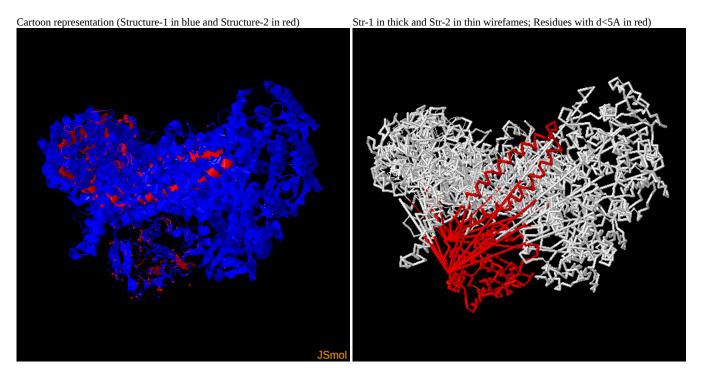
4/15/2018 TM-score Server

## **TM-score Results**

```
TM-SCORE
  A scoring function to assess the similarity of protein structures
  Based on statistics:
  0.0 < TM-score < 0.17, random structural similarity
0.5 < TM-score < 1.00, in about the same fold
Reference: Yang Zhang and Jeffrey Skolnick, Proteins 2004 57: 702-710
  For comments, please email to: zhng@umich.edu
Structure1: A695157
                       Length= 5000
Structure2: B695157
                      Length= 484 (by which all scores are normalized)
Number of residues in common= 2580
RMSD of the common residues=
                               0.000
           = 5.3306
                     (d0=7.83)
TM-score
MaxSub-score= 5.3306 (d0= 3.50)
GDT-TS-score= 5.3306 %(d<1)=5.3306 %(d<2)=5.3306 %(d<4)=5.3306 %(d<8)=5.3306
GDT-HA-score= 5.3306 %(d<0.5)=5.3306 %(d<1)=5.3306 %(d<2)=5.3306 %(d<4)=5.3306
 ----- rotation matrix to rotate Chain-1 to Chain-2
                                                     u(i.3)
i
                       u(i.1)
                                      u(i.2)
       0.0000000000
                     1.000000000 -0.000000000 -0.000000000
1
        0.0000000000 - 0.0000000000 \\
                                   1.0000000000
                                                  0.0000000000
       -0.000000000
                     0.000000000
                                   -0.0000000000
                                                   1.0000000000
Superposition in the TM-score: Length(d<5.0)=*** RMSD= 0.00
Superposition in the in-softe. Length(403.0) - NASE 0.00 (":" denotes the residue pairs of distance < 5.0 Angstrom)
LSQAQKMQAIGQLAGGVAHDFNNLLTAIQLRLDQLLHRHPVGDPSYEGLNEIRQTGVRAADLVRKLLAFSRKQTVQREVLDLGELISEFEVLLRRLLREDVKLITDYGRDLPQVRADKSQLETAVMNLAVNARDAV
\mathsf{KLL}\mathsf{AFSRKQTVQREVLDLGELISEFEVLLRRLLREDVKLITDYGRDLPQVRADKSQLETAVMNLAVNARDAVRAAKGGGVVRIRTARLTRDEAIQLGFPAADGDTAFIEVSDDGPGIPPDVMGKIFDPFFTTKPVG
AVNARDAVRAAKGGGVVRIRTARLTRDEAIQLGFPAADGDTAFIEVSDDGPGIPPDVMGKIFDPFFTTKPVGEGTGLGLATVYGIVKQSDGWIHVHSRPNEGAAFRIFLPVYEALSQAQKMQAIGQLAGGVAHDFN
LSQAQKMQAIGQLAGGVAHDFNNLLTAIQLRLDQLLHRHPVGDPSYEGLNEIRQTGVRAADLVRKLLAFSRKQTVQREVLDLGELISEFEVLLRRLLREDVKLITDYGRDLPQVRADKSQLETAVMNLAVNARDAV
```

## Visualization of TM-score superposition



## **Document downloads**

- Click <u>A695157.pdb</u> to download the first structure that you submitted.
- Click B695157.pdb to download the second structure that you submitted.
- Click C695157.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C695157.pdb' to view the structure).

4/15/2018 TM-score Server

• Click D695157.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D695157.pdb' to view the structure).

## **Reference:**

- Y. Zhang, J. Skolnick, Scoring function for automated assessment of protein structure template quality, Proteins, 57: 702-710 (2004).
  J. Xu, Y. Zhang, How significant is a protein structure similarity with TM-score=0.5? Bioinformatics, 26, 889-895 (2010).

Back to TM-score Homepage