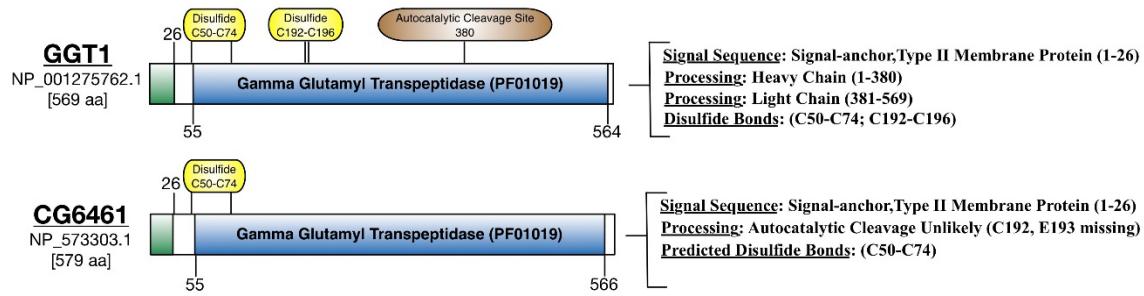


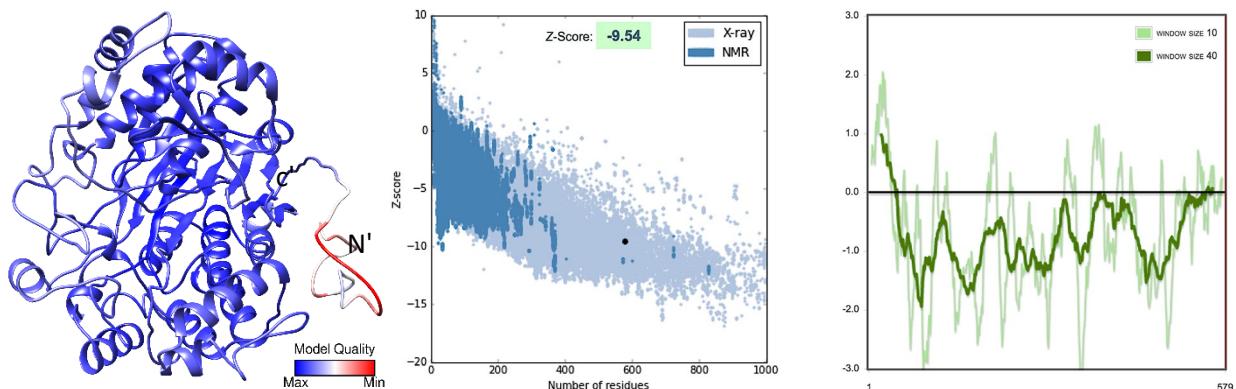
A.



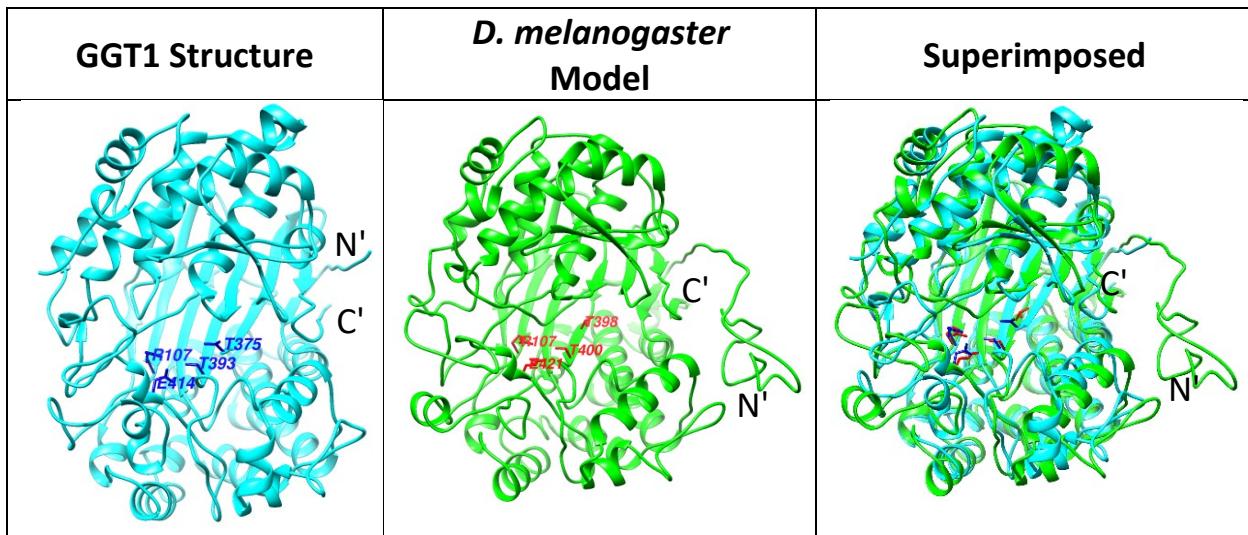
B.

C.

