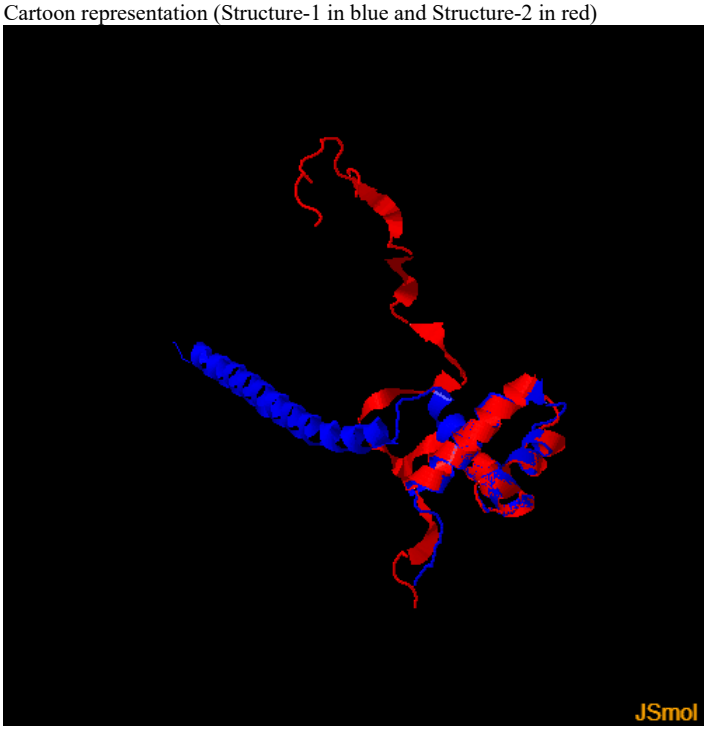
TM-score Results

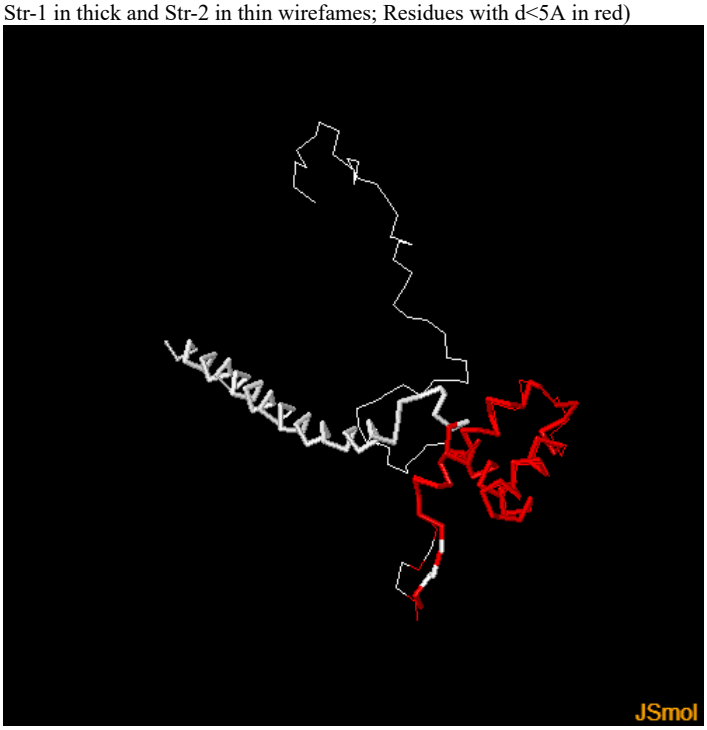
```
 **************************************************************************
 *                              TM-SCORE                                  *
 * A scoring function to assess the similarity of protein structures      *
 * Based on statistics:                                                   *
 *       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: A489609     Length=  108
Structure2: B489609     Length=  108 (by which all scores are normalized)
Number of residues in common=  108
RMSD of  the common residues=   20.964

TM-score    = 0.5020  (d0= 3.82)
MaxSub-score= 0.4710  (d0= 3.50)
GDT-TS-score= 0.4931 %(d<1)=0.4074 %(d<2)=0.4815 %(d<4)=0.5185 %(d<8)=0.5648
GDT-HA-score= 0.4282 %(d<0.5)=0.3056 %(d<1)=0.4074 %(d<2)=0.4815 %(d<4)=0.5185

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1     20.4471422283  -0.0107756369   0.6180814019   0.7860402447
 2     -1.9259114581  -0.7914549725   0.4751586346  -0.3844779557
 3      4.1627404037  -0.6111324833  -0.6262584551   0.4840634620

Superposition in the TM-score: Length(d<5.0)= 55  RMSD=  1.15
(":" denotes the residue pairs of distance < 5.0 Angstrom)
MTKNTRFSPEVRQRAVRMVLESQGEYDSQWATICSIAPKIGCTPETLRVWVRQHERDTGGDDGGLTTAERQRLKEPERENRELRRSNDILRLASAYFAKAEFDRLWKK
::  : ::::::::::::::::::::::::::::::::::::::::::::::::::
MTKNTRFSPEVRQRAVRMVLESQGEYDSQWATICSIAPKIGCTPETLRVWVRQHERDTGGDDGGLTTAERQRLKEPERENRELRRSNDILRLASAYFAKAEFDRLWKK
1234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678
```

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 A489609.pdb to download the first structure that you submitted.
- Click B489609.pdb to download the second structure that you submitted.
- Click C489609.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C489609.pdb' to view the structure).
- Click D489609.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D489609.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