

GGT1
NP_001275762.1
[569 aa]

Gamma Glutamyl Transpeptidase (PF01019)

26 55 380 564

Disulfide C50-C74
Disulfide C192-C196
Autocatalytic Cleavage Site 380

Signal Sequence: Signal-anchor, Type II Membrane Protein (1-26)
Processing: Heavy Chain (1-380)
Processing: Light Chain (381-569)
Disulfide Bonds: (C50-C74; C192-C196)

CG6461
NP_573303.1
[579 aa]

Gamma Glutamyl Transpeptidase (PF01019)

26 55 566

Disulfide C50-C74

Signal Sequence: Signal-anchor, Type II Membrane Protein (1-26)
Processing: Autocatalytic Cleavage Unlikely (C192, E193 missing)
Predicted Disulfide Bonds: (C50-C74)

CG6461/1-579

1 TT 10 20 30 40 50 60

XRIVNSKKILLWILLAAKLVLTALTCLVFLGKLRNRTIVISC AVVSVNGICGAAYVGCENLD

4GDX/33-563 PD.NHAYTRAAVAADAKGCKLGLNDALRD

CG6461/1-579

70 80 90 100 110 120

GGS AVDAATAAL L L C G L L F S M G I G G C F V A T T I Y T R S R K R V T V I A R E S A P A L A H K D M F V

4GDX/33-563 GGS AVDAATAAL L L C G L L N S M G I G G C F I T T I Y T R R K R S E V I N A R E S A P A L A F A T .

CG6461/1-579

130 140 150 160 170

GET... I I G A N S C A V P G E I R G Y K E R M L P W N R L F P S T K L A R E G H V S R Y . L A

4GDX/33-563 . . P N S S T Q S Q R G G T S A V P G E I R G Y P I A H R H R C L P W A R L F C P S T L A R A Q C P F V . K C L A

CG6461/1-579

180 190 200 210 220 230

A A I C G K L D N I K A D I F I S A V T L N A T G P H L E G S I K K K P L A D T F E I T E N G A B E I Y D G S E I

4GDX/33-563 A A I P N K R I V Q C Q I A Q S I D F I S A V T L N A T G P H L E G S I L T P L A D T F E I T E G A C A P Y N . G S I

CG6461/1-579

240 250 260 270 280 290

G R K S V H D I G K C G I L C D F I T R W E . S D G H S A H V S T Y T L V S T P D S G R V A L I L

4GDX/33-563 T A Q V I K I D I A G C G I V A I D I L N F R I L I Z E F L N I S G . . D A V I V M S S D I S G R V A L I L

CG6461/1-579

300 310 320 330 340

N L P A D D L Y . . . D N . . . E F I M U R V E A P R H A Y S Q R N L G M H A D F V S . A A S I N A . T I L

4GDX/33-563 N E I G G Y N F S R E S V S E P E Q K E I T H R V E A S R H A Y A S Q . . L . L G D R K P V D . . . T E Y

CG6461/1-579

350 360 370 380 390 400

R E M L K P F P I S V R K I L H D S S S R D Y I V Y G A N P T V S D F G T A H . N V V A T N C G A V S I T S I

4GDX/33-563 R N I T S E F P I S V R K I L H D S S S R D Y I V Y G A N P T V S D F G T A H . N V V A T N C G A V S I T S I

CG6461/1-579

410 420 430 440 450

N N Y F G S K V A S T Q R C I L I N E M D D F S P G . I T V N G F G V P A S P A N K T Y P G K R P S

4GDX/33-563 N N Y F G S K V R S P V S G I L I N E M D D F S P S I T N E F G V P P S P A N S I O P G K Q P S

CG6461/1-579

460 470 480 490 500 510

S M S C I L I V D Q R . C H V R I V V G A A G G T I T T S V A A V I M K Y L L R K E S T T A V N N C R L H Q L A

4GDX/33-563 S M C I L I V D Q R . C H V R I V V G A A G G T I T T A T A L A I N Y L R F G Y I T K A V A S R C R L H Q L F

CG6461/1-579

520 530 540 550 560

P M R V S G I P R D S S V T D Y I V V C H D M Y E E P V G S S T A V A L C A L E . . . Q E P E Y D R R R I G S

4GDX/33-563 N . V I T V E R N I D A V T A A L I R R R H T Q I A S T . . F I A V V A I V R . . T A G G W A A S S D R R G C R

CG6461/1-579

570

A L I T A K N I K M Q E

4GDX/33-563 P I G Y

C.

