TM-score Results

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 *                              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: A690420     Length=  108
Structure2: B690420     Length=  108 (by which all scores are normalized)
Number of residues in common=  108
RMSD of  the common residues=   10.999

TM-score    = 0.6435  (d0= 3.82)
MaxSub-score= 0.6112  (d0= 3.50)
GDT-TS-score= 0.6296 %(d<1)=0.4167 %(d<2)=0.6389 %(d<4)=0.6852 %(d<8)=0.7778
GDT-HA-score= 0.4769 %(d<0.5)=0.1667 %(d<1)=0.4167 %(d<2)=0.6389 %(d<4)=0.6852

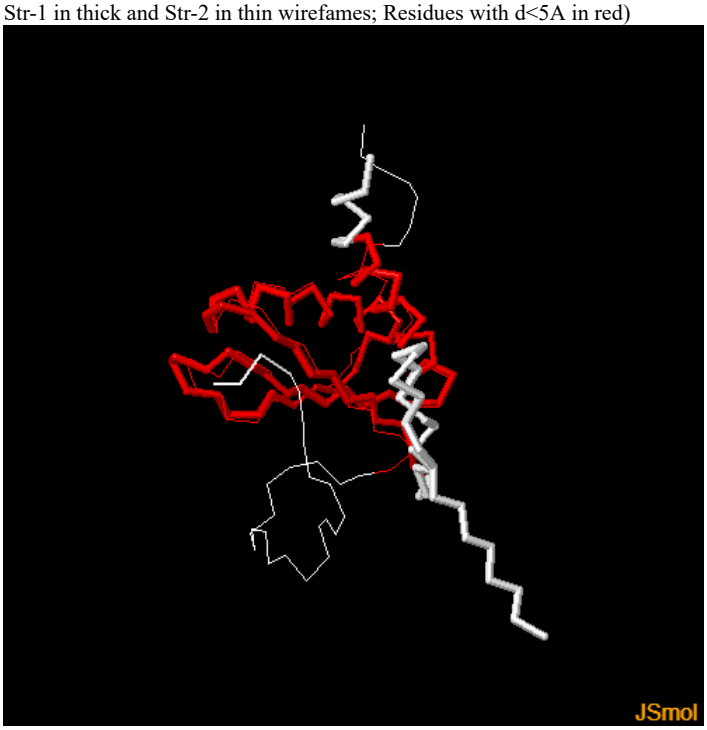
 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1     -0.2073525651   0.2142509350  -0.1119444473  -0.9703427114
 2     -3.8397426394  -0.6318781691  -0.7734344629  -0.0502902681
 3     -0.1487872678  -0.7448667775   0.6239131128  -0.2364443092

Superposition in the TM-score: Length(d<5.0)= 74  RMSD=  1.29
(":" denotes the residue pairs of distance < 5.0 Angstrom)
MSNQTCVENEVCEACGCAGEIGFIIREGDDVAEVSLFGSDKAHLEGKLAEYISLAKQVYANVEYEVAPVADNATELHARFKFEVSAEKLIFELKTRALARLEHHHHHH
                            ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
MSNQTCVENEVCEACGCAGEIGFIIREGDDVAEVSLFGSDKAHLEGKLAEYISLAKQVYANVEYEVAPVADNATELHARFKFEVSAEKLIFELKTRALARLEHHHHHH
12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678
```

Visualization of TM-score superposition

Cartoon representation (Structure-1 in blue and Structure-2 in red)

Str-1 in thick and Str-2 in thin wirefames; Residues with d<5A in red)



Document downloads

- Click A690420.pdb to download the first structure that you submitted.
- Click B690420.pdb to download the second structure that you submitted.
- Click C690420.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C690420.pdb' to view the structure).
- Click D690420.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D690420.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