- Here are the Top 10 threading templates. Based on the sequence identity, coverage, and Normalized Z-score, is thymidylate synthase from W.g.b. an easy or hard target?
- The sequence identity is not very high but in a reasonable range for homology modeling. The coverage is very high and Normalized Z-score is also high, so this not a hard target for I-TASSER.

- The confidence of each model is quantitatively measured by C-score that is calculated based on the significance of threading template alignments and the convergence parameters of the structure assembly simulations. C-score is typically in the range of [-5, 2], where a C-score of a higher value signifies a model with a higher confidence and vice-versa. TM-score and RMSD are estimated based on C-score and protein length…
- Is I-TASSER confident about its final model?

Top 5 final models predicted by I-TASSER

(For each target, I-TASSER simulations generate a large ensemble of structural quantitatively measured by C-score that is calculated based on the significance on C-score and protein length following the correlation observed between these rank models as seen in our benchmark tests. If the I-TASSER simulations conv

- More about C-score
- Local structure accuracy profile of the top five models

(By right-click on the images, you can export image file or change the
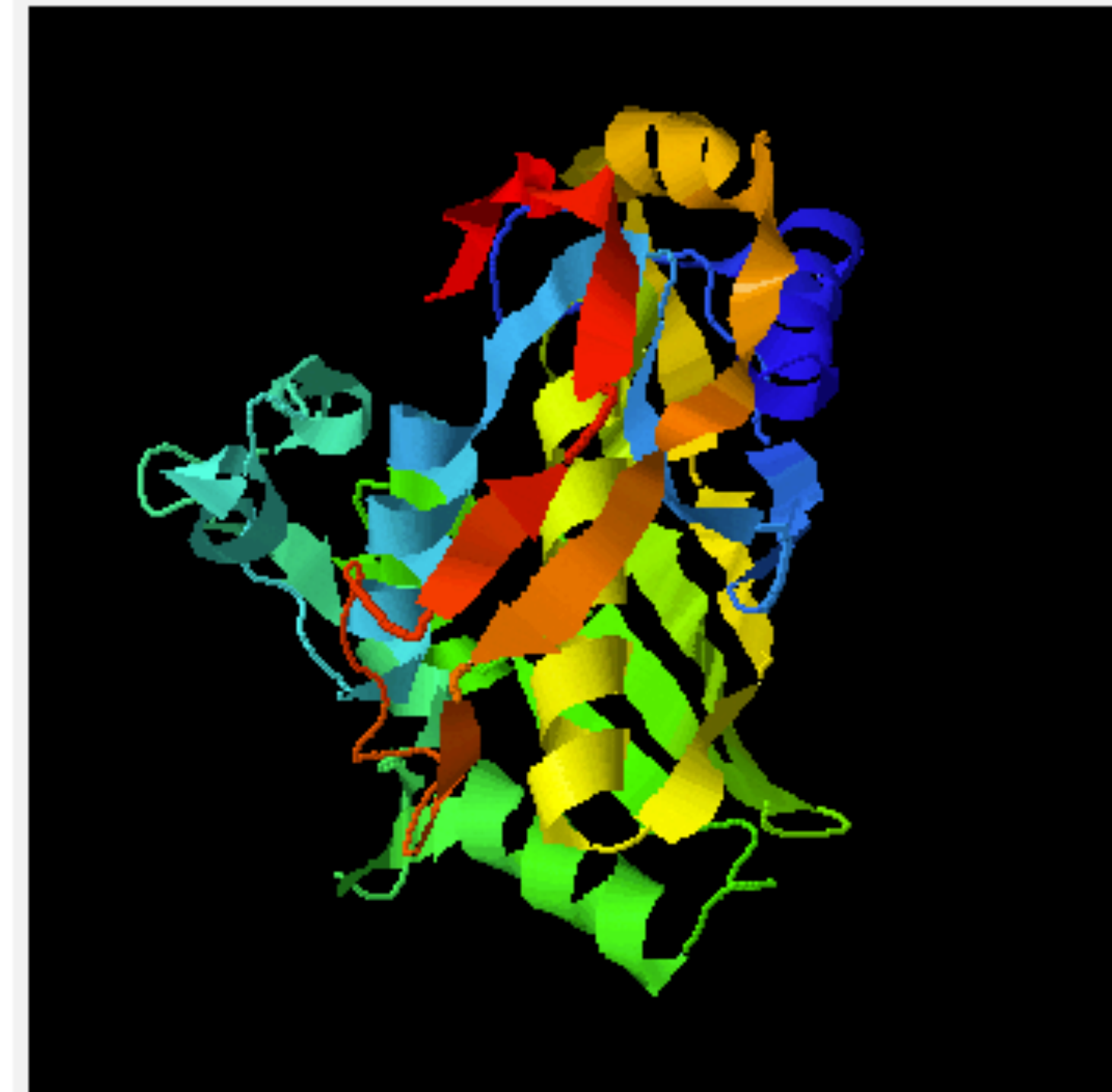
Reset to initial orientation ☐ Spin On/Off

- Download Model 1
- C-score=1.91 (Read more about C-score)
- Estimated TM-score = 0.99±0.04
- Estimated RMSD = 2.2±1.7Å