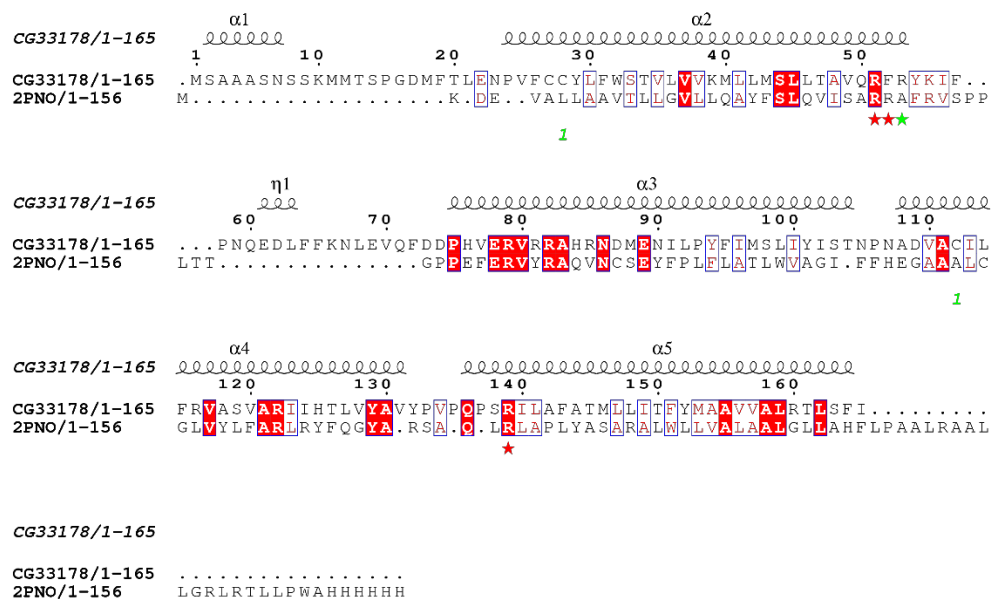




B.



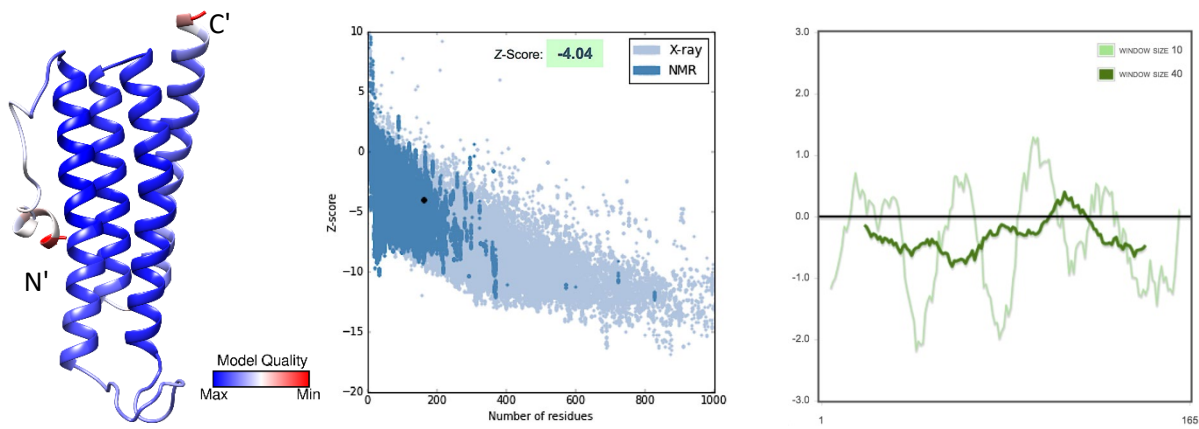
C.

CG33178/1-165 1 -MSAAASNSSMMTTSFGDMFTLLENRYFCCYLFWSTVLVYVKMLLMSLLTAVQFRKKIF-----INQEDLFFKNLEVQ71
2PNO/1-156 1 M-----K-DE-----VALLAAVTLGLVLLQAYFLQVYLAIRAFVSPPLT-----148

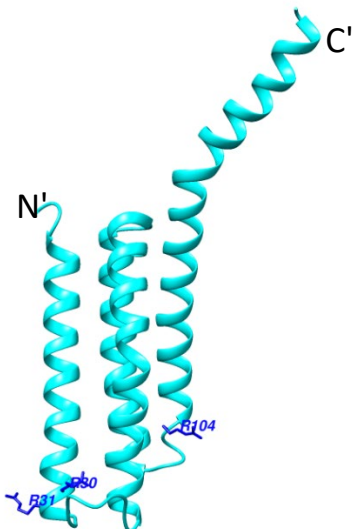
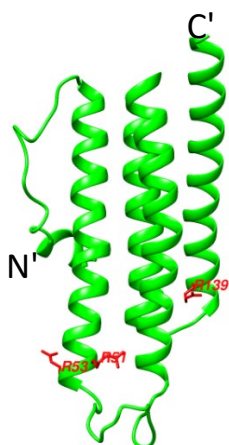
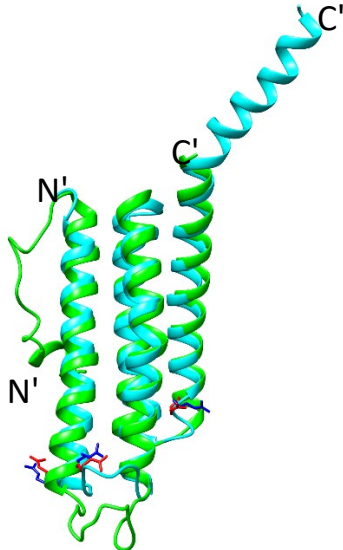
CG33178/1-165 72 FDDPHVYVYRAHRMDMENLIFYMSLTYISTNNADVACGLFRVASVATITLTVYAVYVPVQPSILAFATML149
2PNO/1-156 42 -GPPEFERYVRAQVCSGYFLFLFATLWVAGI-FHEHSAALCGLVYLFAELRMFQGYA-RSA-Q-L-LAPLYASAR113

CG33178/1-165 149 ITFYMAAVVALRTLSFIFLPAALRAALLRLRTLTPWAHHHHHHH 165
2PNO/1-156 141 ALWLLVALAALQLLAHFLPAALRAALLRLRTLTPWAHHHHHHH 165

D.



E.

LTC4S 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)
Leukotriene C4 synthase (LTC4S, NP_665874.1, PDB: 2PNO)	150	MAPEG domain (PF01124) 8-131	R30, R31 and R104	18% ID 31% SIM	1.257 Å
Uncharacterized protein (CG33178, NP_788904.1)	165	MAPEG domain (PF01124) 29-159	R51, R53 and R139		

S17 Fig. Sequence and structural details of the modeled fly LTC4S candidate. A. Domain architecture of LTCS4 and CG33178 and known/predicted functional residues B. Pairwise alignment of CG33178 and 2PNO generated from structural superposition showing shared secondary structure elements and known/predicted functional residues (marked with red asterisks; the green asterisk denotes the analog for R31) C. Pairwise alignment of CG33178 and 2PNO generated from structural superposition with conserved residues highlighted using the physiochemical color scheme (CLUSTALX) D. Validation of the CG33178 model: ProQ2 quality score mapped to a 3D model of CG33178 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. LTCS4 (2PNO, cyan-blue) superimposed on the predicted structure of CG33178 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by LTCS4 and potential *D. melanogaster* ortholog CG33178.