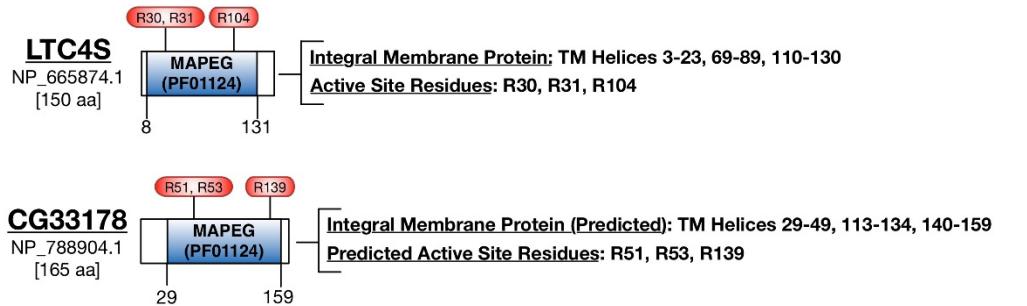
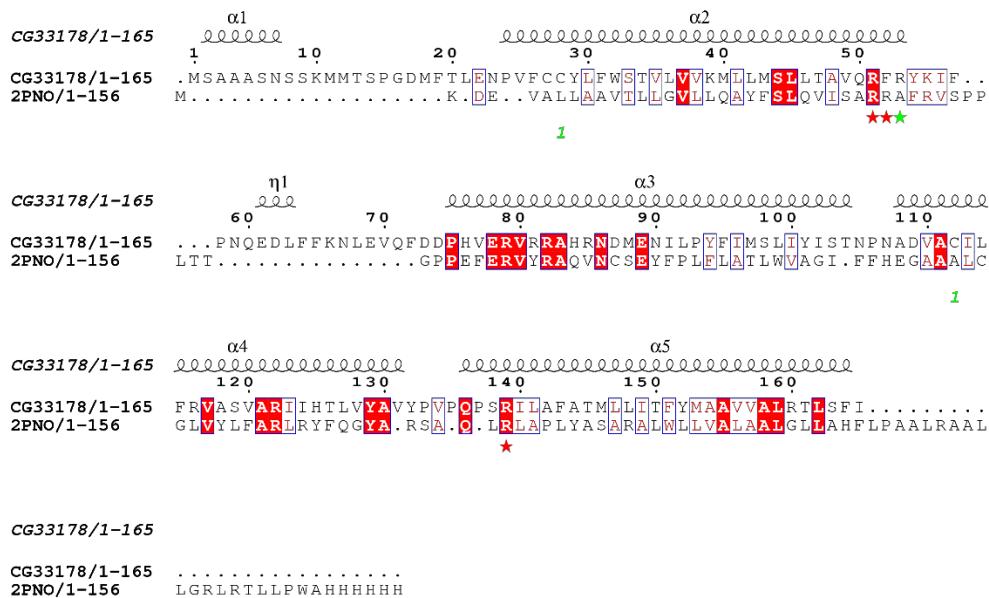


A.



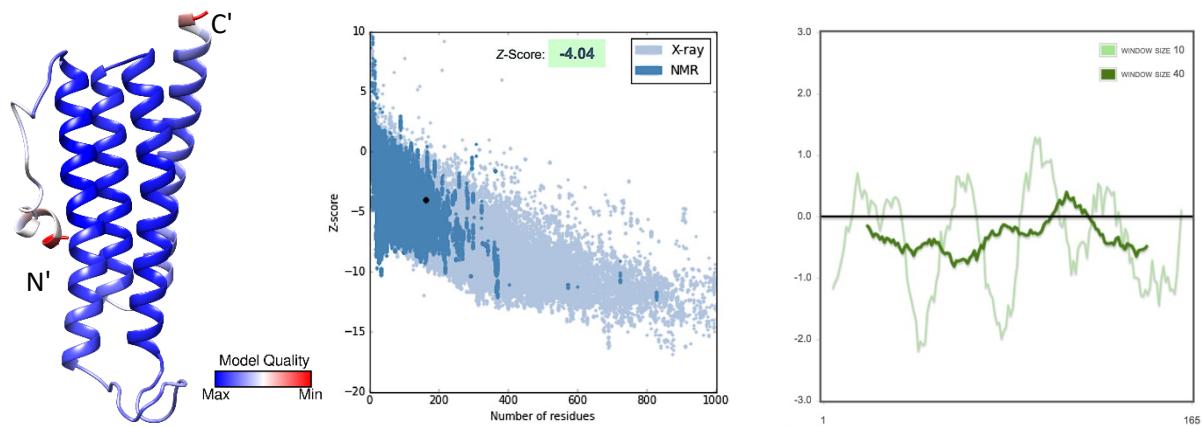
B.



