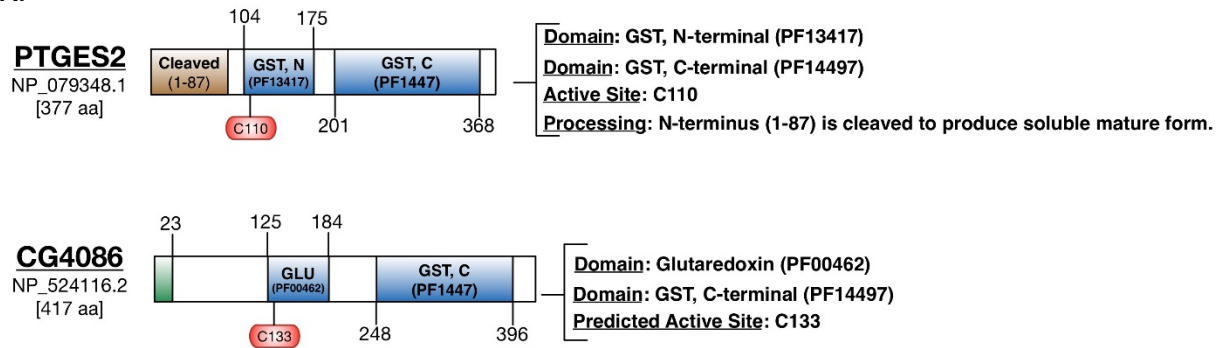
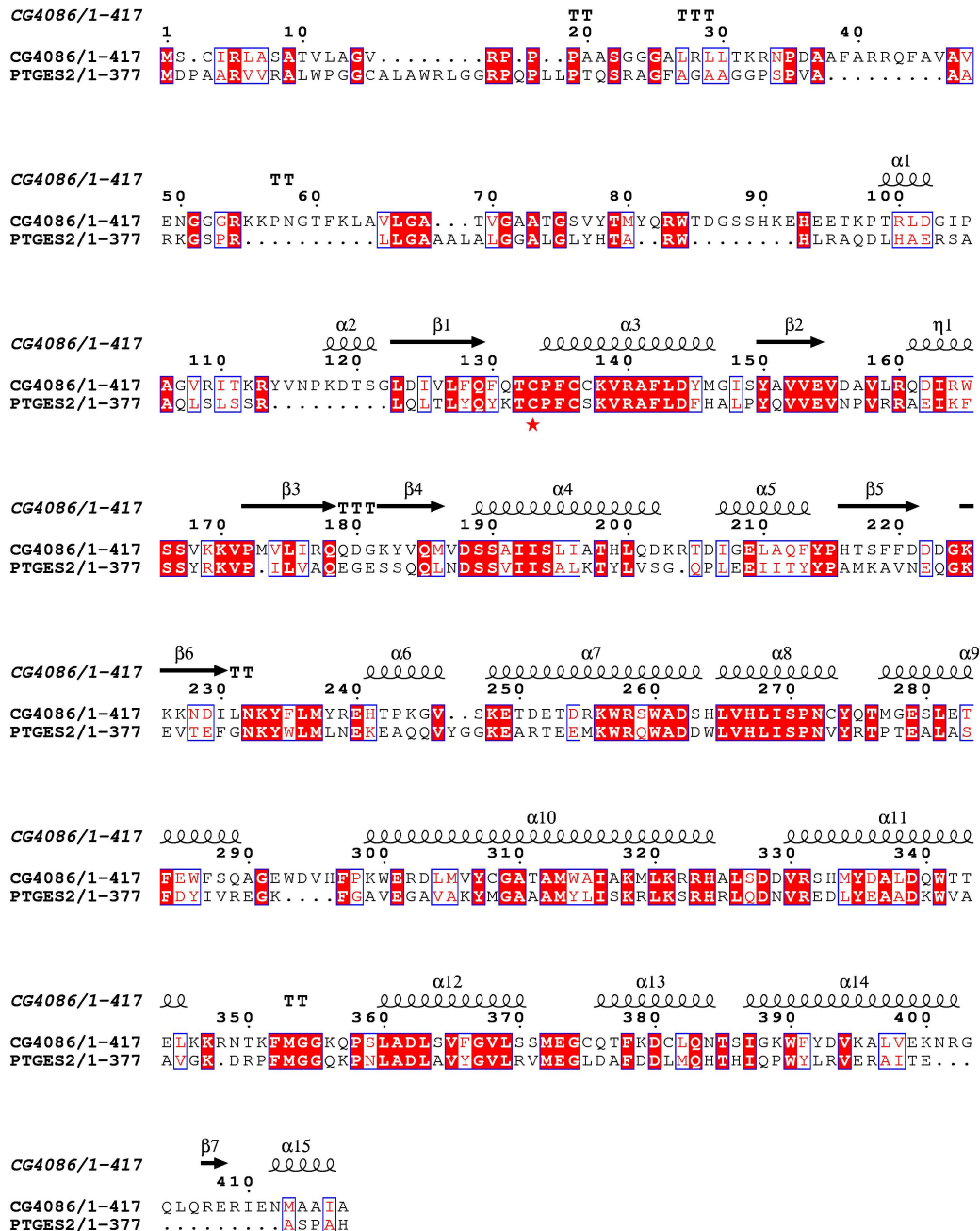


A.