1-579
4GDX/33-563
1 MRI VWSKKLLWLLLAALMVTA LTLGLVFGLKNRDTLYISGAVVS 45
33 - - - - - PD- NHVYTRAAVAA 45

CG6461/1-579
4GDX/33-563
46 NGIGCAAVGGEMLTGGGSAVDAAIATLLCEGLLLPHSMGI GGGFV 90
46 DAKQCCKI GRDALRDGGSAVDAAIAALLGVGLMNAHSMGI GGGLF 90

CG6461/1-579
4GDX/33-563
91 ATITYRSSRKVETVIARESAPAAHKDMFVGET- - - S- ITGAKS 130
91 LTIYNSTIRKAEVINAREVAPRLAFAT- M- - - FNSSEQSQKGGLS 131

CG6461/1-579
4GDX/33-563
131 GAVPGEILGYWEMHRRYGI LPWKHLFEPISIKLAREGHVVSRY- LA 174
132 VAVPGEIRGYELAHQHHGRLPWAHLFQPSIQLARQGFPVG- KGLA 175

CG6461/1-579
4GDX/33-563
175 AAIQSKLDNIKADPGLSAVFLNATGDPHLEGDYMKRPA LADTLER 219
176 AALENKRTVIEQQPVLCFVFCR- DRKVLREGERLTLPQLADTYET 219

CG6461/1-579
4GDX/33-563
220 IAENGAKFHYDGGETGRKFVEIDQKMGGITEDQLRDYTVRWE- S 263
220 LAIEGAQAFYN- GSLTAQIVKDIQAAGGIVTADLNNYRAELIEH 263

CG6461/1-579
4GDX/33-563
264 DGHVSAHVSGETTLYSTPMPSSGPVLAFLNLNLMADLYT- - - DN- - 303
264 PLNISLG- - - DAVLYMP SAPLSGRVLALILNLKGYNFSRESVES 305

CG6461/1-579
4GDX/33-563
304 - - - EPIYWQRVVEAFKHAYGQRTNLGDMYADPVS- AASTNA- T- L 342
306 PEQCKGLTYHRIVEAFRFAYAKR- T- L- - LGDPKFVD- - V- - TEV 342

CG6461/1-579
4GDX/33-563
343 EEMLKPEFLESVFKLIHONSTSEDYLYYGANFTVEEDHGT- - - 383
343 RNMTSEFFAAQLRAQISDTHPI SYK- - P- - - - - - EFTY 375

CG6461/1-579
4GDX/33-563
384 - HM- NVLATNGDAVSITSTINNYFGSKVASTQTGILNDEMDFS 426
376 AH- LSVVAEDGSASATSTINLYFGSKVRSPVSGILFNDEMDFS 419

