

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: zhang@umich.edu                             *
*****
```

```
Structure1: A196059      Length=    84
Structure2: B196059      Length=    84 (by which all scores are normalized)
Number of residues in common= 84
RMSD of the common residues= 7.785
```

TM-score = 0.6882 (d0= 3.29)
MaxSub-score= 0.6814 (d0= 3.50)
GDT-TS-score= 0.6964 %(d<1)=0.5357 %(d<2)=0.6905 %(d<4)=0.7619 %(d<8)=0.7976
GDT-HA-score= 0.5804 %(d<0.5)=0.3333 %(d<1)=0.5357 %(d<2)=0.6905 %(d<4)=0.7619

```

----- rotation matrix to rotate Chain-1 to Chain-2 -----
i          t(i)          u(i,1)          u(i,2)          u(i,3)
1    68.7257023885    -0.5381893876    0.4563427227    -0.7085926210
2    -2.0496179616    -0.6265079558    0.3457661781    0.6985223915
3    2.9491839929    0.5637729724    0.8198762526    0.0998146587

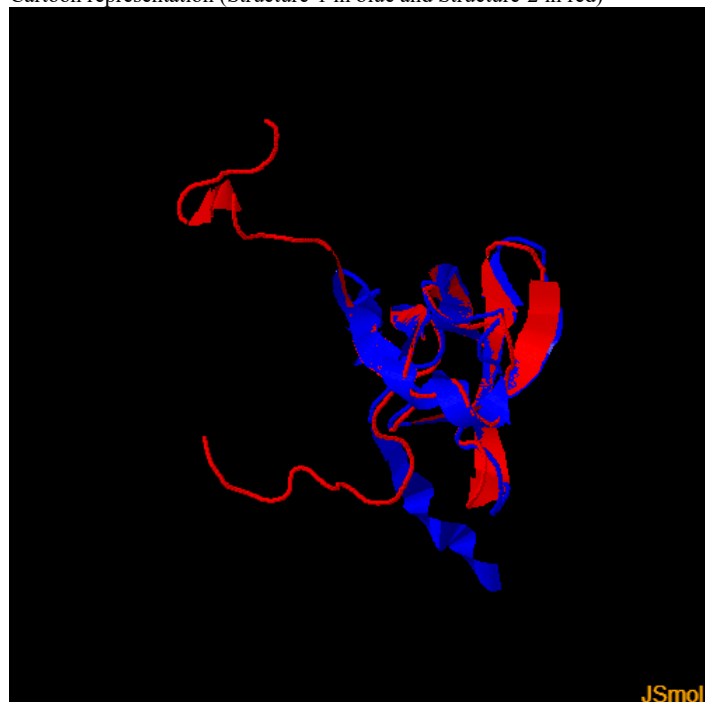
```

Superposition in the IM-space: Length(<5.0) = 64 RMSD= 1.33
 ("." denotes the residue pairs of distance < 5.0 Angstrom)
 MAGDPLPKYWSYPVGLAVEINNARYGCPHHVGRKGKIEHLHSATYDAVSDETGDIYFKEHELTPLKGGGLAYVLEHHHHHH

 MAGDPLPKYWSYPVGLAVEINNARYGCPHHVGRKGKIEHLHSATYDAVSDETGDIYFKEHELTPLKGGGLAYVLEHHHHHH
 1234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234

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 wireframes; Residues with $d < 5\text{\AA}$ in red)



Document downloads

- Click [A196059.pdb](#) to download the first structure that you submitted.
- Click [B196059.pdb](#) to download the second structure that you submitted.
- Click [C196059.pdb](#) to download the superposed structure in C-alpha trace (This file is in a Rasmol script format, you can run 'rasmol -script C196059.pdb' to view the structure).
- Click [D196059.pdb](#) to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D196059.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](#)