TM-score Results

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*                              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                           *
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Structure1: A853690     Length=   73
Structure2: B853690     Length=   73 (by which all scores are normalized)
Number of residues in common=   11
RMSD of  the common residues=    0.407

TM-score    = 0.1481  (d0= 3.00)
MaxSub-score= 0.1488  (d0= 3.50)
GDT-TS-score= 0.1473 %(d<1)=0.1370 %(d<2)=0.1507 %(d<4)=0.1507 %(d<8)=0.1507
GDT-HA-score= 0.1438 %(d<0.5)=0.1370 %(d<1)=0.1370 %(d<2)=0.1507 %(d<4)=0.1507

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i        t(i)         u(i,1)         u(i,2)         u(i,3)
 1     4.2541864975    0.7122720658   -0.6971421019    0.0816173631
 2     8.9488459818    0.4195807867    0.5161080436    0.7467157764
 3     2.0418661158   -0.5626903835   -0.4976197113    0.6601167740

Superposition in the TM-score: Length(d<5.0)= 11  RMSD=  0.41
(":" denotes the residue pairs of distance < 5.0 Angstrom)
VADDWLKQYANREKAIQHAIERFNTKPIQTIKKHDYQRFVDDISAQYSKNYVDSIVASTNMIFKYAYDTRLIK------------------------------------------------------------
                                                      ::::::::::::
----------------------------------------------------VADDWLKQYAN-------REKAIQHAIERFNTKPIQTIKKHDYQRFVDDISAQYSKNYVDSIVASTNMIFKYAYDTRLIK
12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345
```
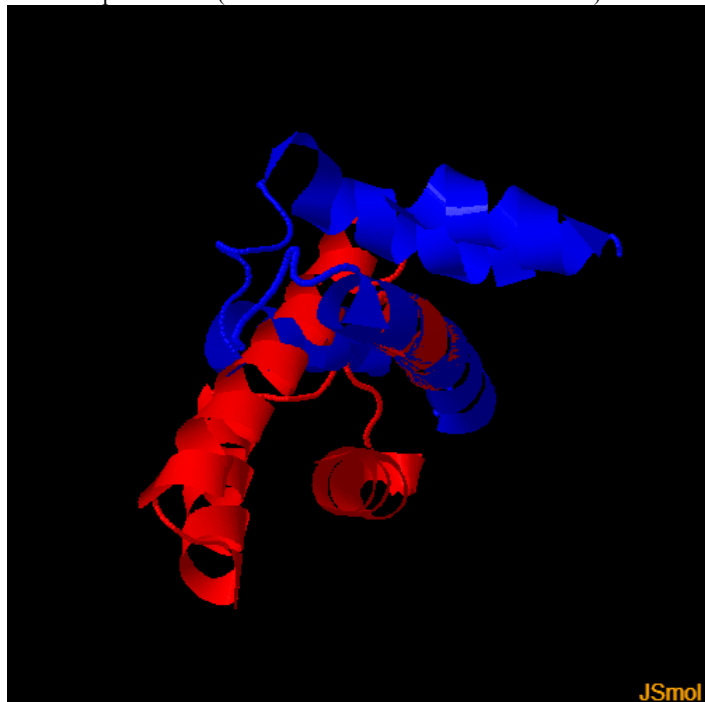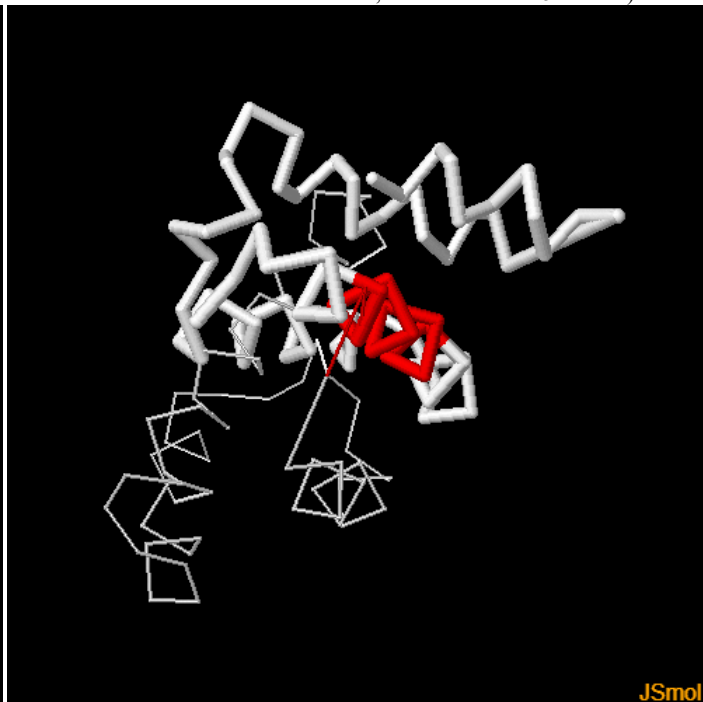
Visualization of TM-score superposition

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 A853690.pdb to download the first structure that you submitted.
- Click B853690.pdb to download the second structure that you submitted.
- Click C853690.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C853690.pdb' to view the structure).
- Click D853690.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D853690.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