

```
*****
*                               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: A680874      Length=    74
Structure2: B680874      Length=   209 (by which all scores are normalized)
Number of residues in common=    74
RMSD of the common residues=   11.897

TM-score    = 0.1022 (d0= 5.38)
MaxSub-score= 0.0441 (d0= 3.50)
GDT-TS-score= 0.0658 %(d<1)=0.0239 %(d<2)=0.0335 %(d<4)=0.0766 %(d<8)=0.1292
GDT-HA-score= 0.0383 %(d<0.5)=0.0191 %(d<1)=0.0239 %(d<2)=0.0335 %(d<4)=0.0766

```

```

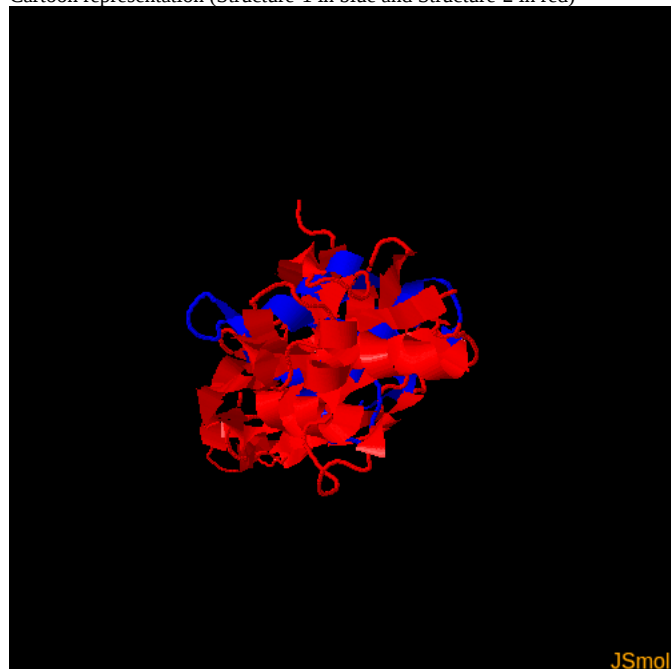
----- rotation matrix to rotate Chain-1 to Chain-2 -----
i          t(i)          u(i,1)          u(i,2)          u(i,3)
1      9.4562730067      -0.8736472868      -0.4037069519      -0.2715899764
2      7.8366495505      -0.3894786939      0.9148050850      0.1069486020
3      77.9687855429      0.2916277856      0.0123431533      -0.9564522368

```

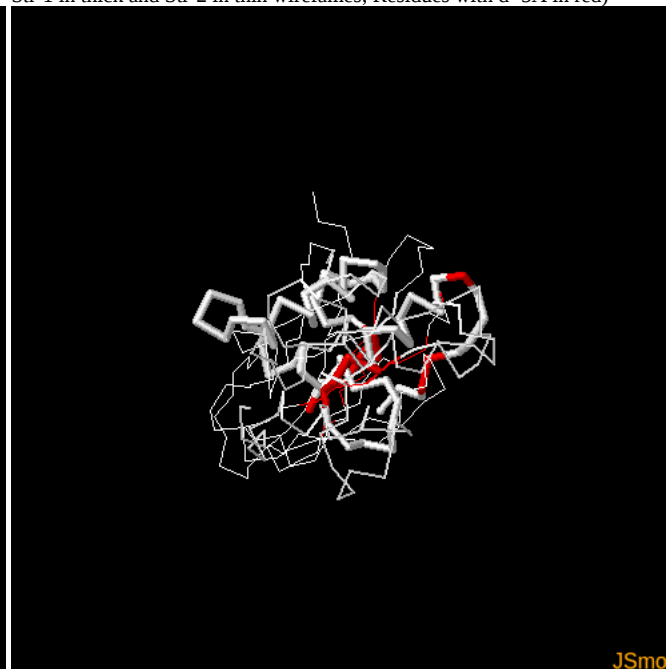
Superposition in the TM-score: Length(d<5.0)= 13 RMSD= 2.91
(":" denotes the residue pairs of distance < 5.0 Angstrom)

[illegible]

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



Str-1 in thick and Str-2 in thin wireframes; Residues with $d < 5\text{\AA}$ in red)



- Click [A680874.pdb](#) to download the first structure that you submitted.
- Click [B680874.pdb](#) to download the second structure that you submitted.
- Click [C680874.pdb](#) to download the superposed structure in C-alpha trace (This file is in a Rasmol script format, you can run 'rasmol -script C680874.pdb' to view the structure).
- Click [D680874.pdb](#) to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D680874.pdb' to view the structure).

- 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](#)