1-579	1 M R I V W S K K L L L W L L A A L M V T A L T L G L V F G L K N R D T L Y I S G A V V S 45
4GDX/33-563	33 - - - - - P D - N H V Y T R A A V A A 45
CG6461/1-579	46 N G I G C A A V G G E M I L T D G G S A V D A A I A T L L C E G L L L P H S M G I G G G F V 90
4GDX/33-563	46 D A K Q C S K I G R D A L R D G G S A V D A A I A A L L C V G L M N A H S M G I G G G L F 90
CG6461/1-579	91 A T I Y T R S S R K V E T V I A R E S A P A A A H K D M F V G E T - - - S - I T G A K S 130
4GDX/33-563	91 L T I Y N S I T T R K A E V I N A R E V A P R L A F A T - M - - F N S S E Q S Q K G G L S 131
CG6461/1-579	131 G A V P G E I L G Y W E M H R R Y G I L P W K R L F E P S I K L A R E G H V V S R Y - L A 174
4GDX/33-563	132 V A V P G E I R G Y E L A H Q R H G R L P W A R L F Q P S I Q L A R Q G F P V G - K C L A 175
CG6461/1-579	175 A A I Q S K L D N I K A D P G L S A V F L N A T G D P H I E G D Y M K R P A L A D T L E R 219
4GDX/33-563	176 A A L E N X A R T V I E Q Q P V I C E V F C R - D R K V L R E G E R L T L P Q L A D T Y E T 219
CG6461/1-579	220 I A E N G A K E F Y D G G E T G R K F V E D I Q K M G G I T E C D L R D Y T V R W E - S 263
4GDX/33-563	220 L A I E Q A Q A F Y N - G S L T A Q I V K D I Q A A G G I V T A E D L N N Y T R A E L I E H 263
CG6461/1-579	264 D G H V S A H V S G T Y T L Y S T P M P S S G P V L A F I L N L M A D L Y T - - - D N - - 303
4GDX/33-563	264 P L N I S L G - - D A V L Y M P S A P L S G P V L A L I L N L K G Y N F S R E V E S 305
CG6461/1-579	304 - - - E P I Y W Q R V V E A F K H A Y G Q F T N L G D M Y A D P V S - A A S I N A - T - L 342
4GDX/33-563	306 P E Q K G U T Y H R I V E E A F R F A Y A K R - T - L - L C D P K F V D - - V - - T E V V 342
CG6461/1-579	343 E E M L K P E F F L E S V R K L I H D N S T S E D Y L Y Y G A N F T V E E D H G T A - - - 383
4GDX/33-563	343 R N M T S E F F A A Q L R A Q I S D D T T H P I S Y Y K - P - - - - - E F Y T 375
CG6461/1-579	384 - H M - N V L A T N G D A V S I T S T I N N Y F G S K V A S T Q T G I I L N D E M D D F S 426
4GDX/33-563	376 A H - L S V V A E D G S A V S A T S T I N L Y F G S K V R S P V S G I L F N N E M D D F S 419
CG6461/1-579	427 T P G - V I N G F G V P A S - - - P A N Y I Y P G K R P M S S M S P C I I V D Q 462
4GDX/33-563	420 S P - S I T - - - N E F G V P P S P A N F I Q P G K Q F L S S M C P T I M V - G 454
CG6461/1-579	463 E - G N V R L L V G A A G G T R I T T S V A A V I M K Y L L R K E S L T A A V N N G R L H 506
4GDX/33-563	455 Q D G Q V R M V V G A A G G T Q I T T A T A L A I I Y N L W F G Y D V K R A V E E P R L H 499
CG6461/1-579	507 H O L - A P M R V S Y E Q E V D S S V T D Y L K Q V G H E M Y E E P V G S S F A A V T A I 550
4GDX/33-563	500 N Q L L P N - V T T V E R N I D Q A V T A A L E T R H H T Q I A S T - - F I A V V Q A I 541
CG6461/1-579	551 G A L E - - - Q P E P F Y D R R R I G S A L T L A K T N K M Q H 579
4GDX/33-563	542 V R - - T A Q G W A A A S D S R K G G E P A Q Y - - - - - - - 563

D.

E.



F.

	Length (AA)	Domain Architecture (Pfam, range)	Functional Residues (aligned matches in <i>D. melanogaster</i>)	Sequence ID%	Structural Overlap (RMSD)
Gamma-glutamyltranspeptidase 1 (GGT1, NP_001275762.1, PDB: 4GDX)	569	Gamma-glutamyltranspeptidase (PF01019) 55-564	T381	39% ID 54% SIM	1.126 Å
Gamma-glutamyltranspeptidase (CG6461, NP_573303.1)	579	Gamma-glutamyltranspeptidase (PF01019) 56-566	T382		

S5 Fig. Sequence and structural details of the modeled fly GGT1 candidate. A. Domain architecture of GGT1 and CG6461 and known/predicted functional residues B. Pairwise alignment of CG6461 and 4GDX generated from structural superposition showing shared secondary structure elements and known/predicted functional residues (marked with red asterisks) C. Pairwise alignment of CG6461 and 4GDX generated from structural superposition with conserved residues highlighted using the physicochemical color scheme (CLUSTALX) D. Validation of the CG6461 model: ProQ2 quality score mapped to a 3D model of CG6461 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. GGT1 (4GDX, cyan-blue) superimposed on the predicted structure of CG6461 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by GGT1 and potential *D. melanogaster* ortholog CG6461.

