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: A569581     Length=   95
Structure2: B569581     Length=   95 (by which all scores are normalized)
Number of residues in common=   95
RMSD of  the common residues=    6.198

TM-score    = 0.8056  (d0= 3.54)
MaxSub-score= 0.7928  (d0= 3.50)
GDT-TS-score= 0.7947 %(d<1)=0.5263 %(d<2)=0.8211 %(d<4)=0.8947 %(d<8)=0.9368
GDT-HA-score= 0.6184 %(d<0.5)=0.2316 %(d<1)=0.5263 %(d<2)=0.8211 %(d<4)=0.8947

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1      1.2217504482   0.8532279868  -0.4038640551  -0.3299936782
 2      0.9135659324   0.5210892720   0.6863913428   0.5072798982
 3      2.9939956092   0.0216326871  -0.6047815718   0.7960975300

Superposition in the TM-score: Length(d<5.0)= 85  RMSD=  1.38
(":" denotes the residue pairs of distance < 5.0 Angstrom)
MGHHHHHHSHGKSDFIKVNVSNSHNDAVAFEVKLAKDLTVAQLKTKLEILTGGCAGTMKVQVFKGDTCVSTMDNNDAQLGYYANSDGLRLHVVDS
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
MGHHHHHHSHGKSDFIKVNVSNSHNDAVAFEVKLAKDLTVAQLKTKLEILTGGCAGTMKVQVFKGDTCVSTMDNNDAQLGYYANSDGLRLHVVDS
12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345
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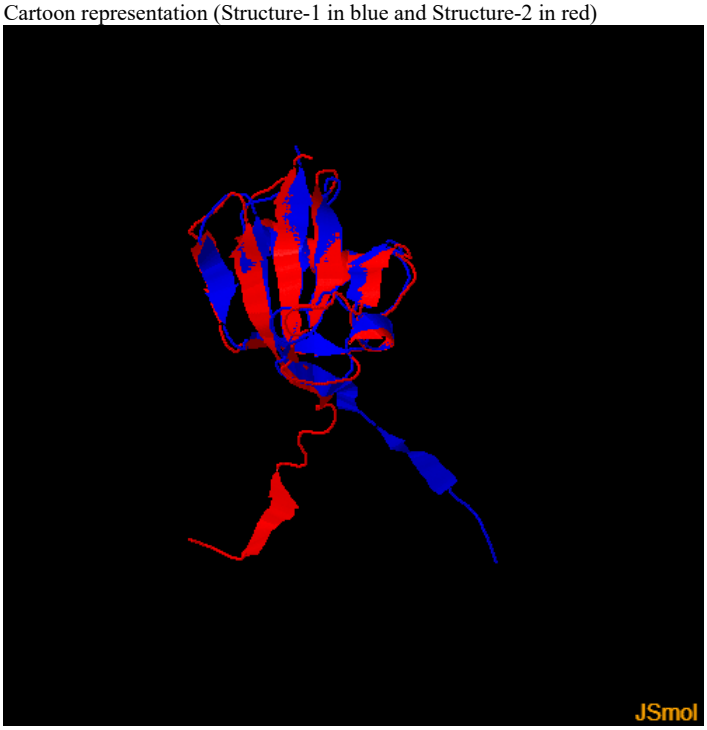
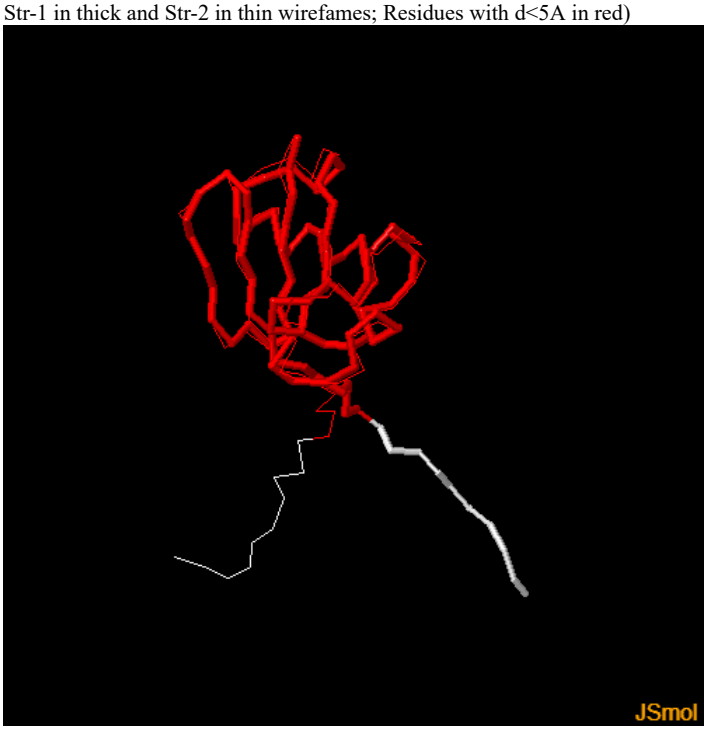
Visualization of TM-score superposition

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 A569581.pdb to download the first structure that you submitted.
- Click B569581.pdb to download the second structure that you submitted.
- Click C569581.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C569581.pdb' to view the structure).
- Click D569581.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D569581.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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