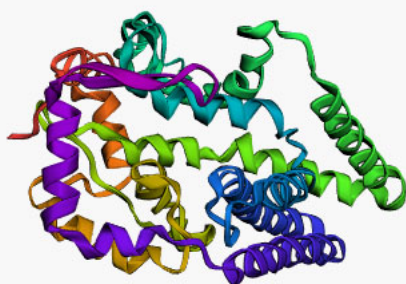


[Click on [TR027389\\_results.tar.bz2](#) (TR027389\_results.tar.bz2) to download the tarball file including all modeling results listed on this page]

## Summary of predicted models



- The confidence of the predicted model or the left is **high** (with estimated TM-score=0.675).
- The model was built by trRosetta based on **de novo folding**, guided by deep learning restraints.
- You can download other lower-ranked models: model2 (model2.pdb), model3 (model3.pdb), model4 (model4.pdb), model5 (model5.pdb).
- Download the multiple sequence alignment (seq.a3m) used by trRosetta.
- Download the predicted inter-residue distance and orientations (seq.npz).

(seq.cont.png) Contact      (seq.dist.png) Distance      (seq.omega.png) Omega      (seq.theta.png) Theta      (seq.phi.png) Phi

[illegible]

• J Yang, I Anishchenko, H Park, Z Peng, S Ovchinnikov, D Baker, *Improved protein structure prediction using predicted interresidue orientations*, PNAS, 117: 1496-150 (2020)