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Supporting information for article:

**The structure of the *Gemella haemolysans* M26 IgA1 protease
trypsin-like domain**

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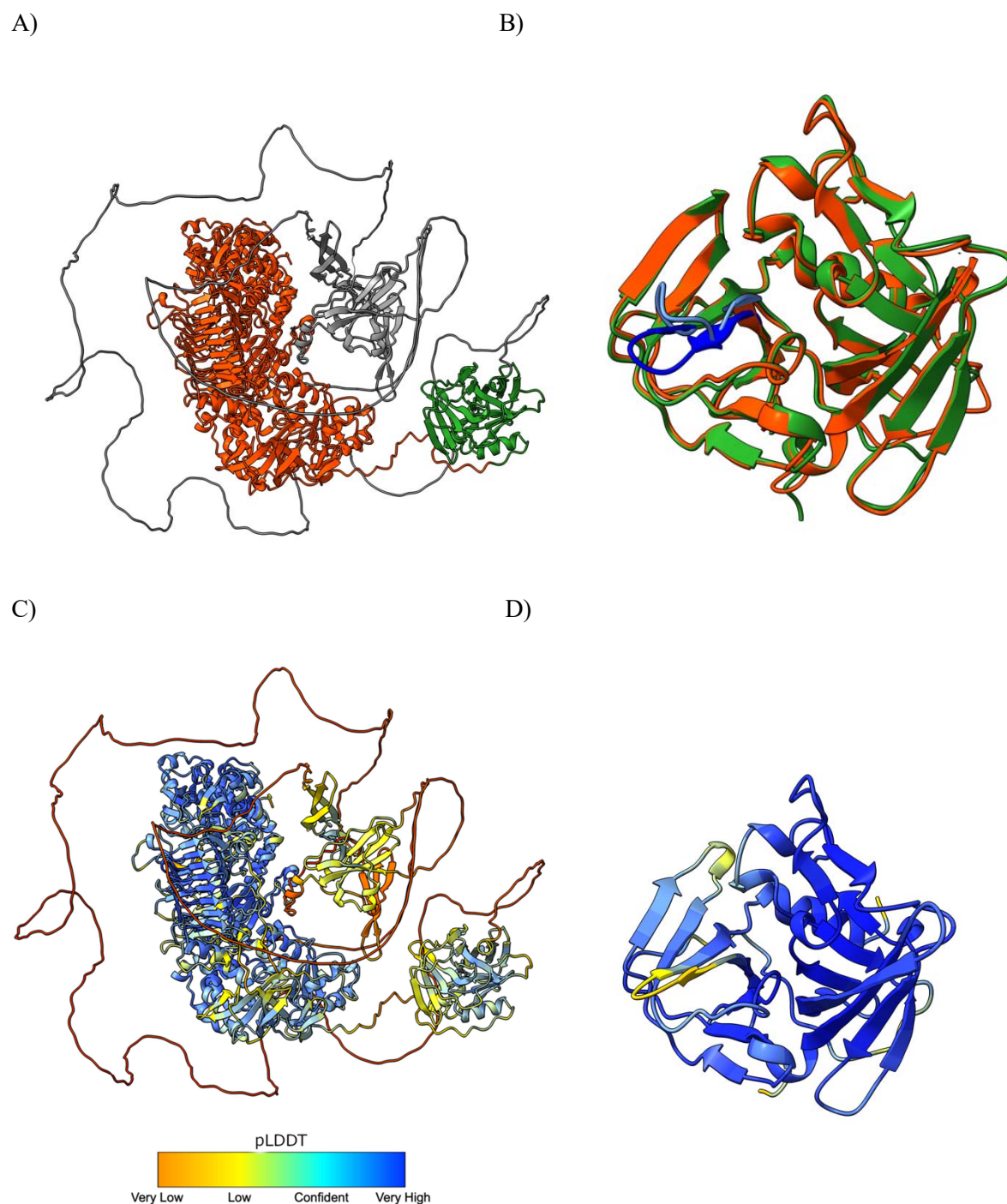


Figure S1 A comparison of the AlphaFold3-predicted model of *GhIgAP* with the *GhTrp* crystal structure. The Google webserver (<https://alphafoldserver.com>) for AlphaFold3 was used to generate the full-length model using default settings. A) the complete modelled structure of *GhIgAP* with the IgAP domain rendered in orange and the trypsin domain in green. The remainder of the N-terminal structure is rendered in grey. B) superimposition of the *GhTrp* domain from the AlphaFold model (green) with the crystallographic structure (orange). Loop 2 in the modelled and crystallographic structures is rendered in dark and light blue, respectively. The two structures align well with a C α RMSD of 1.4Å. The complete *GhIgAP* (C) and the *GhTrp* domain (D) AlphaFold3 predicted

structures colored by pLDDT values. The color key corresponds to Very high (pLDDT > 90), Confident (90 > pLDDT > 70), Low (70 > pLDDT > 50), Very low (pLDDT < 50).

