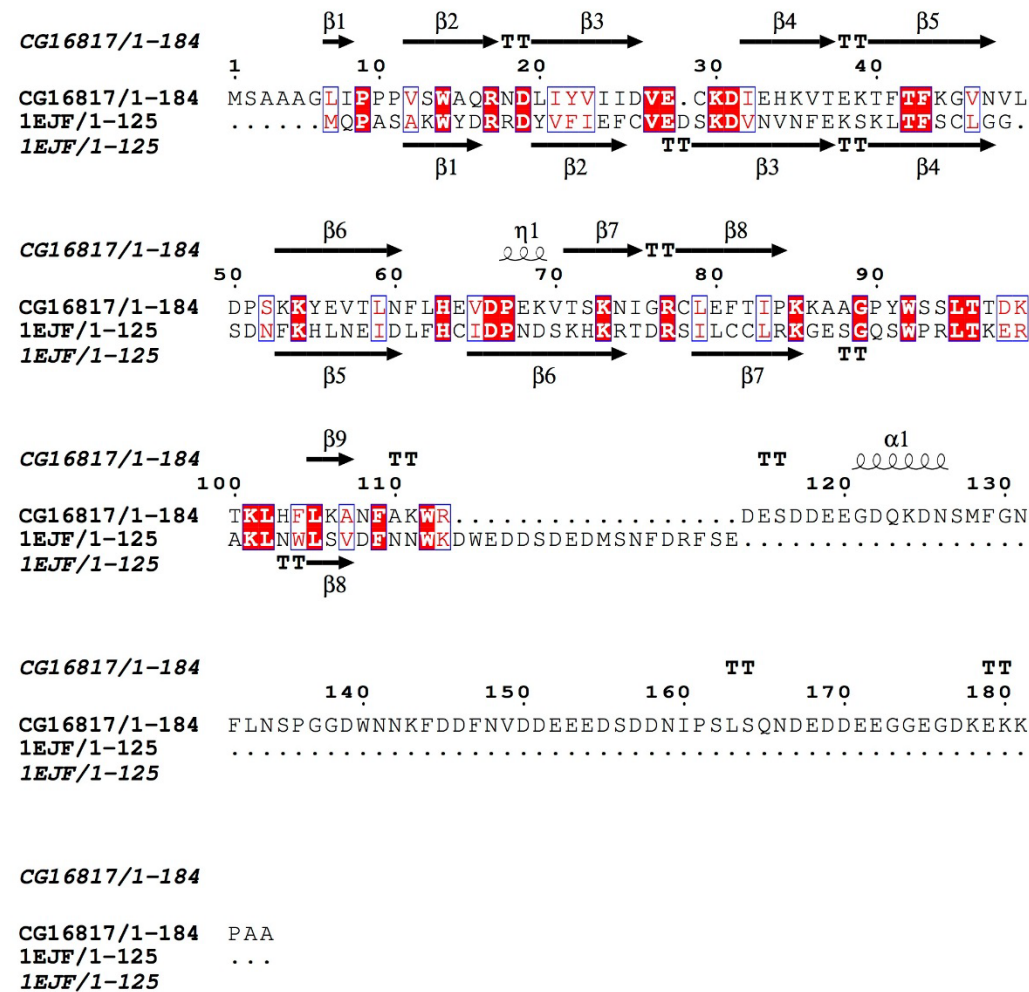


**B.**



**C.**

CG168171-184  
1EJF1-125

1 MSAAAGLIPPPVSWAQRNDLIYVILDVE-CKDIEHKVTEKTFTFKGVNVLDP SKKYEVTLNLFHEVDP EKVTS 72  
1-----MQPASAKWYDRDYVYFIEFCVDSKDVNNVFESKSLTFSC LGG-SDNF KHLNEIDL FHCIDPND SKH 66

