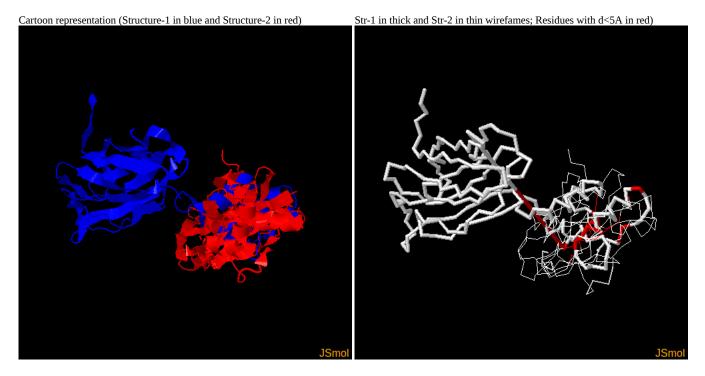
4/15/2018 TM-score Server

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
  Length= 212
Length= 209 (by which all scores are normalized)
Structure1: A926245
Structure2: B926245
Number of residues in common=
                            74
                            11.897
RMSD of the common residues=
          = 0.1022
                   (d0 = 5.38)
TM-score
MaxSub-score= 0.0441
                  (d0=3.50)
GDT-TS-score= 0.0658 %(d<1)=0.0239 %(d<2)=0.0335 %(d<4)=0.0766 %(d<8)=0.1292
GDT-HA-score= 0.0383 %(d<0.5)=0.0191 %(d<1)=0.0239 %(d<2)=0.0335 %(d<4)=0.0766
 ----- rotation matrix to rotate Chain-1 to Chain-2
                                                 u(i.3)
i
                      u(i.1)
                                    u(i.2)
       9.4562730067
                  -0.8736472868 -0.4037069519 -0.2715899764
1
       7.8366495505
                   -0.3894786939
                                  0.9148050850 -0.1069486020
      77.9687855429
                    0.2916277856
                                  0.0123431533
                                              -0.9564522368
Superposition in the TM-score: Length(d<5.0)= 13 RMSD= 2.91
    denotes the residue pairs of distance < 5.0 Angstrom)
.
PVANADVVFDFONYTAKAGDEVTVDVLVDSKNKPISADVKFKVDSPLTIEEIDKESLAFNTTVTNAILGANFKSLDDKGEPLVPKDGAAVFTLYVNVPANTPDGTYYVGFNGKNEVHKSNDGSQFTVASKNGAITV
```

Visualization of TM-score superposition



Document downloads

- Click <u>A926245.pdb</u> to download the first structure that you submitted.
- Click <u>B926245.pdb</u> to download the second structure that you submitted.
- Click <u>C926245.pdb</u> to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C926245.pdb' to view the structure).
- Click <u>D926245.pdb</u> to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D926245.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).

Back to TM-score Homepage