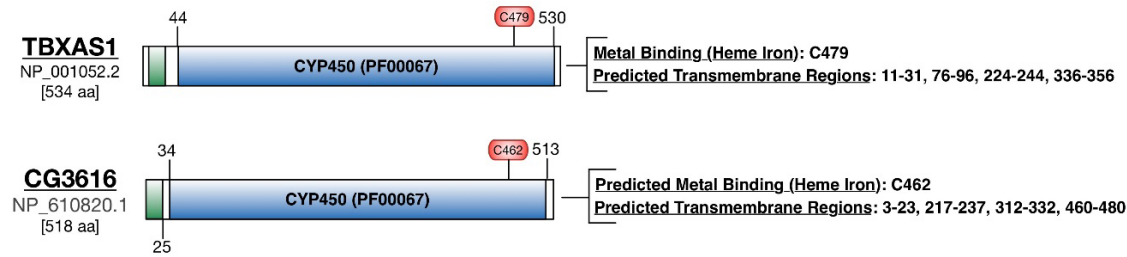
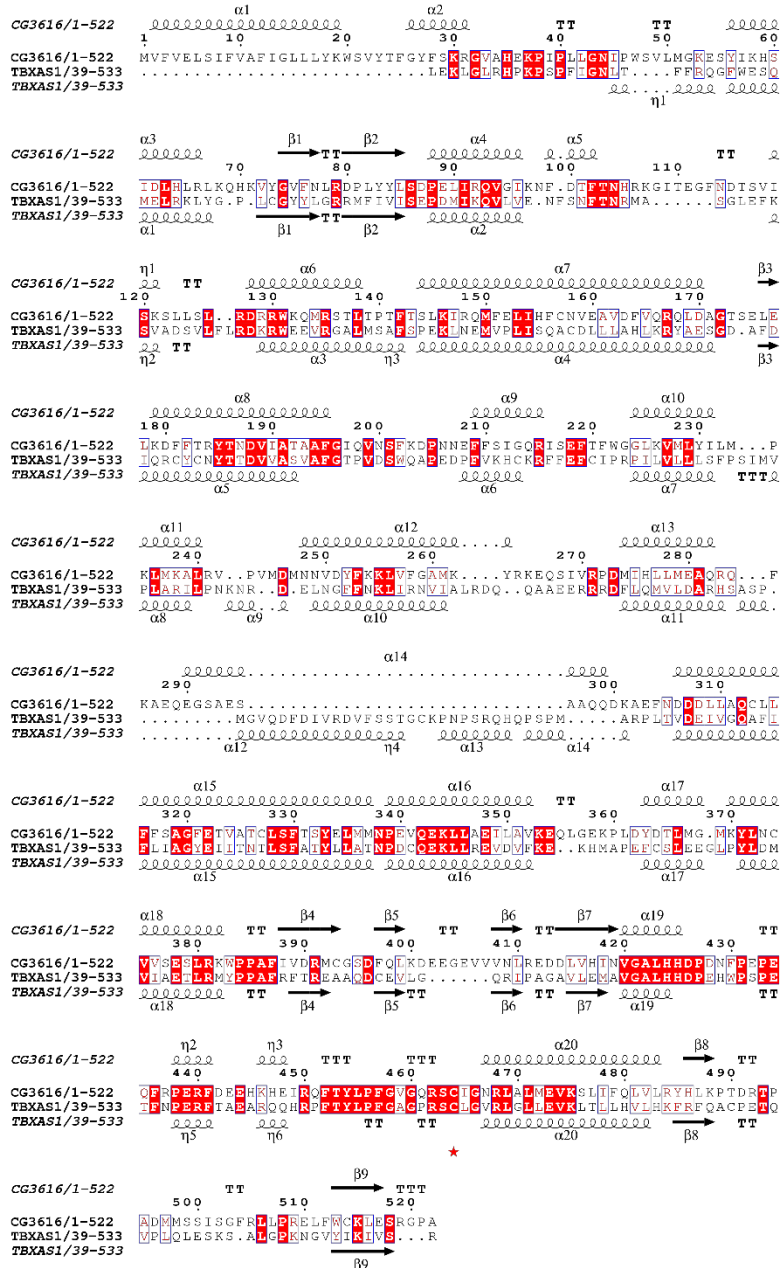


A.



