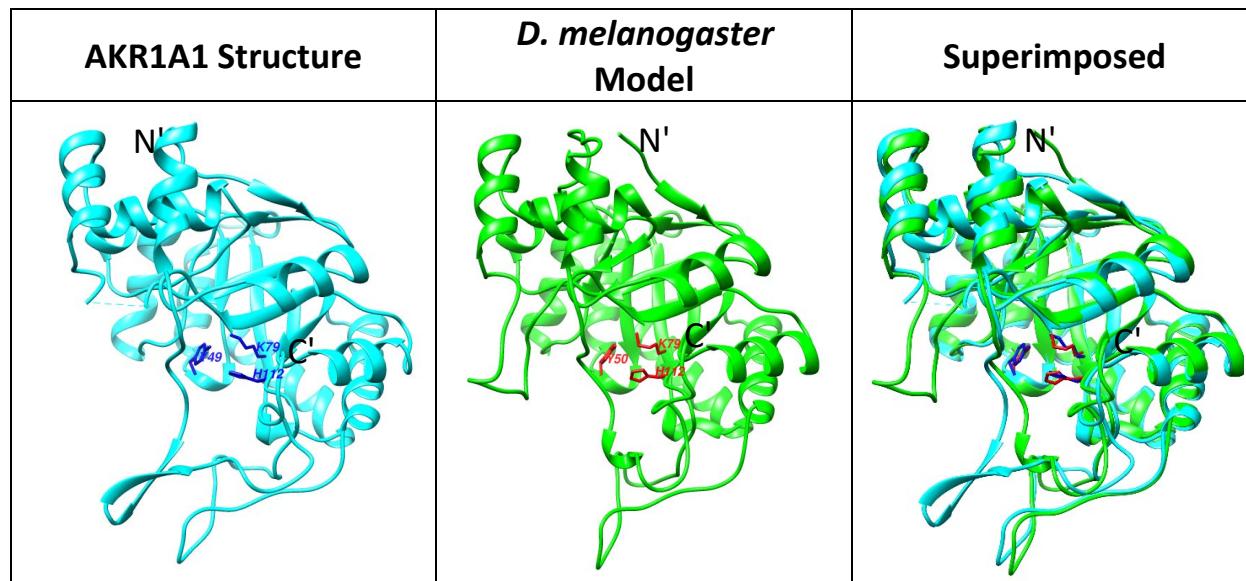
C.

<i>CG6084</i> /1-316 2ALR/1-324	1 - - MAVP N V K F N NG K E V P I I G L G T W G S P K G Q V T E A V K V A I D A G Y R H I D C A Y V V Y Q N E D E V G D G V E A K I - - - KEG 6 7
	1 AA - - S C V L L H T G Q K M P L I G L G T W K S E P G Q V K A A V K Y AL S V G Y R H I D C A A I Y G N E P E I G E A L K E D V G P G - - K 6 7
<i>CG6084</i> /1-316 2ALR/1-324	68 V V V K R E D L F I T S K L W N T F H R P D L V K S A E N T L S S L K L K Y L D L Y L I H W P M G Y K E G C D L F P T D K D G K T L Y S P V D Y 1 39
	68 A V P F R E E L F V T S K L W N T K H H P E D V E P A L R K T L A D L Q L E Y L D Y L M H W P Y A F E R G D N P F P K N A D G T I C Y D S T H Y 1 39
<i>CG6084</i> /1-316 2ALR/1-324	140 V D T W K A M E K L V E E G L V K S I G V S N F N R R Q I E R V L E A V T P V T N Q I E C H P Y L T Q K K L I D F C K S K D I I T I T A Y S P 2 11
	140 K E T W K A L E A L V A K G L V Q A L G L S N F N R S Q I I D D I I L S V A S V R P A V L Q V E C H P Y L A Q N E L I A H C Q A R G L E V T A Y S P211
<i>CG6084</i> /1-316 2ALR/1-324	212 L G - - - - - S P N R P W A K G D P V I L E E A K I K E I A A K K K K T P G Q I I L I R Y Q V Q R A N I I V I P K S V T K D R I E S 2 71
	212 L G S S D R A W R D P E P - - - - V L L E E P V V V L A A E K Y G R S P A Q I L L R W Q Q R K V I C I P K S I T P S R I L Q 3 71
<i>CG6084</i> /1-316 2ALR/1-324	272 N F Q V F D E L T P E E I I I I E S F E C N G R L V P L - - - - - L N Q Y G G H P H H P F E K D E Y 3 16
	272 N I K V F D F T F S P E E M K Q L N A N K N W R Y I V P M L T V D G K R V P R D A G H P L Y P F N D -PY 3 24

D.



E.



F.	Length (AA)	Domain Architecture (Pfam, range)	Functional Residues (aligned matches in <i>D. melanogaster</i>)	Sequence ID%	Structural Overlap (RMSD)
Prostacyclin F synthase (AKR1B1, NP_001619.1)	316	Aldo/keto reductase family (PF00248) 4-289	Y49, K78, H111	48% ID 62% SIM	0.847 Å
Uncharacterized protein (CG6084, NP_648484.1)	316	Aldo/keto reductase family (PF00248) 9-282	Y50, K79, H112		

S3 Fig. Sequence and structural details of the modeled fly Prostacyclin F synthase candidate. A. Domain architecture of AKR1A1 and CG6084 and known/predicted functional residues B. Pairwise alignment of CG6084 and 2ALR generated from structural superposition showing shared secondary structure elements and known/predicted functional residues (marked with a red asterisk) C. Pairwise alignment of CG6084 and 2ALR generated from structural superposition with conserved residues highlighted using the physiochemical color scheme (CLUSTALX) D. Validation of the CG6084 model: ProQ2 quality score mapped to a 3D model of CG6084 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. AKR1A1 (2ALR, cyan-blue) superimposed on the predicted structure of CG6084 (green-red). RMSD: 0.847 Å with potential matches for conserved functional residues highlighted F. Summary of features shared by Prostacyclin F synthase and potential *D. melanogaster* ortholog CG6084.