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: A732053     Length=  109
Structure2: B732053     Length=  109 (by which all scores are normalized)
Number of residues in common=  109
RMSD of  the common residues=    4.807

TM-score    = 0.8751  (d0= 3.84)
MaxSub-score= 0.8554  (d0= 3.50)
GDT-TS-score= 0.8761 %(d<1)=0.7064 %(d<2)=0.8991 %(d<4)=0.9266 %(d<8)=0.9725
GDT-HA-score= 0.7225 %(d<0.5)=0.3578 %(d<1)=0.7064 %(d<2)=0.8991 %(d<4)=0.9266

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1      0.6227171204  -0.8009108155  -0.2241043709  -0.5552648886
 2     -0.5737271324  -0.5755268755   0.0321780659   0.8171495503
 3      0.8916082558  -0.1652594357   0.9740337792  -0.1547498494

Superposition in the TM-score: Length(d<5.0)=100  RMSD=  1.00
(":" denotes the residue pairs of distance < 5.0 Angstrom)
MEPQLTKIVDIVENGQWANLKAKVIQLWENTHESISQVGLLGDETGIIKFTIWKNAELPLLEQGESYLLRSVVVGEYNDRFQVQVNKNSSIEKLSEPIEVGLEHHHHHH
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
MEPQLTKIVDIVENGQWANLKAKVIQLWENTHESISQVGLLGDETGIIKFTIWKNAELPLLEQGESYLLRSVVVGEYNDRFQVQVNKNSSIEKLSEPIEVGLEHHHHHH
12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789
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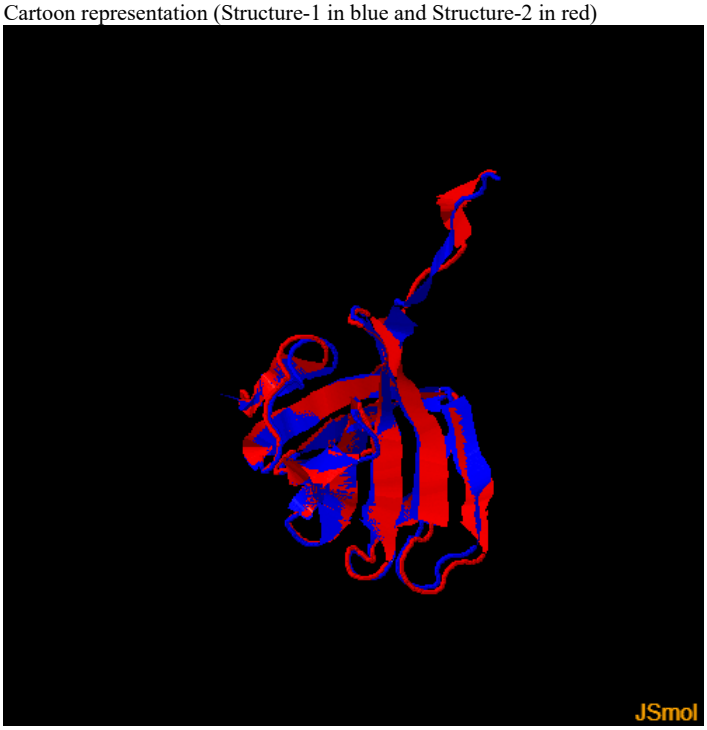
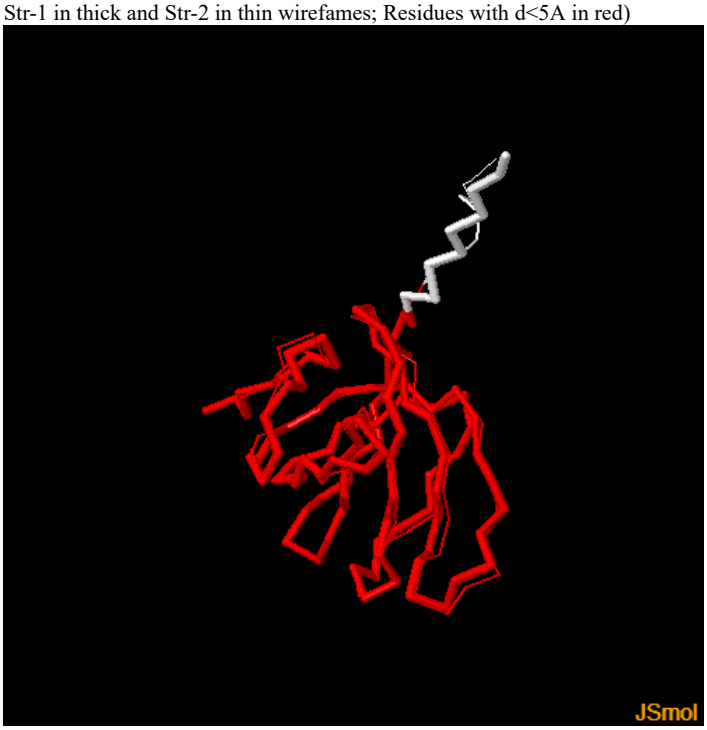
Visualization of TM-score superposition

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 A732053.pdb to download the first structure that you submitted.
- Click B732053.pdb to download the second structure that you submitted.
- Click C732053.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C732053.pdb' to view the structure).
- Click D732053.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D732053.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