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: A659661     Length=  260
Structure2: B659661     Length=  260 (by which all scores are normalized)
Number of residues in common=  260
RMSD of  the common residues=    0.642

TM-score    = 0.9905  (d0= 5.96)
MaxSub-score= 0.9751  (d0= 3.50)
GDT-TS-score= 0.9904 %(d<1)=0.9692 %(d<2)=0.9962 %(d<4)=0.9962 %(d<8)=1.0000
GDT-HA-score= 0.9115 %(d<0.5)=0.6846 %(d<1)=0.9692 %(d<2)=0.9962 %(d<4)=0.9962

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1     -6.6407886887   0.2346782280   0.9709904092   0.0458667045
 2     44.6807806514  -0.7820265845   0.2166125669  -0.5843914929
 3     -1.0573249440  -0.5773738394   0.1012749777   0.8101745667

Superposition in the TM-score: Length(d<5.0)=259  RMSD=  0.53
(":" denotes the residue pairs of distance < 5.0 Angstrom)
AVTQRELFEFVLNDPLLASSLYINIALAGLSILLFVFMTRGLDDPRAKLIAVSTILVPVVSIASYTGLASGLTISVLEMPAGHFAEGSSVMLGGEEVDGVVTMWGRYLTWALSTPMILLALGLLAGSNATKLFTAIT
 ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
AVTQRELFEFVLNDPLLASSLYINIALAGLSILLFVFMTRGLDDPRAKLIAVSTILVPVVSIASYTGLASGLTISVLEMPAGHFAEGSSVMLGGEEVDGVVTMWGRYLTWALSTPMILLALGLLAGSNATKLFTAIT
12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567
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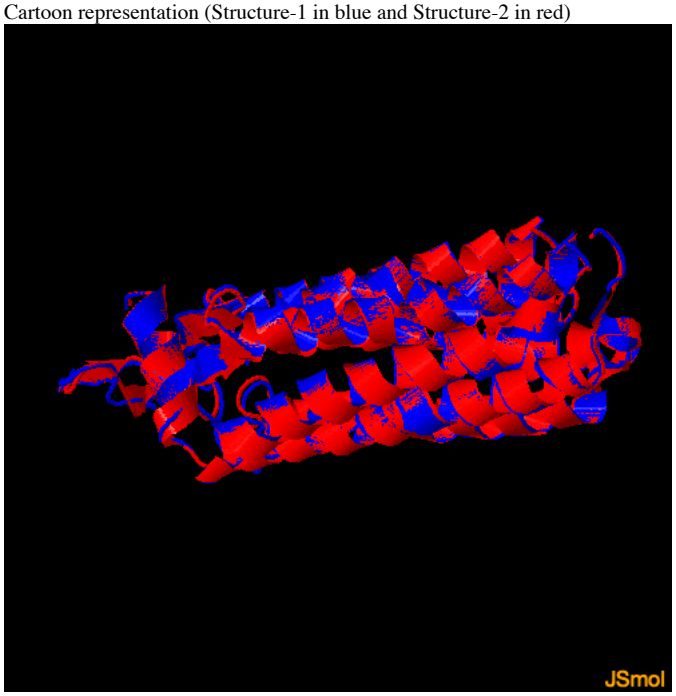
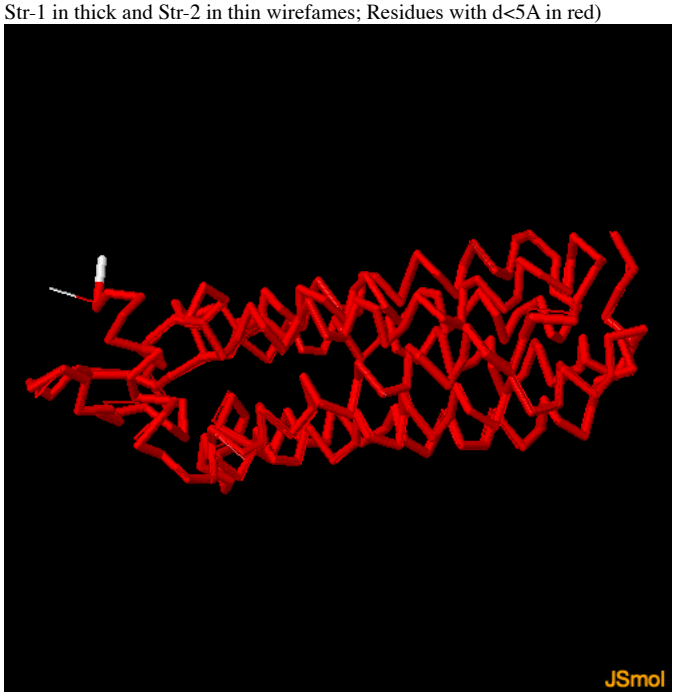
Visualization of TM-score superposition

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 A659661.pdb to download the first structure that you submitted.
- Click B659661.pdb to download the second structure that you submitted.
- Click C659661.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C659661.pdb' to view the structure).
- Click D659661.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D659661.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).