B.



C.

CG3616/1-522 1 M V F V E L S I F V A F I G L L L Y K W S V Y T F G Y F S R G V A H E K P I P L L G N I P W S V L M G K E S Y I K H S I D L H L R L K Q H K V Y 73  
TBXAS1/39-533 39 - - - - - L E L G L R H P K P S P F I G N L T - - - - F F R G G F W E S Q M E L R K L Y G - P - L C 78

CG3616/1-522 74 G V F N L H D P L Y Y L S D P E L I R Q V G I K N F - D T F T N H R K G I T E G F N D T S V I S K S L L S L - - R D R R W K Q M R S T L T P T F T 143  
TBXAS1/39-533 79 G Y Y L G H R M F I V I S E P D M I K Q V L V E - N F S N F T N R M A - - - - - S G L E F K S V A D S V L F L R D K R W E E V R G A L M S A F S 144

CG3616/1-522 144 S L K I R M F E L I H F C N V E A V D F V Q R Q L D A G T S E L E L K D F F T R Y T N D V I A T A A F G I Q V N S F K D P N N E F F S I G Q R I 216  
TBXAS1/39-533 145 P E K L N E M V P L I S Q A C D L L L A H L K R Y A E S G D - A F D I Q R C Y C N Y T T D V V A S V A F G T P V D S W Q A P E D P F V K H C K R F 216

CG3616/1-522 217 S E F T F W G G L K V M L Y I I L M - - - P K L M K A L R V - - P V M D M N V D Y F K K L V F G A M K - - - - Y R E Q S I V R P D M I H L L M E 280  
TBXAS1/39-533 217 F E F C I P R P I L V L L L S F P S I M V P L A R I L P N K N R - - - D - E L N G F F N K L I R N V I A L R D Q - - Q A A E E R R R F L Q M V L F 284

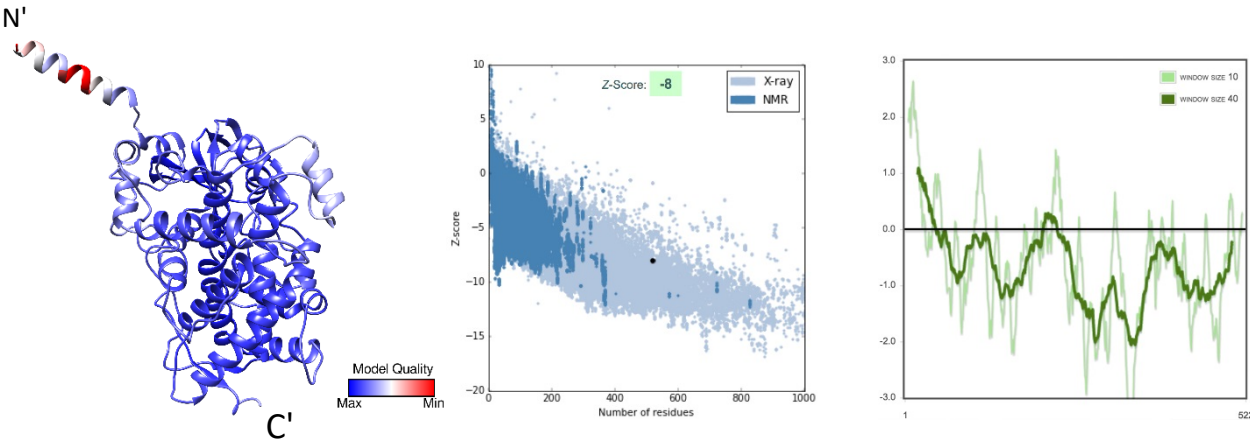
CG3616/1-522 281 A Q R Q - - - F K A E Q E G S A E S - - - - - M G V Q D F D I V R D V F S S T G C K P N R S R Q H Q P S P M - - - - - A A Q Q D K A E F N D D L L A Q C L L F F S A G 320  
TBXAS1/39-533 285 A R H S A S P - - - - - M G V Q D F D I V R D V F S S T G C K P N R S R Q H Q P S P M - - - - - A R P L T V D E I V G Q A F I F L I A G 342

