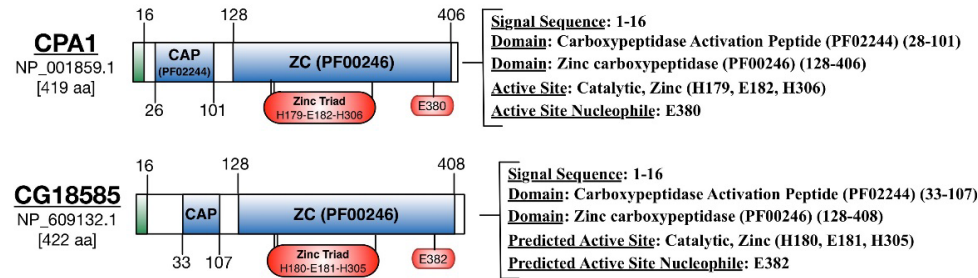
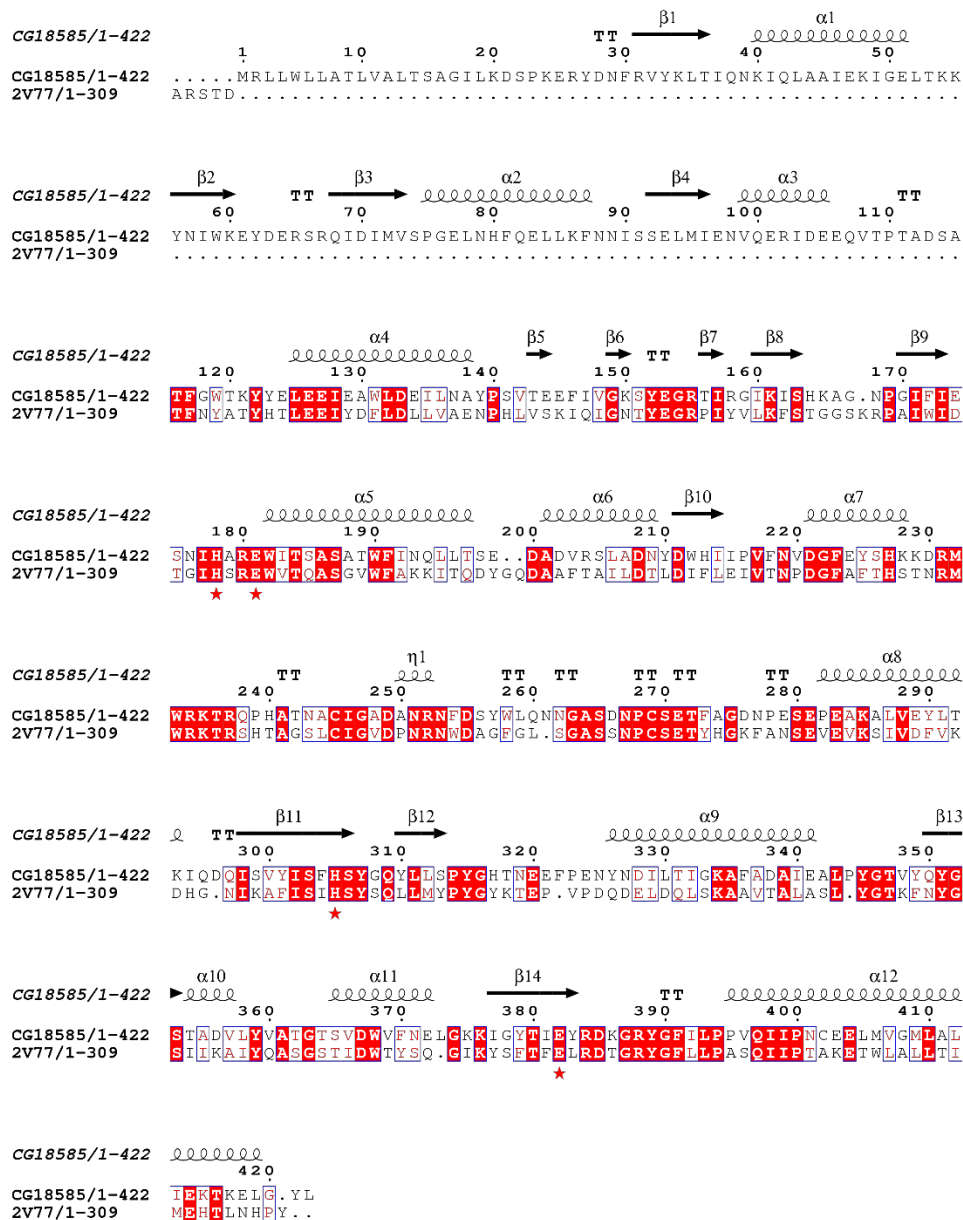


A.



