# 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: A604910     Length=  338
Structure2: B604910     Length=  338 (by which all scores are normalized)
Number of residues in common=  338
RMSD of  the common residues=   22.014

TM-score    = 0.5607  (d0= 6.71)
MaxSub-score= 0.5420  (d0= 3.50)
GDT-TS-score= 0.5459 %(d<1)=0.5385 %(d<2)=0.5414 %(d<4)=0.5473 %(d<8)=0.5562
GDT-HA-score= 0.5414 %(d<0.5)=0.5385 %(d<1)=0.5385 %(d<2)=0.5414 %(d<4)=0.5473

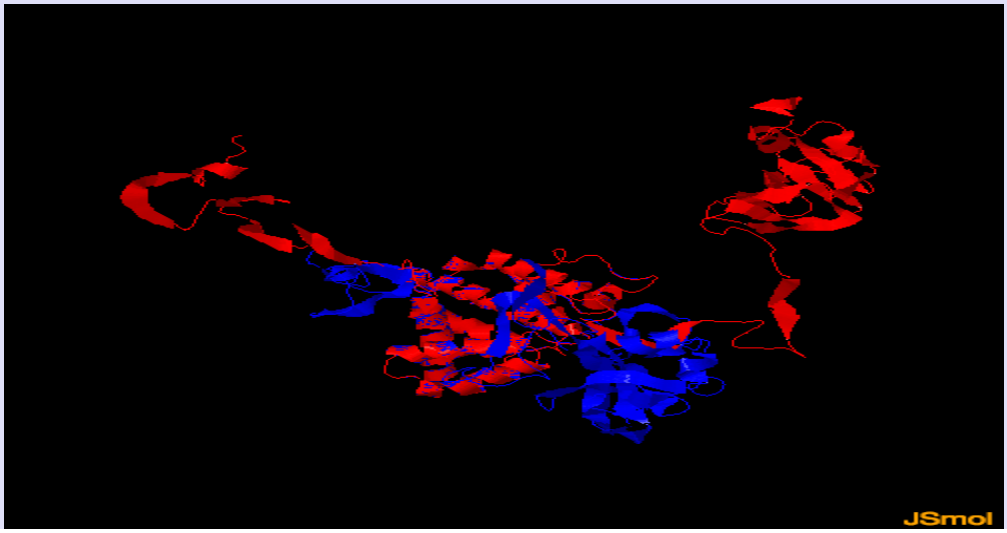
 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1    -97.6315560285   0.1820812596   0.0765116225   0.9803021914
 2   -102.1311558933   0.6071798765   0.7754352828  -0.1732995089
 3    -24.8596813915  -0.7734203336   0.6267743564   0.0947359155

Superposition in the TM-score: Length(d<5.0)=185  RMSD=  0.44
(":" denotes the residue pairs of distance < 5.0 Angstrom)
GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI

GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI
1234567890123456789012345678901234567890123456789012345678901234567890123456789012
```

# Visualization

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



## Document downloads

- Click A604910.pdb to download the first structure that you submitted.
- Click B604910.pdb to download the second structure that you submitted.
- Click C604910.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C604910.pdb' to view the structure).
- Click D604910.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D604910.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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