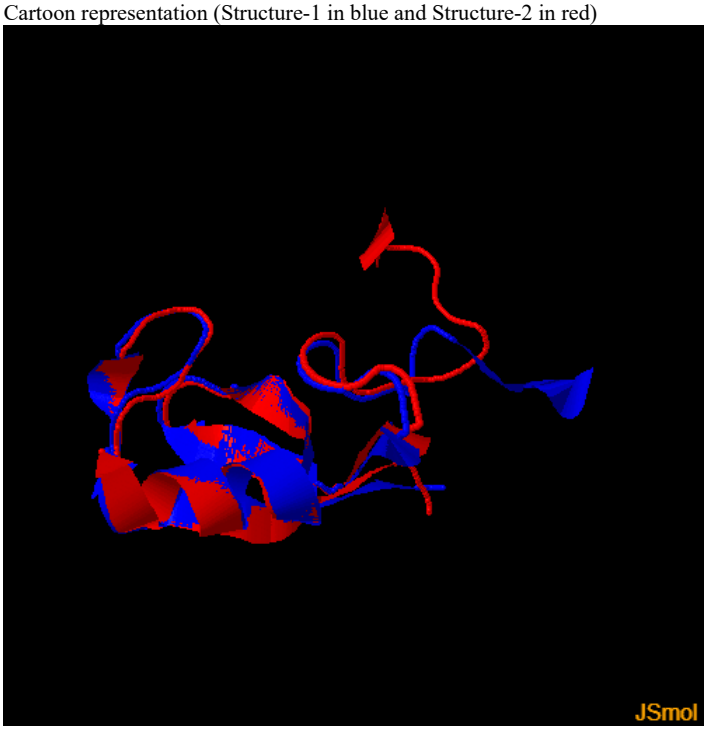
TM-score Results

```
 ***************************************************************************
 *                              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: A807922     Length=   61
Structure2: B807922     Length=   61 (by which all scores are normalized)
Number of residues in common=   61
RMSD of  the common residues=    4.105

TM-score    = 0.8293  (d0= 2.64)
MaxSub-score= 0.8448  (d0= 3.50)
GDT-TS-score= 0.8689 %(d<1)=0.7705 %(d<2)=0.8689 %(d<4)=0.9016 %(d<8)=0.9344
GDT-HA-score= 0.7418 %(d<0.5)=0.4262 %(d<1)=0.7705 %(d<2)=0.8689 %(d<4)=0.9016

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1     -6.9984097960   0.7877803716  -0.0136924767  -0.6158040291
 2    -11.2968651468  -0.4210719006   0.7176987321  -0.5546232816
 3     -8.2451381614   0.4495559373   0.6962191078   0.5596234567

Superposition in the TM-score: Length(d<5.0)= 55  RMSD=  0.96
(":" denotes the residue pairs of distance < 5.0 Angstrom)
SHMPTSEEDLCPICYAHPISAVFQPCGHKSCKACINQHLMNNKDCFFCKTTIVSVEDWEKG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::::
SHMPTSEEDLCPICYAHPISAVFQPCGHKSCKACINQHLMNNKDCFFCKTTIVSVEDWEKG
12345678901234567890123456789012345678901234567890123456789012345678901
```

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 A807922.pdb to download the first structure that you submitted.
- Click B807922.pdb to download the second structure that you submitted.
- Click C807922.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C807922.pdb' to view the structure).
- Click D807922.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D807922.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