B.



C.

CG4086/1-417 1 -----MSCIRLASATVLAGVRPPPAASGGGALRLLTKRNPDAAFARRQFAVAVENGGGRKKPNQTF 61
1Z9H/88-377 88 ERSAVQLSLSSR----- 99

CG4086/1-417 62 KLAVLGATVGAATGSVYTMQRWTDGSSHKEHEETKPTRLDGIPAGVRITKRYVNPKDTSGLDIVLFQFQTC 134
1Z9H/88-377 100 -----LQLTLYQYKTC 111

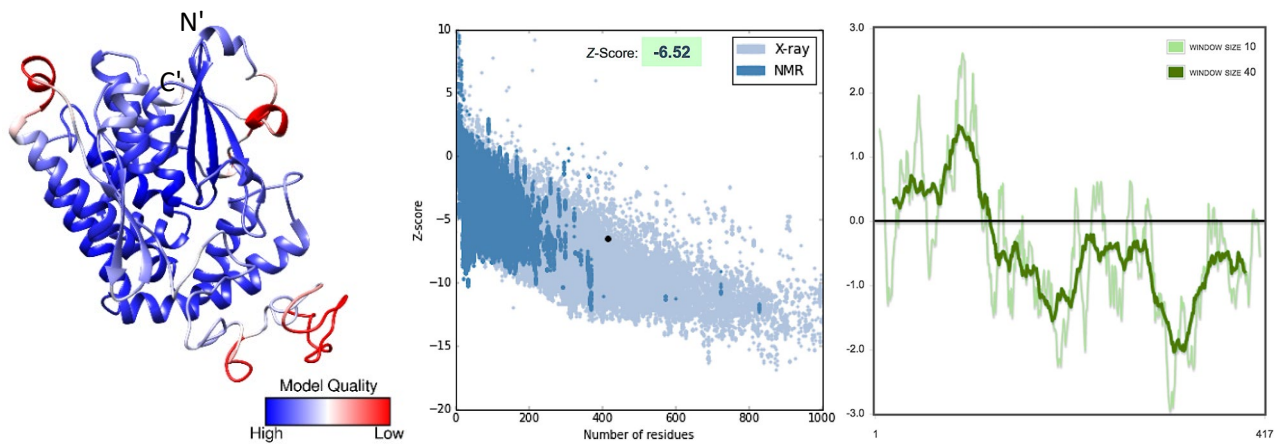
CG4086/1-417 135 FCCKVFAFLDYMGISYAVVEVDAVLQDRIWSSVKKVPMVLIHQDQGYVQMVDSAAIISLIATHLQDKRTDI 207
1Z9H/88-377 112 FCSKVAFLDFHALPYQVVEVNPVLRAEIKFSSYRKVPILVAQE-GESSQQLNDSSVLIISALKTYLVSGQ-PL 182

CG4086/1-417 208 GELAQFYPHTSFFDDDGKKKNDILNKYFLMYREHTPKG-V-SKETDETDRKWRSWADSHLVHLISPNCYQTMG 278
1Z9H/88-377 183 EEIITYYPAMKAVNDQGGKEVTEFGNKYWLMLNEKEAQQVYSGKEARTEEMKWRQWADDWLVHLISPNVYRT 255

CG4086/1-417 279 ESLETFEWFSSQAGEWDVHFPKWERDLMVYCGATAMWAIKMLKRRHALSDDVRSHMYDALDQWTTTELKKRNTK 351
1Z9H/88-377 256 EALASFDYIVREGK----FGAVEGAVAKYMGAAAMYLIKRLKSRHRLQNVREDLYEADKWAAVG-KDRP 323

CG4086/1-417 352 FMGGGKQPSLADLSVFGVLSMMEGCQTFKDCLONTSISGKWFYDVKALVEKN---RQLQRERIENMAAIA 417
1Z9H/88-377 324 FMGGGKQPNLADLAVYGVLRVMEGLDAFDLMOHTHIQPYWLVERAITEASPAH----- 377

D.



E.

PTGES 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)
Prostaglandin-E- synthase 2 (PTGES2, NP_079348.1, PDB: 1Z9H)	377	GST-N3 domain (PF13417) 104-175 GST-C3 (PF14497) 201-368	C110	33% ID 49% SIM	0.814 Å
Suppressor of ref(2)P sterility (CG4086, NP_524116.2)	417	Glutaredoxin domain (PF00462) 125-184 GST-C domain (PF14497) 248-396	C133		

S2 Fig. Sequence and structural details of the modeled fly PTGES2 candidate. A. Domain architecture of PTGES2 and CG4086 and known/predicted functional residues B. Pairwise alignment of CG4086 and 1Z9H generated from structural superposition showing shared secondary structure elements and known/predicted functional residues (marked with a red asterisk) C. Pairwise alignment of CG4086 and 1Z9H generated from structural superposition with conserved residues highlighted using the physiochemical color scheme (CLUSTALX) D. Validation of the CG4086 model: ProQ2 quality score mapped to a 3D model of CG4086 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. Truncated PTGES2 (1Z9H, cyan-blue) superimposed on the predicted structure of CG4086 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by PTGES2 and potential *D. melanogaster* ortholog CG4086.