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: A891283     Length=  729
Structure2: B891283     Length=  729 (by which all scores are normalized)
Number of residues in common=  729
RMSD of  the common residues=   65.620

TM-score    = 0.4227  (d0= 9.28)
MaxSub-score= 0.4060  (d0= 3.50)
GDT-TS-score= 0.4071 %(d<1)=0.4060 %(d<2)=0.4060 %(d<4)=0.4060 %(d<8)=0.4102
GDT-HA-score= 0.4060 %(d<0.5)=0.4060 %(d<1)=0.4060 %(d<2)=0.4060 %(d<4)=0.4060

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1    101.3128030685   0.3128497595  -0.9311254747   0.1874309962
 2    165.1243898323   0.2618047376   0.2742306264   0.9253409333
 3     91.2363601823  -0.9130078353  -0.2404223657   0.3295660461

Superposition in the TM-score: Length(d<5.0)=296  RMSD=  0.00
(":" denotes the residue pairs of distance < 5.0 Angstrom)
GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI
       :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI
12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012
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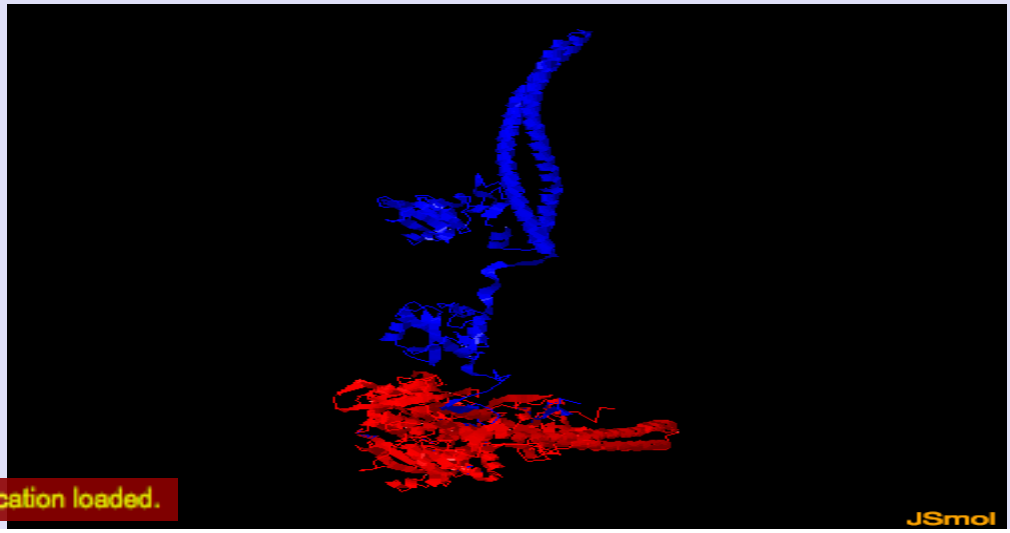
Visualization

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



Document downloads

- Click A891283.pdb to download the first structure that you submitted.
- Click B891283.pdb to download the second structure that you submitted.
- Click C891283.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C891283.pdb' to view the structure).
- Click D891283.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D891283.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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