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: A148826     Length=  338
Structure2: B148826     Length=  338 (by which all scores are normalized)
Number of residues in common=  338
RMSD of  the common residues=   24.919

TM-score    = 0.5572  (d0= 6.71)
MaxSub-score= 0.5385  (d0= 3.50)
GDT-TS-score= 0.5451 %(d<1)=0.5385 %(d<2)=0.5385 %(d<4)=0.5444 %(d<8)=0.5592
GDT-HA-score= 0.5399 %(d<0.5)=0.5385 %(d<1)=0.5385 %(d<2)=0.5385 %(d<4)=0.5444

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1     68.0445433300  -0.4682241625   0.0727806615  -0.8806072388
 2      7.0905763866   0.6827023218   0.6624983364  -0.3082425896
 3     89.9246985260   0.5609667312  -0.7455192349  -0.3598852553

Superposition in the TM-score: Length(d<5.0)=185  RMSD=  0.59
(":" denotes the residue pairs of distance < 5.0 Angstrom)
GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI

GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI
1234567890123456789012345678901234567890123456789012345678901234567890123456789012
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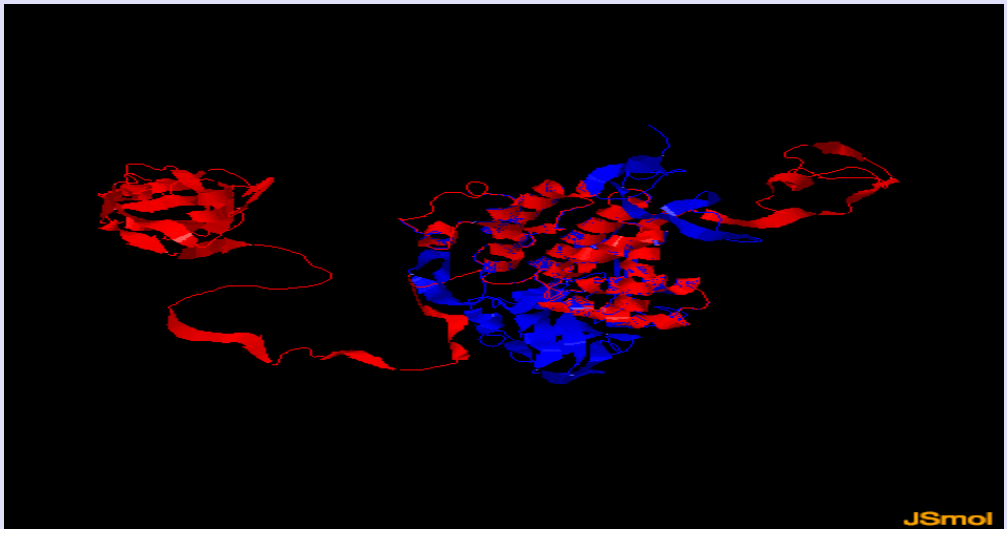
Visualization

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



Document downloads

- Click A148826.pdb to download the first structure that you submitted.
- Click B148826.pdb to download the second structure that you submitted.
- Click C148826.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C148826.pdb' to view the structure).
- Click D148826.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D148826.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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