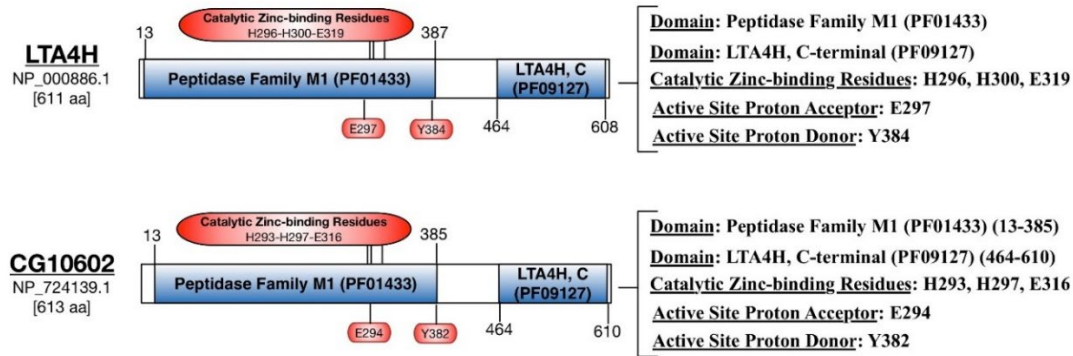
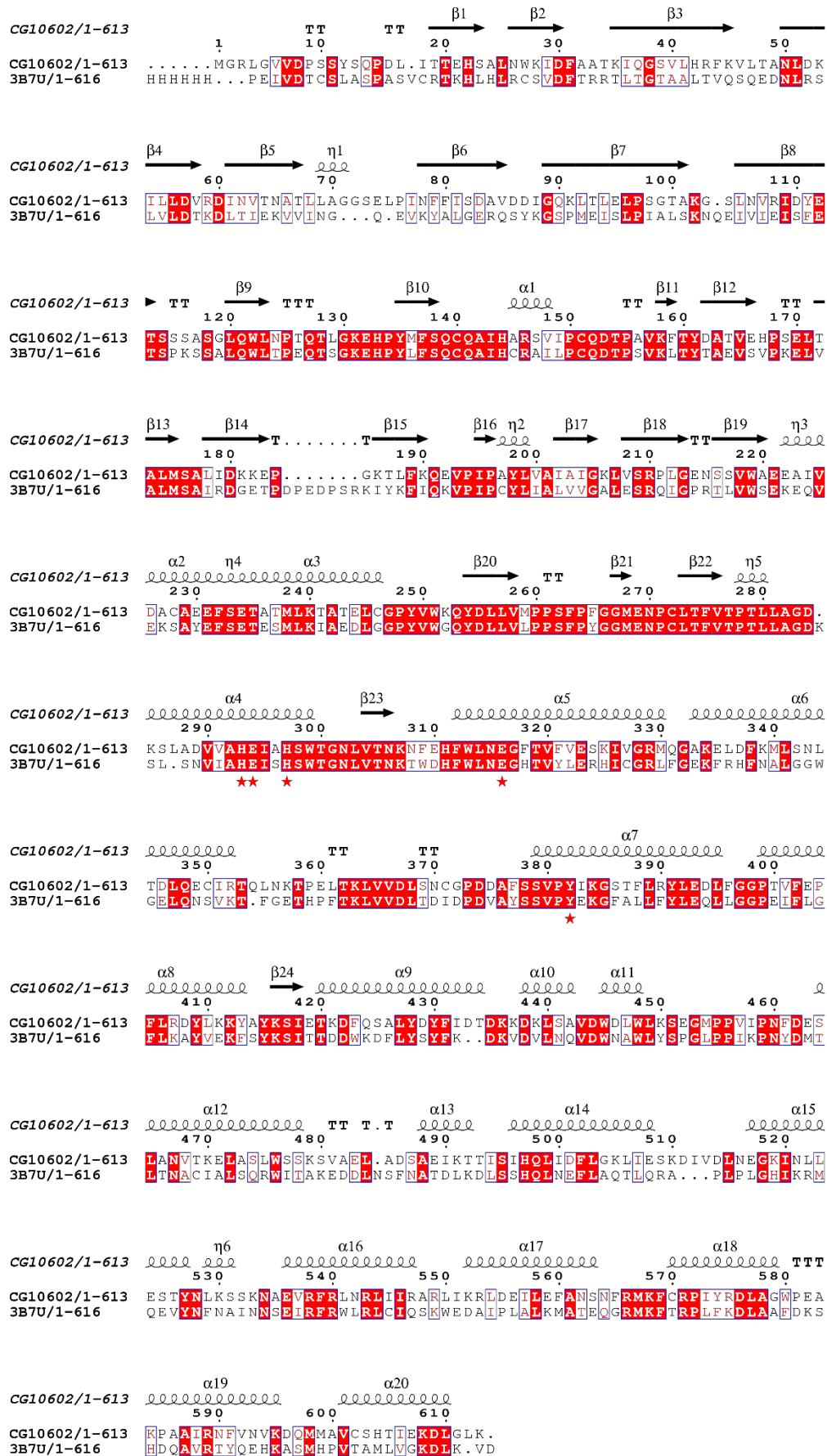


