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                          *
 **************************************************************************

Structure1: A444159     Length=   92
Structure2: B444159     Length=   92 (by which all scores are normalized)
Number of residues in common=   92
RMSD of  the common residues=    4.801

TM-score    = 0.7333  (d0= 3.48)
MaxSub-score= 0.6999  (d0= 3.50)
GDT-TS-score= 0.7255 %(d<1)=0.3913 %(d<2)=0.7065 %(d<4)=0.8587 %(d<8)=0.9457
GDT-HA-score= 0.5353 %(d<0.5)=0.1848 %(d<1)=0.3913 %(d<2)=0.7065 %(d<4)=0.8587

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1      3.0358118098  -0.2319123359   0.9429160684  -0.2390103687
 2     -2.9946983979   0.8362843925   0.0677696901  -0.5440916136
 3      1.6774951143  -0.4968350665  -0.3260621980  -0.8042626186

Superposition in the TM-score: Length(d<5.0)= 79  RMSD=  1.79
(":" denotes the residue pairs of distance < 5.0 Angstrom)
MPHKEKHPLQDMFTSAIEAVARDSGWAELSAVGSYLAKNDPSFDPRNWGHGRLSQMVKKLDFLTVQESRNGSKLHSEIRLRHDGLEHHHHHH
      ::::::::::::::::  :::::::::::::::::::::::: ::::::::::::::::::::::::::::::::::::::
MPHKEKHPLQDMFTSAIEAVARDSGWAELSAVGSYLAKNDPSFDPRNWGHGRLSQMVKKLDFLTVQESRNGSKLHSEIRLRHDGLEHHHHHH
12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012
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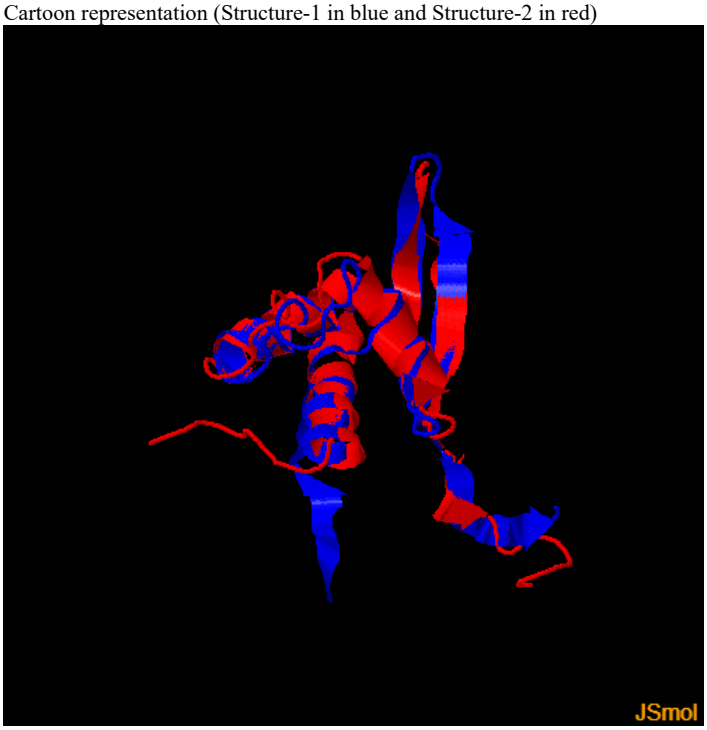
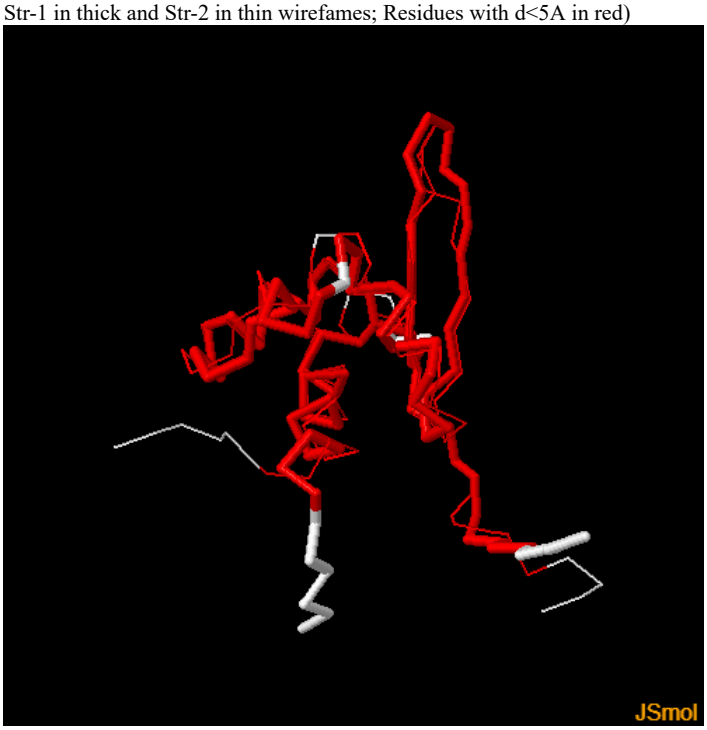
Visualization of TM-score superposition

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 A444159.pdb to download the first structure that you submitted.
- Click B444159.pdb to download the second structure that you submitted.
- Click C444159.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C444159.pdb' to view the structure).
- Click D444159.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D444159.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).

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