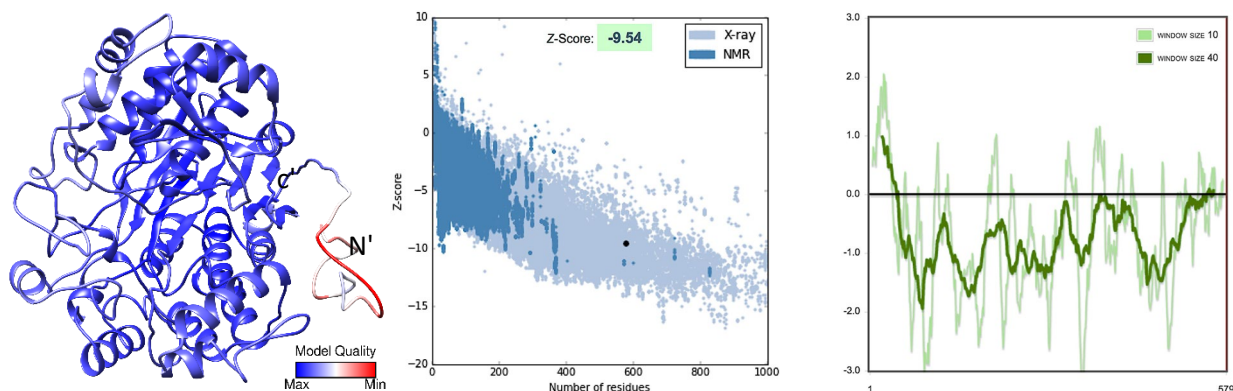
CG6461/1-579
4GDX/33-563
427 TPG- VINGFGVPA- - - - - PANYIYPGKRPMSSMSPCIIVDQ 462
420 SP- SIT- - - - - NEFGVPPSPANFIQPGKQLSSMCP TIMV- G 454

CG6461/1-579
4GDX/33-563
463 E- GNVRLLVGAAGGTIRITTSVAAVIMKYLRLKESLTAAYNNGRLH 506
455 DGQVRMVVGAAGGTQITATATAIAIYNLWFGYDVKRAVEEPRLH 499

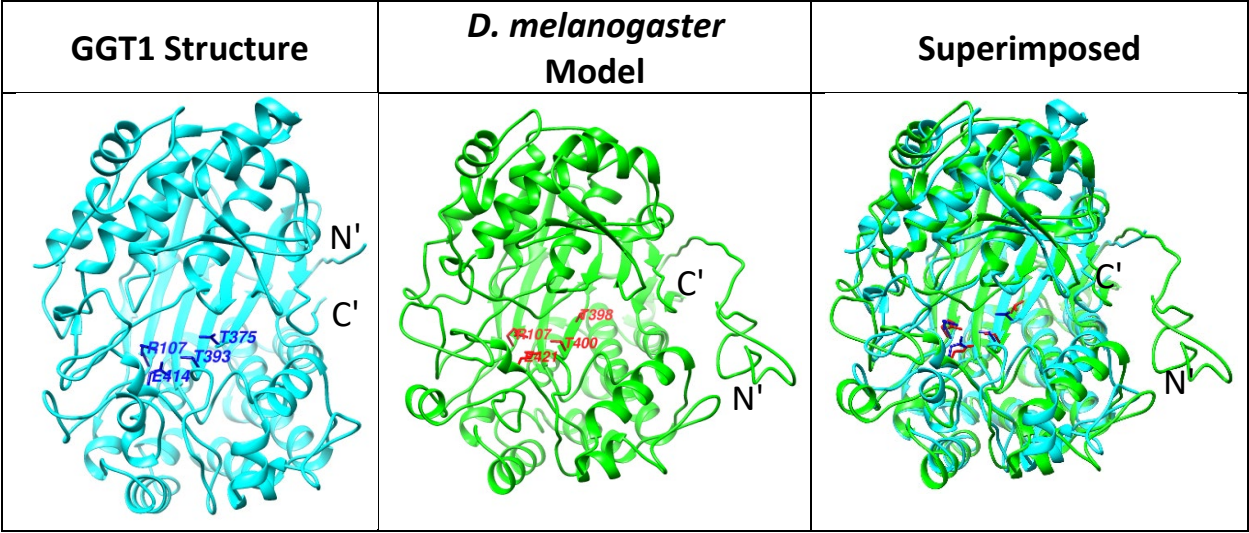
CG6461/1-579
4GDX/33-563
507 HQL- APMRVSYEQEVDSSVTDY LKQVGHMEYEEFVGSFAAVTAI 550
500 NQLLPN- VTTVERNIDQAVTAALETRHHHTQIAST- - FIAVVQAI 541

CG6461/1-579
4GDX/33-563
551 GALE- - - QPEPFYDRRI GSALT LAKTNKMQH 579
542 VR- - TAGGWAAASDSKGGEPAGY- - - - - 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 physiochemical 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.