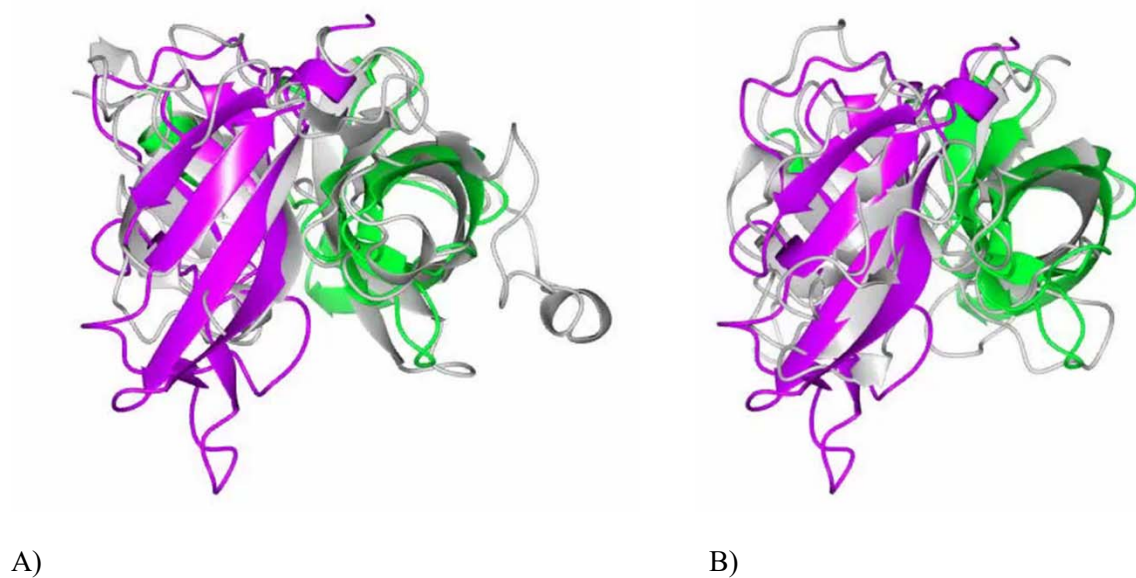


Figure S2 Superimposition of *GhTrp* with previously unsuccessful molecular-replacement search models. The N-terminal (purple) and C-terminal (green) lobes of the *GhTrp* trypsin-like fold are superimposed with A) the highest sequence identity model at the time (31.2% identity; C α RMSD of 2.46 Å) and B) the I-TASSER homology model (C α RMSD of 3.03 Å). These search models are shown in gray.

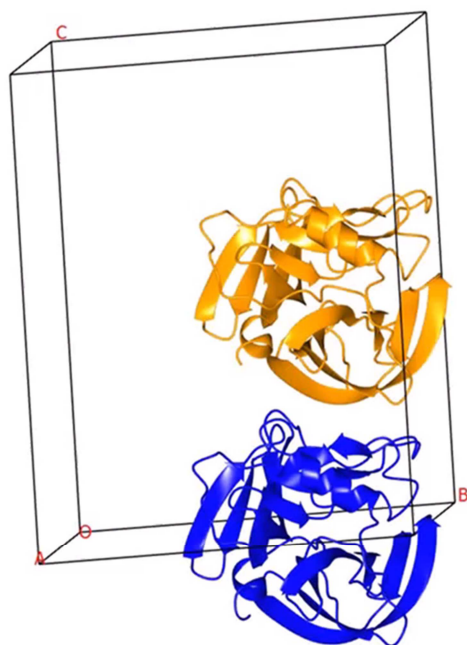


Figure S3 Asymmetric unit of the *GhTrp* in the context of the unit cell. The two molecules of the *GhTrp* asymmetric unit are shown in blue and orange. They are related to each other by translational non-crystallographic symmetry along the c-axis of the unit cell.