A.



B.



C.

-----J/1-613 1 - - - - - MGR L G V V D P S S Y S Q P D L - I T T E H S A L N W K I D F A A T K I Q G S V L H R F K V L T A N L D K I L L D V R D I N V T N A T L L A 70
3B7U/1-616 1 H H H H H H - - - P E I V D T C S L A S P A S V C R I K H L H L R C S V D F T R R T L T G T A A L T V Q S Q E D N L R S L V L D T K D L T I E K V V I N G 74

CG10602/1-613 71 G G S E L P I N F F I S D A V D D I G Q K L T L E L F S G T A K G - S L N V R I D Y E T S S S A S G L Q W L N P T Q T L G K E H P Y M F S Q C Q A I H A R 146
3B7U/1-616 75 - - - Q - E V K Y A L G E R Q S Y K G S P M E I S L P I A L S K N Q E I V I E I S F E T S P K S A L Q W L T P E Q T S G K E H P Y L F S Q C Q A I H C R 147

CG10602/1-613 147 S V I P C Q D T P A V K F T Y D A T V E H P S E L T A L M S A L I D K K E P - - - - - G K T L F K Q E V P I P A Y L V A I A I G K L V S R P L G E N S 216
3B7U/1-616 148 A I L P C Q D T P S V K L T Y T A E V S V P K E L V A L M S A I R D G E T P D P E D P S R K I Y K F I K V P I P C Y L I A L V V G A L E S R Q I G P R I 224

CG10602/1-613 217 S V W A E A I V D A C A E E F S E T A T M L K T A T E L C G P Y V W K Q Y D L L V M P P S F P F G G M E N P C L T F V T P T L L A G D - K S L A D V V A 292
3B7U/1-616 225 L V W S E K E Q V K S A Y E F S E T E S M L K I A E D L G G P Y V W G Q Y D L L V L P P S F P Y G G M E N P C L T F V T P T L L A G D K S L - S N V I A 300

CG10602/1-613 293 H E I A H S W T G N L V T N K N F E H F W L N E G F T V F V E S K I V G R M Q G A K E L D F K M L S N L T D L Q E C I R T Q L N K T P E L T K L V V D L S 369
3B7U/1-616 301 H E I S H S W T G N L V T N K T W D H F W L N E G H T V Y L E R H I C G R L F G E K F R H F N A L G G W G E L Q N S V K T - F G E T H P F T K L V V D L T 376

