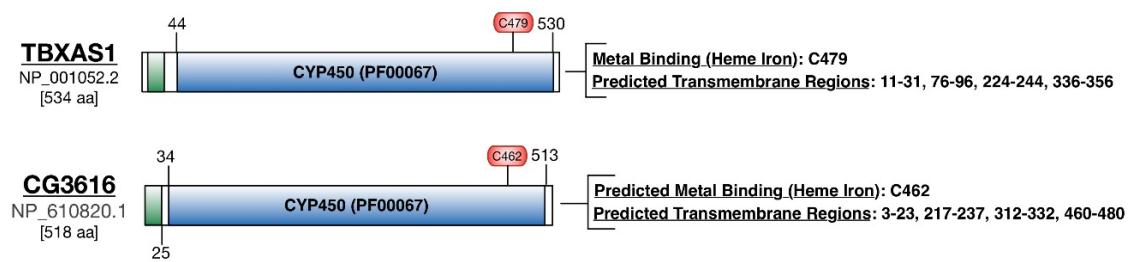
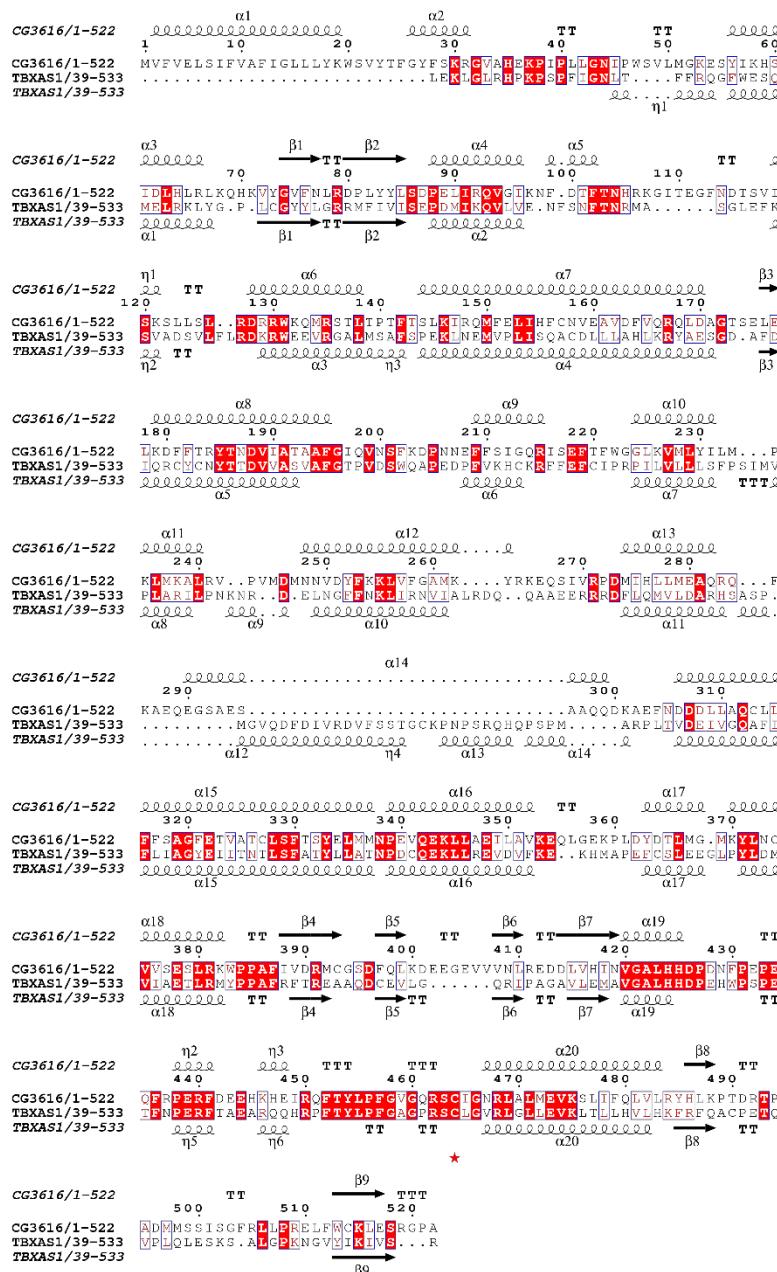
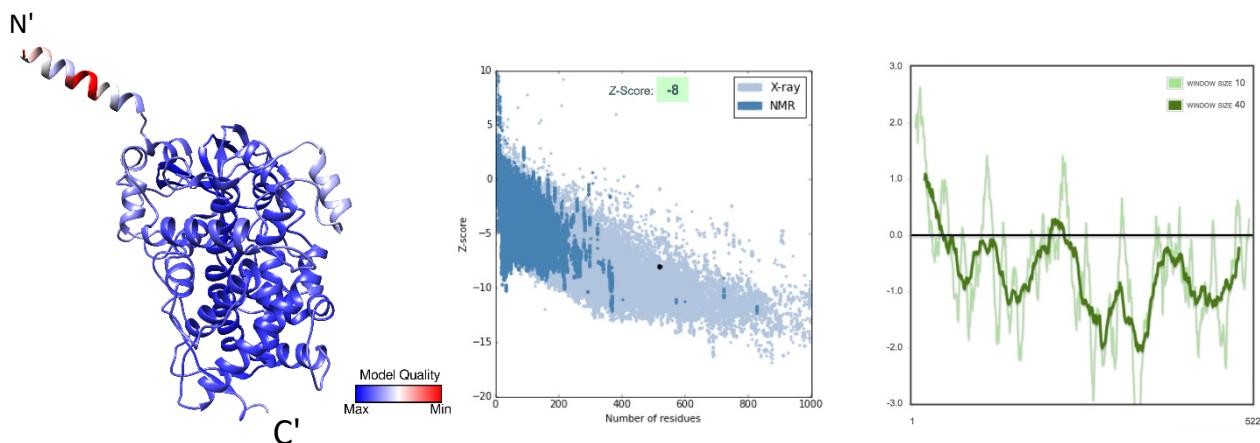


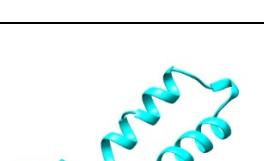
A.**B.**

C.

D.



E.

TBXAS1 Model	<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)
Thromboxane A synthase (TBXAS1, NP_001052.2, PDB: N/A (modeled))	534	Cytochrome P450 domain (PF00067) 44-530	C479	27% ID 45% SIM	0.699 Å
Cytochrome P450-9c1 (CG3616, NP_610820.1)	518	Cytochrome P450 domain (PF00067) 34-513	C462		

S13 Fig. Sequence and structural details of the modeled fly TBXAS1 candidate. A. Domain architecture of TBXAS1 and CG3616 and known/predicted functional residues B. Pairwise alignment of CG3616 and the modeled human TBXAS1 generated from structural superposition showing shared secondary structure elements and known/predicted functional residues (marked with a red asterisk) C. Pairwise alignment of CG3616 and the modeled human TBXAS1 generated from structural superposition with conserved residues highlighted using the physiochemical color scheme (CLUSTALX) D. Validation of the CG3616 model: ProQ2 quality score mapped to a 3D model of CG3616 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. TBXAS1 (model, cyan-blue) superimposed on the predicted structure of CG3616 (green-red) F. Summary of features shared by TBXAS1 and potential *D. melanogaster* ortholog CG3616.