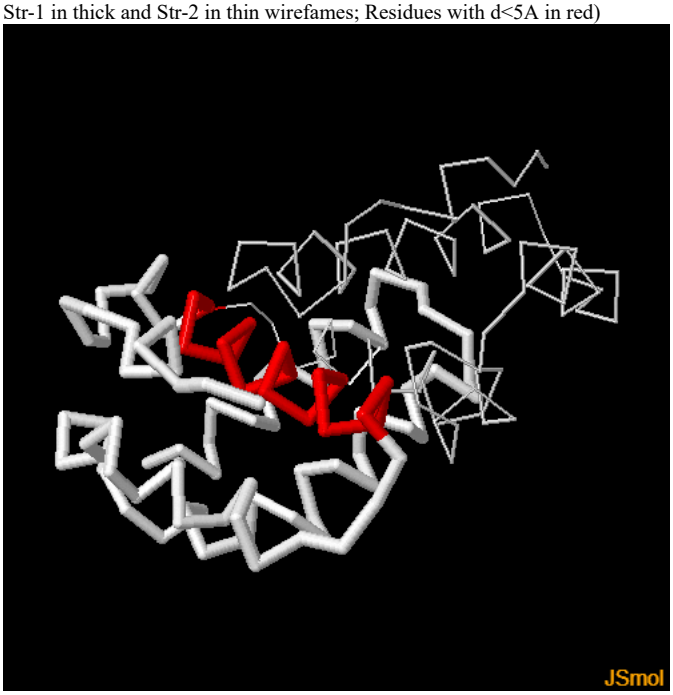
TM-score Results

```
 **************************************************************************
 *                            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: A528290     Length=   94
Structure2: B528290     Length=   94 (by which all scores are normalized)
Number of residues in common=   34
RMSD of  the common residues=    5.729

TM-score    = 0.1870  (d0= 3.52)
MaxSub-score= 0.1784  (d0= 3.50)
GDT-TS-score= 0.2154 %(d<1)=0.1809 %(d<2)=0.1809 %(d<4)=0.1809 %(d<8)=0.3191
GDT-HA-score= 0.1755 %(d<0.5)=0.1596 %(d<1)=0.1809 %(d<2)=0.1809 %(d<4)=0.1809

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1     -9.5895507140   0.9368562759  -0.1678872644   0.3067803526
 2     -5.9157216824  -0.1855743430  -0.9821962501   0.0292008477
 3     -6.2278703019   0.2964160614  -0.0842875598  -0.9513322899

Superposition in the TM-score: Length(d<5.0)= 17  RMSD=  0.41
(":" denotes the residue pairs of distance < 5.0 Angstrom)
SFGDWAEKFLKSKEADGVSVSQLNSYKNYCRNHLSPLYMKSLSEILPADIQSIINETKLAKNTLKAIRNTASQIFRLAIENRAIDFNPADYVRI----------------------------------------------------------
                                                                ::::::::::::::::
----------------------------------------------------------SFGDWAEKFLKSKEADGVSVSQLNSYKNYCRNHLSPLYMKSLSEILPADIQSIINETKLAKNTLKAIRNTASQIFRLAIENRAIDFNPA
12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789
```

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 A528290.pdb to download the first structure that you submitted.
- Click B528290.pdb to download the second structure that you submitted.
- Click C528290.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C528290.pdb' to view the structure).
- Click D528290.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D528290.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