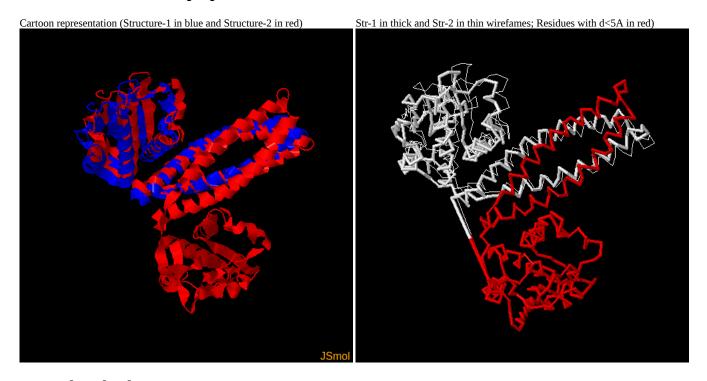
4/15/2018 TM-score Server

TM-score Results

```
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
                            Length= 484
Length= 484 (by which all scores are normalized)
Structure1: A917421
Structure2: B917421
Number of residues in common= 242
                                       0.000
RMSD of the common residues=
             = 0.5000
                          (d0 = 7.83)
TM-score
MaxSub-score= 0.5000
                         (d0=3.50)
GDT-TS-score= 0.5000 %(d<1)=0.5000 %(d<2)=0.5000 %(d<4)=0.5000 %(d<8)=0.5000
GDT-HA-score= 0.5000 %(d<0.5)=0.5000 %(d<1)=0.5000 %(d<2)=0.5000 %(d<4)=0.5000
 ----- rotation matrix to rotate Chain-1 to Chain-2 -----
                                                                  u(i.3)
 i
                              u(i.1)
                                                u(i.2)
                           1.00000000000
         0.000000000
                                             0.000000000
                                                               0.0000000000
 1
         -0.000000000
                           0.000000000
                                             1.0000000000
         0.000000000
                           0.000000000
                                              0.0000000000
                                                               1.0000000000
Superposition in the TM-score: Length(d<5.0)=242 RMSD= 0.00 (":" denotes the residue pairs of distance < 5.0 Angstrom) LSQAQKMQAIGQLAGGVAHDFNNLLTAIQLRLDQLLHRHPVGDPSYEGLNEIRQTGVRAADLVRKLLAFSRKQTVQREVLDLGELISEFEVLLRRLLREDVKLITDYGRDLPQVRADKSQLETAVMNLAVNARDAV
LSQAQKMQAIGQLAGGVAHDFNNLLTAIQLRLDQLLHRHPVGDPSYEGLNEIRQTGVRAADLVRKLLAFSRKQTVQREVLDLGELISEFEVLLRRLLREDVKLITDYGRDLPQVRADKSQLETAVMNLAVNARDAV
```

Visualization of TM-score superposition



Document downloads

- Click <u>A917421.pdb</u> to download the first structure that you submitted.
- Click <u>B917421.pdb</u> to download the second structure that you submitted.
- Click <u>C917421.pdb</u> to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C917421.pdb' to view the structure).
- Click <u>D917421.pdb</u> to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D917421.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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