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: A952383     Length=  338
Structure2: B952383     Length=  338 (by which all scores are normalized)
Number of residues in common=  338
RMSD of  the common residues=   18.374

TM-score    = 0.5600  (d0= 6.71)
MaxSub-score= 0.5402  (d0= 3.50)
GDT-TS-score= 0.5466 %(d<1)=0.5385 %(d<2)=0.5385 %(d<4)=0.5414 %(d<8)=0.5680
GDT-HA-score= 0.5392 %(d<0.5)=0.5385 %(d<1)=0.5385 %(d<2)=0.5385 %(d<4)=0.5414

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1    -23.1043923245  -0.9431572642  -0.0712425050   0.3246211336
 2     91.6544324992  -0.1228424255   0.9823119352  -0.1413258666
 3     18.9284987167  -0.3088108052  -0.1731697651  -0.9352262395

Superposition in the TM-score: Length(d<5.0)=183  RMSD=  0.21
(":" denotes the residue pairs of distance < 5.0 Angstrom)
GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI

GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI
12345678901234567890123456789012345678901234567890123456789012345678901234567890123
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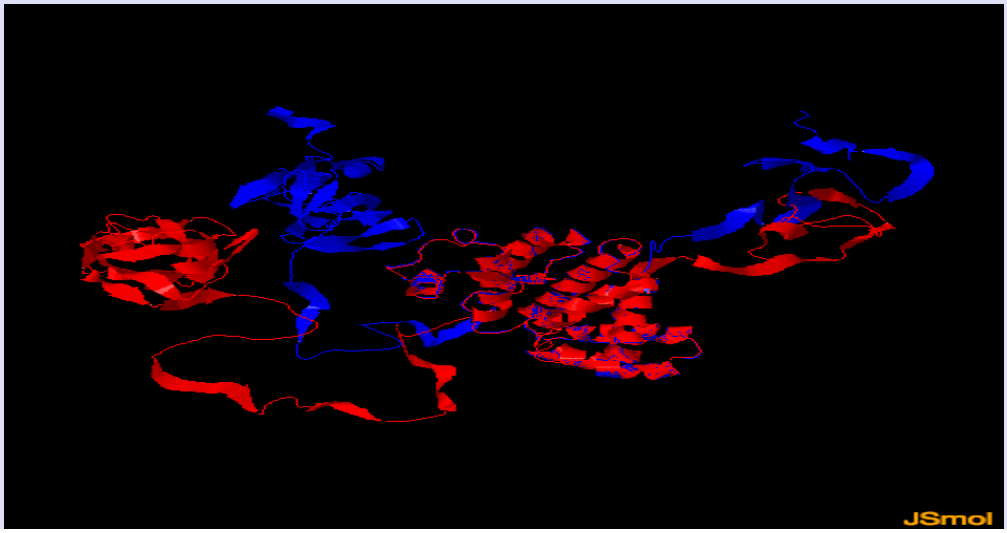
Visualization

TM-score superposition (Structure-1 in blue and Structure-2 in red)



Document downloads

- Click A952383.pdb to download the first structure that you submitted.
- Click B952383.pdb to download the second structure that you submitted.
- Click C952383.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C952383.pdb' to view the structure).
- Click D952383.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D952383.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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