# 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: A924759     Length=  729
Structure2: B924759     Length=  729 (by which all scores are normalized)
Number of residues in common=  729
RMSD of  the common residues=   61.839

TM-score    = 0.4298  (d0= 9.28)
MaxSub-score= 0.4067  (d0= 3.50)
GDT-TS-score= 0.4091 %(d<1)=0.4060 %(d<2)=0.4060 %(d<4)=0.4088 %(d<8)=0.4156
GDT-HA-score= 0.4067 %(d<0.5)=0.4060 %(d<1)=0.4060 %(d<2)=0.4060 %(d<4)=0.4088

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1    -83.2898551840   0.2948969942   0.8292855574  -0.4746801314
 2     37.1732252857   0.7632443945   0.0944459902   0.6391697343
 3    -62.7899341735   0.5748858644  -0.5507861829  -0.6050957145

Superposition in the TM-score: Length(d<5.0)=298  RMSD=  0.33
(":" denotes the residue pairs of distance < 5.0 Angstrom)
GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI
    : ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI
12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012
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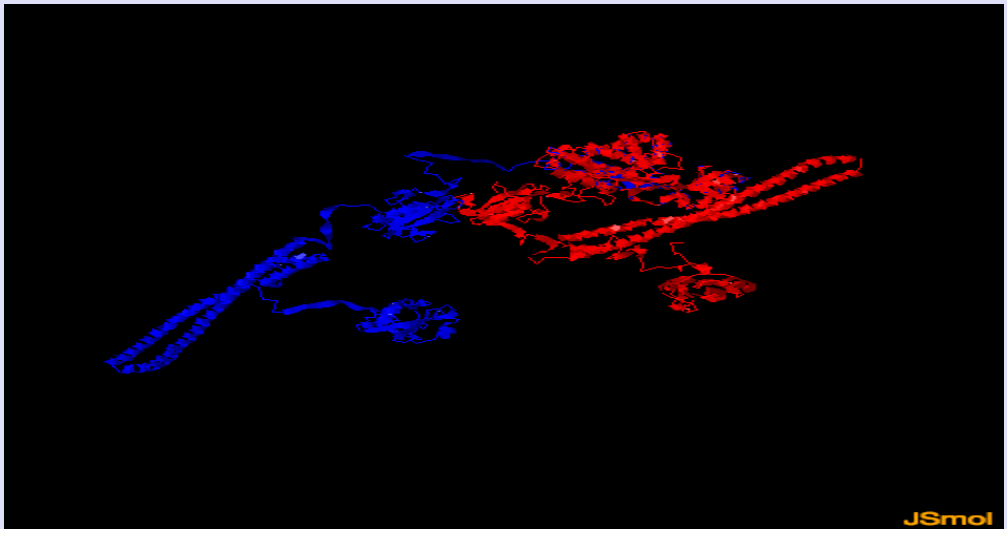
# Visualization

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



## Document downloads

- Click A924759.pdb to download the first structure that you submitted.
- Click B924759.pdb to download the second structure that you submitted.
- Click C924759.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C924759.pdb' to view the structure).
- Click D924759.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D924759.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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