B.



|                             |  |            |
|-----------------------------|--|------------|
| CG18585/1-422<br>2V77/1-309 | 1 - - - - MRLWLLATLVALTSAGILKDSPKERYDNFRVYKLTIQNKIQLAAIEIKIGELTKKYNIWKEYDERSRQID | 70<br>5    |
| CG18585/1-422<br>2V77/1-309 | 71 IMVSPGELNHFQELLKFNNISSELMIEINVQERIDEEQVTPADSAITFGWTKYEEIEAWLDELINAYPSVTEE     | 145<br>30  |
| CG18585/1-422<br>2V77/1-309 | 146 FIVGKSYEGGTRIGIKISHKAG-NPGIFIESNIHAREWITSASATWFNQLTSE--DADVRSLLADNYDWHIIPV   | 217<br>36  |
| CG18585/1-422<br>2V77/1-309 | 218 FNVDFGEYSHKKDRMWRKTRQPHATNACIGADANRNFDSYWLQNNGASDNPCCSETFAGDNPESEPEAKALVEYLT | 292<br>111 |
| CG18585/1-422<br>2V77/1-309 | 293 KIQDQTSVYISFHSYGGVLLSPYGHNTPEFPENYNDILTIKAFADAIEALPYGTVYQYGSTADVLYVATGTSVD   | 367<br>185 |
| CG18585/1-422<br>2V77/1-309 | 368 WVFNELGKIKGYTIEYRDKGRYGFLPPVQIINPCEELMVGLMALIEKTKELG-YL                      | 422<br>30  |

| CPA1 Structure | <i>D. melanogaster</i> Model | Superimposed |
|----------------|------------------------------|--------------|
|                |                              |              |

| F.   | Length<br>(AA) | Domain<br>Architecture<br>(Pfam, range)  | Functional<br>Residues<br>(aligned matches<br>in <i>D.<br/>melanogaster</i> ) | Sequence<br>ID%   | Structural<br>Overlap<br>(RMSD) |
|--|----------------|--|---|-------------------|---------------------------------|
| Carboxypeptidase A1<br>(CPA1, NP_001859.1,<br>PDB: 3FJU) | 419            | Carboxypeptidase<br>activation peptide<br>(PF02244)<br>26-100<br><br>Zinc carboxypeptidase<br>(PF00246)<br>128-406 | H179, E182, H306<br>and E380  | 34% ID<br>54% SIM | 0.753 Å                         |
| CPA (CG18585,<br>NP_609132.1)                            | 422            | Carboxypeptidase<br>activation peptide<br>(PF02244)<br>33-106<br><br>Zinc carboxypeptidase<br>(PF00246)<br>128-408 | H178, E181, H305<br>and E382  |                   |                                 |

**S8 Fig. Sequence and structural details of the modeled fly CPA1 candidate.** A. Domain architecture of CPA1 and CG18585 and known/predicted functional residues B. Pairwise alignment of CG18585 and 3FJU generated from structural superposition showing shared secondary structure elements and known/predicted functional residues ( marked with red asterisks) C. Pairwise alignment of CG18585 and 3FJU generated from structural superposition with conserved residues highlighted using the physiochemical color scheme (CLUSTALX) D. Validation of the CG18585 model: ProQ2 quality score mapped to a 3D model of CG18585 (left); ProSA global quality score ranking (middle) and per-residue quality graph (right) E. CPA1 (3FJU, cyan-blue) superimposed on the predicted structure of CG18585 (green-red) with potential matches for conserved functional residues highlighted F. Summary of features shared by CPA1 and potential *D. melanogaster* ortholog CG18585.