## trRosetta results for job TR027389 (DEGS1 NP 003667)

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

#### **Predicted Structure Models**



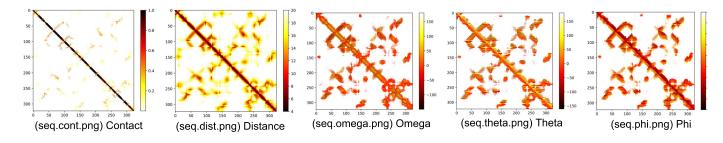
Download Model 1 (model1.pdb) (colored by rainbow from N to C terminus)

Estimated TM-score: 0.675

# Summary of predicted models

- The confidence of the predicted model or the left is **high** (with esitmated TMscore=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).

### Predicted 2D Information



#### Predicted 1D Information

------10------20------30------40------50------60------70------80------90------100-----110------120----123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|123456789|12

H: Helix; S: Strand; C: Coil.

D: Disorder; .: Order

## Reference

• 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)