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: A635248     Length=  108
Structure2: B635248     Length=  108 (by which all scores are normalized)
Number of residues in common=   48
RMSD of  the common residues=    8.199

TM-score    = 0.1888  (d0= 3.82)
MaxSub-score= 0.1553  (d0= 3.50)
GDT-TS-score= 0.2060 %(d<1)=0.1574 %(d<2)=0.1574 %(d<4)=0.1852 %(d<8)=0.3241
GDT-HA-score= 0.1597 %(d<0.5)=0.1389 %(d<1)=0.1574 %(d<2)=0.1574 %(d<4)=0.1852

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1     -9.3870264867   0.9302705588  -0.1395785091   0.3392853183
 2     -5.7647338262  -0.1612275531  -0.9862483567   0.0363298087
 3     -6.1767115563   0.3295487271  -0.0884986931  -0.9399817114

Superposition in the TM-score: Length(d<5.0)= 18  RMSD=  1.04
(":" denotes the residue pairs of distance < 5.0 Angstrom)
RDSFGDWAEKFLKSKEADGVSVSQLNSYKNYCRNHLSPLYMKSLSEILPADIQSIINETKLAKNTLKAIRNTASQIFRLAIENRAIDFNPADYVRIPKIALEHHHHHH----------------------------------------
                                                                ::::::::::::::::                      :
----------------------------------------------------------------RDSFGDWAEKFLKSKEADGVSVSQLNSYKNYCRNHLSPLYMKSLSEILPADIQSIINETKLAKNTLKAIRNTASQIFRLAIENRAIDFN
1234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789
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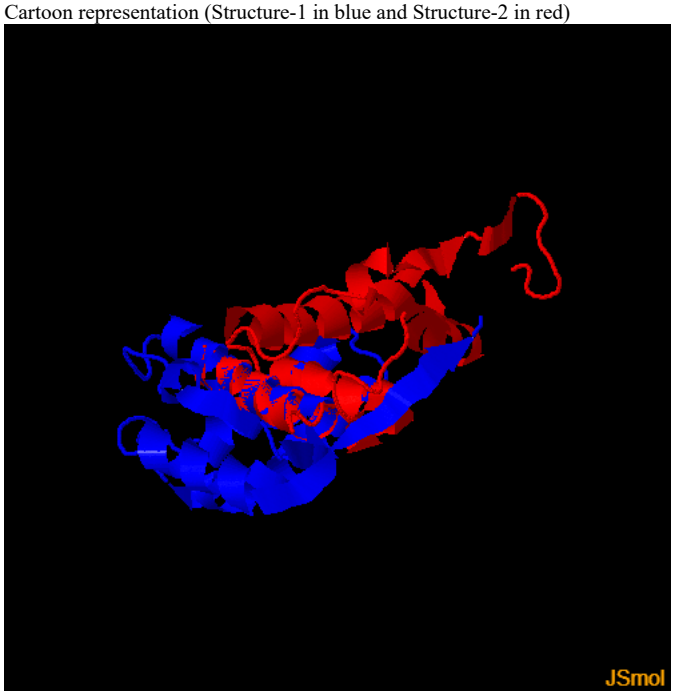
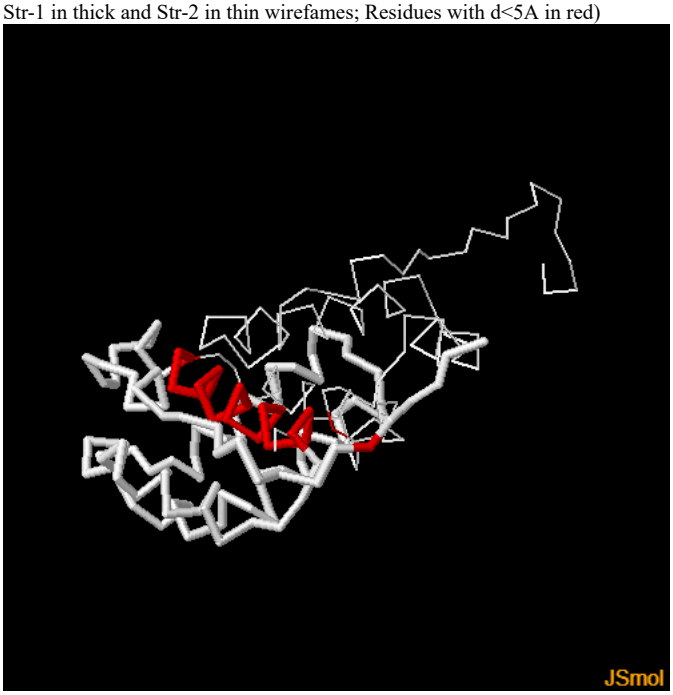
Visualization of TM-score superposition

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 A635248.pdb to download the first structure that you submitted.
- Click B635248.pdb to download the second structure that you submitted.
- Click C635248.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C635248.pdb' to view the structure).
- Click D635248.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D635248.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