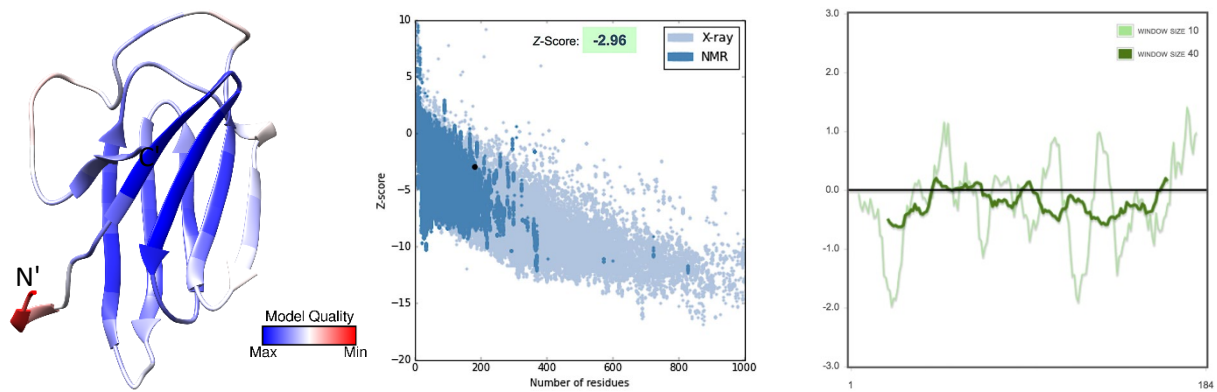
CG168171-184  
1EJF1-125

73 KNIGRCLEFTIPKKAAGPIYWSSLTIDKTKLHFLKANFAKWR-----DES DDEEGDQKDNS 127  
67 KRTDSILCCLRKGESGQSWPRLTKERAKLNWLSVDFNNWKDWEDDSDEDMNSFDRFSE-----125

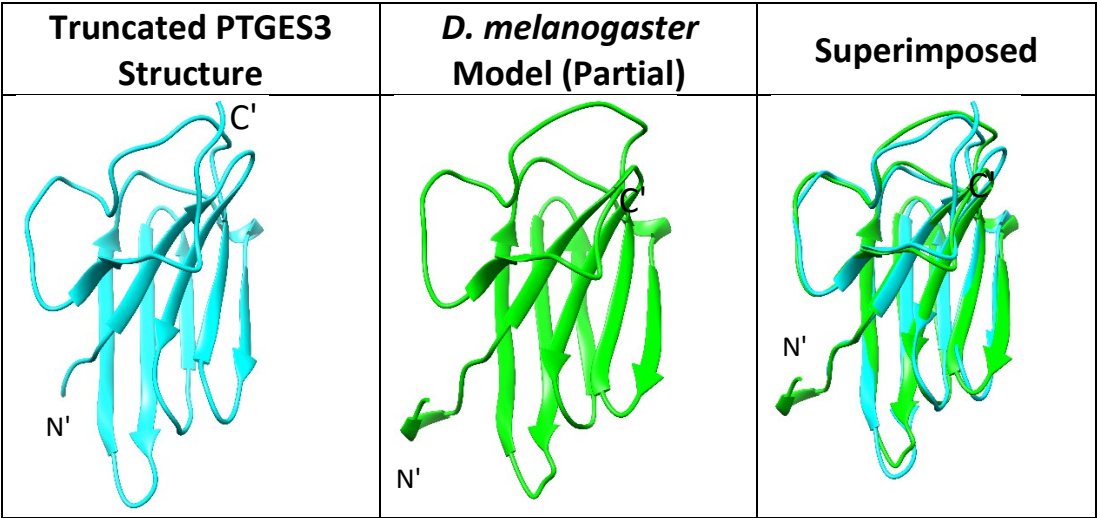
CG168171-184  
1EJF1-125

128 MFGNFLNSPGGDWNKNKFDNFVDDDEEDSDDNIPSLSQNDEDEEGGEGDKEKKPAA 184

D.



E.



F.

	Length (AA)	Domain Architecture (Pfam, range)	Functional Residues (aligned matches in <i>D. melanogaster</i> )	Sequence ID%	Structural Overlap (RMSD)
Prostaglandin E synthase 3 (PTGES3, NP_006592.3, PDB: 1EJF)	160	CS Domain (PF04969) 4-79	N/A	24% ID 40% SIM	0.823 Å
Uncharacterized protein (CG16817, NP_649925.1)	184	CS Domain (PF04969) 10-85	N/A		

**S10 Fig. Sequence and structural details of the modeled fly PTGES3 candidate.** A. Domain architecture of PTGES3 and CG16817 and known/predicted functional residues B. Pairwise alignment of CG16817 and 1EFJ generated from structural superposition showing shared secondary structure elements C. Pairwise alignment of CG16817 and 1EFJ generated from structural superposition with conserved residues highlighted using the physiochemical color scheme (CLUSTALX) D. Validation of the CG16817 model: ProQ2 quality score mapped to a 3D model of CG16817 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. CPA1 (1EFJ, cyan-blue) superimposed on the predicted structure of CG16817 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by PTGES3 and potential *D. melanogaster* ortholog CG16817.