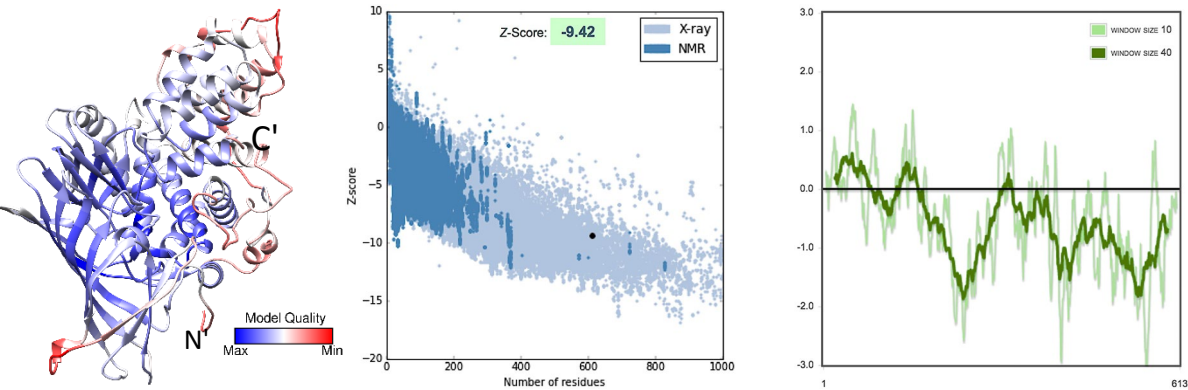
CG10602/1-613 370 N C G P D D A F S S V P Y I K G S T F L R Y L E D L F G G P T V F E P F L R D Y L K K Y A Y K S I E T K D F Q S A L Y D Y F I D T D K K D K L S A V D W D 446
3B7U/1-616 377 D I D P V A Y S S V P Y E K G F A L L F Y L E Q L L G G P E I F L G F L K A Y V E K S Y K S I T D D W K D F L Y S Y F K - - D K V D L N Q V D W N 451

CG10602/1-613 447 L W L K S E G M P P V I P N F D E S L A N V T K E L A S L W S K S V A E L - A D S A E I K T T I S I H Q L I D F L G K L I E S K D I V D L N E G K I N L 522
3B7U/1-616 452 A W L Y S P L P P I K P N Y D M L T N A C I A L S Q R W I T A K E D D L N S F N A T D L K D L S S H Q L N E F L A Q T L Q R A - - - P L P L G H I K R 525

CG10602/1-613 523 L E S T Y N L K S S K N A E V R F R L N R L I I R A R L I K R L D E I L E F A N S N F R M K F C R P I Y R D L A G W P E A K P A A I R N F V N V K D Q M M 599
3B7U/1-616 526 M Q E V Y N F N A I N N S E I R F F W L R L C I Q S K W E D A I P L A L K M A T E Q G R M K F T R P L F K D L A A F D K S H D Q A V R T Y Q E H K A S M H 602

CG10602/1-613 600 A V C S H T I E K D L G L K - 613
3B7U/1-616 603 P V T A M L V G K D L K - V D 616

D.



E.

LTA4H 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 A4 hydrolase (LTA4H, NP_000886.1, PDB: 3B7U)	611	Peptidase family M1 (PF01433) 13-387 LTA4H, C-term (PF09127) 464-608	H296, E297, H300, E319, D376 and Y384	58% SIM	0.891 Å
Uncharacterized protein (CG10602, NP_724139.1)	613	Peptidase family M1 (PF01433) 8-420 LTA4H, C-term (PF09127) 464-610	H293, E294, H297, E316, D374 and Y382		

S4 Fig. Sequence and structural details of the modeled fly LTA4H candidate. A. Domain architecture of LTA4H and CG10602 and known/predicted functional residues B. Pairwise alignment of CG10602 and 3B7U generated from structural superposition showing shared secondary structure elements and known/predicted functional residues (marked with red asterisks) C. Pairwise alignment of CG10602 and 3B7U generated from structural superposition with conserved residues highlighted using the physiochemical color scheme (CLUSTALX) D. Validation of the CG10602 model: ProQ2 quality score mapped to a 3D model of CG10602 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. LTA4H (3B7U, cyan-blue) superimposed on the predicted structure of CG10602 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by LTA4H and potential *D. melanogaster* ortholog CG10602.