CG3616/1-522 321 F E T V A T C L S F T S Y E L M M N P E V Q E K L L A E I L A V K E Q L G E K P L D Y D T L M G - M K Y L N C V V S E S L K W P P A F I V D M 392  
TBXAS1/39-533 343 Y E I I T N T L S F A T Y L L A T N P D C Q E K L L R E V D V F K E - - K H M A P E F C S L E E G L P Y L D M V I A E T L M Y P P A F R F T E 413

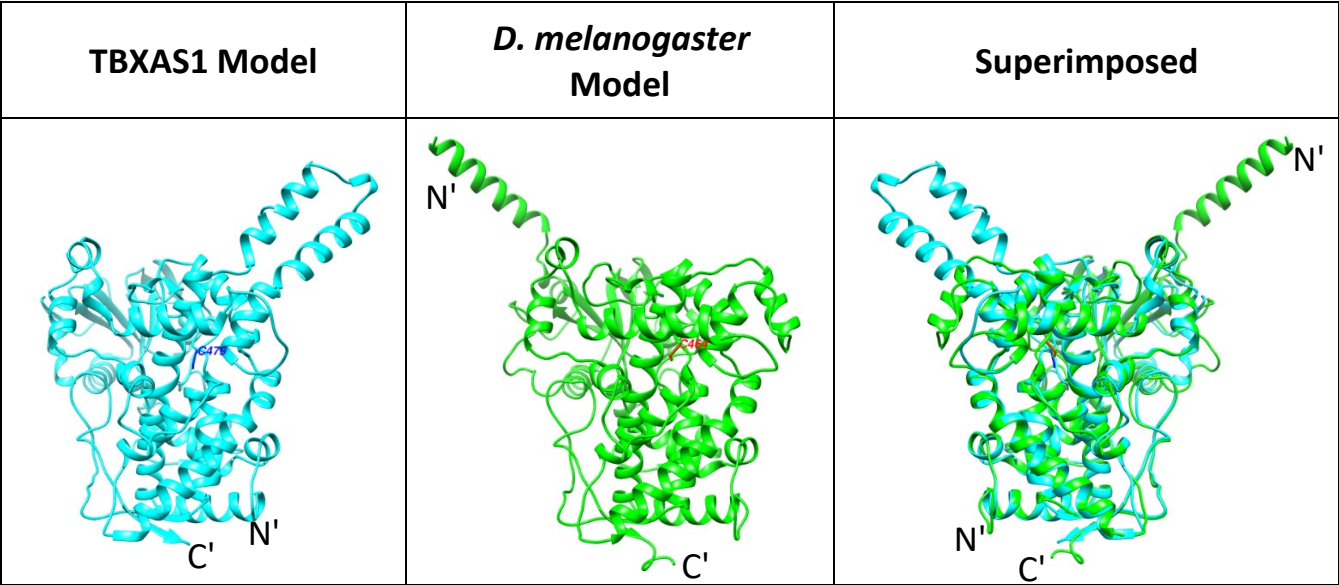
CG3616/1-522 393 C G S D F Q L K D E E G E V V N L R E D D L V H I N V G A L H D P D N F R P E Q F R P E R F D E E H K H E I R Q F T Y L P F G V G Q R S C I 465  
TBXAS1/39-533 414 A A Q D C E V L G - - - - - Q R I P A G A V L E M A V G A L H D P E H W P S P E T F N P E R F T A E A R Q Q H R P F T Y L P F G A G P R S C L 480

CG3616/1-522 466 G N R L A L M E V K S L I F Q L V L R Y H L K P T D R T P A D M M S S I S G F R L L P R E L F W C K L E R G P A 522  
TBXAS1/39-533 481 G V R L G L L E V K L T L L H V L H K E R F Q A C P E T Q V P L Q L E S K S - A L G P A N G V Y I K I V S - - - R 533

D.



E.



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.