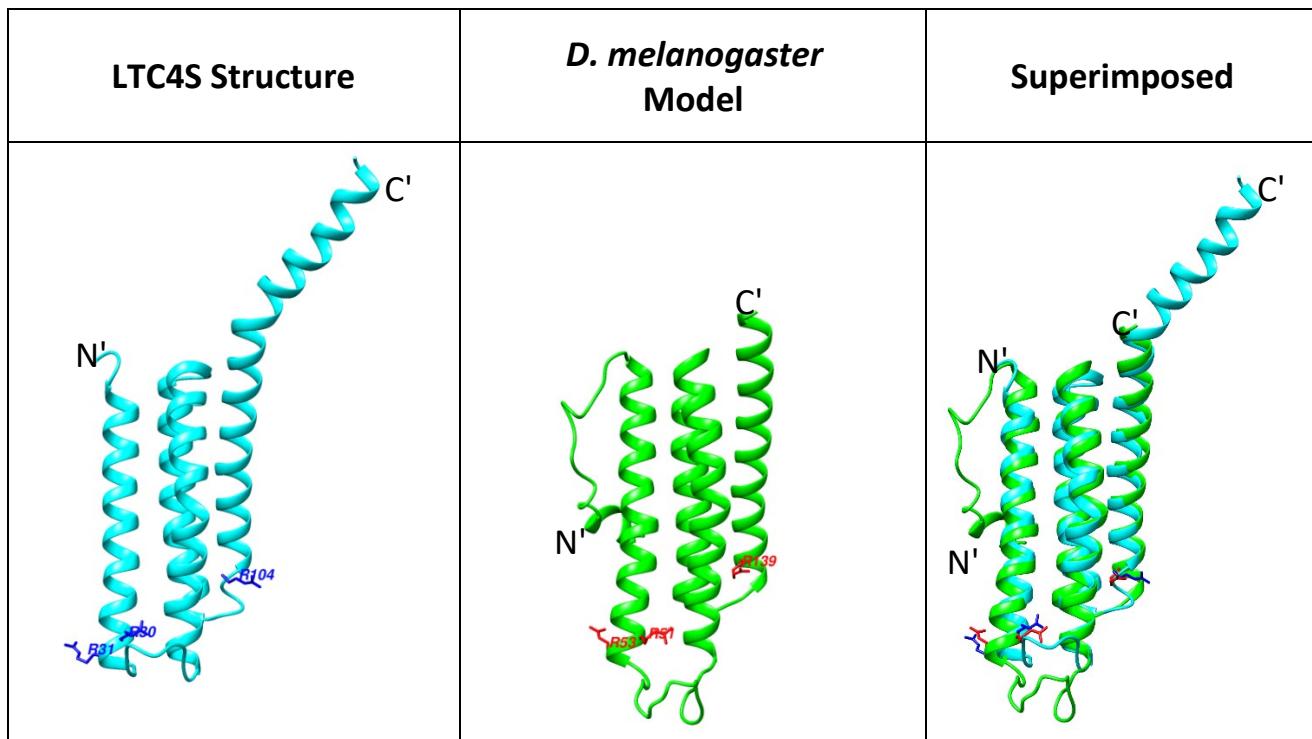
C.

<i>CG33178/1-165</i>	1 -MSAAASNSKKMNTSPGDMFTLENPVFCYLFWSTLVVVKMLMSLLTAVQRFRYKIF-----PNQEDLFFKNLEVQ 71
<i>2PNO/1-156</i>	1 M-----K-DE---VALLAAVITLGVLQLAYFSLQVI SARAFRVSPPLT-----41
<i>CG33178/1-165</i>	72 FDDPHVERVRFAHRIDMENILPYFIMSLIVISTNPNADVCACILFRVASVARIIHTLVYAVYVPVPOPSRILAFATML 148
<i>2PNO/1-156</i>	72 PDDPEFVERVYFAQVNCSEYFPFLATLWVAGI-FFHEGAAALCGLVYL FABRLYFQGYA-RSA-D-LBLAPLYASAR 113
<i>CG33178/1-165</i>	149 ITFYMAAVALRTLSFI-----165
<i>2PNO/1-156</i>	149 ALWLLVALAALGGLAHFLPAALRAALGRLRTLWLWAHHHHHHH 156

**D.**



**E.**



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		
Uncharacterized protein (CG33178, NP_788904.1)	165	MAPEG domain (PF01124) 29-159	R51, R53 and R139	18% ID 31% SIM	1.257 Å

**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 physicochemical 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.