# 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: A325474     Length=  729
Structure2: B325474     Length=  729 (by which all scores are normalized)
Number of residues in common=  729
RMSD of  the common residues=   35.040

TM-score    = 0.2924  (d0= 9.28)
MaxSub-score= 0.2497  (d0= 3.50)
GDT-TS-score= 0.2572 %(d<1)=0.2497 %(d<2)=0.2497 %(d<4)=0.2524 %(d<8)=0.2771
GDT-HA-score= 0.2503 %(d<0.5)=0.2497 %(d<1)=0.2497 %(d<2)=0.2497 %(d<4)=0.2524

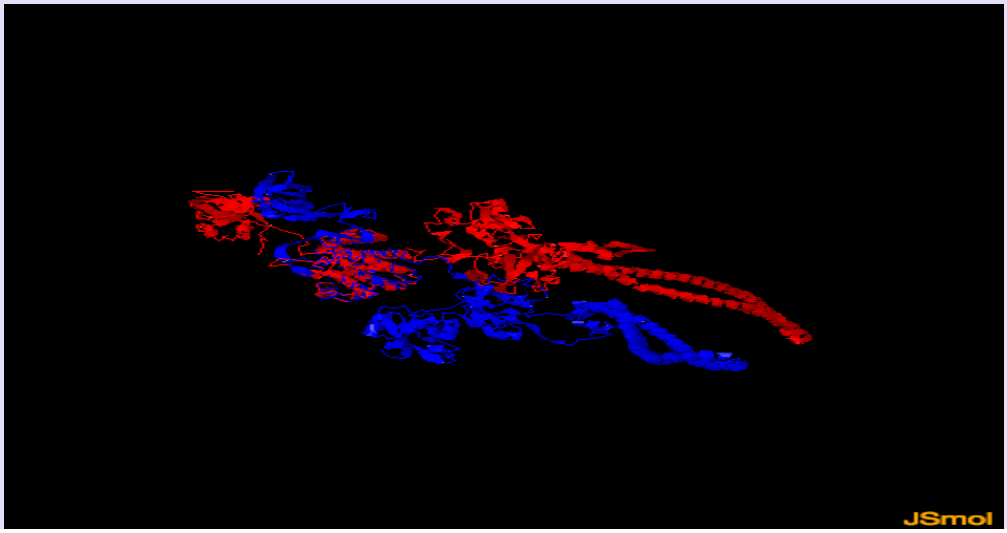
 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1     27.5611062652  -0.6994566772  -0.5368655057   0.4717369876
 2     11.3346597073   0.5118527096  -0.8369759616  -0.1935924674
 3    186.8648027070   0.4987656367   0.1060503114   0.8602244888

Superposition in the TM-score: Length(d<5.0)=185  RMSD=  0.64
(":" denotes the residue pairs of distance < 5.0 Angstrom)
GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI

GPLGSMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYI
12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012
```

# Visualization

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



## Document downloads

- Click A325474.pdb to download the first structure that you submitted.
- Click B325474.pdb to download the second structure that you submitted.
- Click C325474.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C325474.pdb' to view the structure).
- Click D325474.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D325474.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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