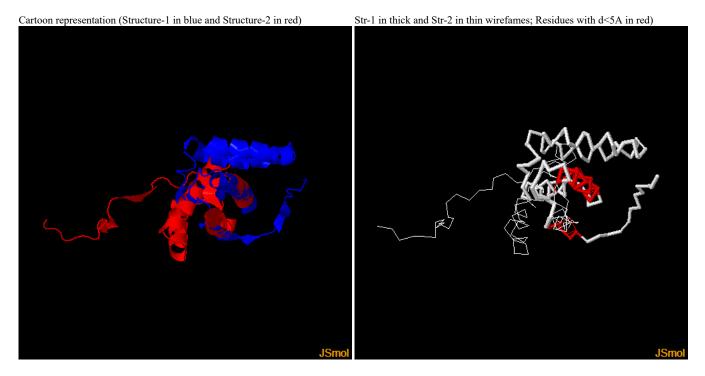
TM-score Results

```
TM-SCORE
 A scoring function to assess the similarity of protein structures \ensuremath{\mathsf{A}}
 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
RMSD of the common residues=
       = 0.2007 (d0 = 3.88)
TM-score
MaxSub-score= 0.1563 (d0= 3.50)
GDT-TS-score= 0.2027 %(d<1)=0.1351 %(d<2)=0.1532 %(d<4)=0.2072 %(d<8)=0.3153
GDT-HA-score= 0.1554 \%(d<0.5)=0.1261\%(d<1)=0.1351\%(d<2)=0.1532\%(d<4)=0.2072
----- rotation matrix to rotate Chain-1 to Chain-2 -----
i
                u(i,1)
                          u(i,2)
                                    u(i,3)
     3.3717297946
              0.5957183635 -0.8027147088 -0.0277259390
1
     7.9874519741
              0.5276285994
                       0.3650755926
                                  0.7670253404
     2.3904662000
              -0.6055804591 -0.4715600789
Superposition in the TM-score: Length(d<5.0)= 22 RMSD= 1.94
 :" denotes the residue pairs of distance < 5.0 Angstrom)
------fkQvADDWLKQYANDVKVSSVRAREKAIQHAIERFNTKPIQTIKKHDYQRFVDDISAQYSKNYVDSIVASTNMIFKYAYDTRLIK
```

Visualization of TM-score superposition



Document downloads

- Click A537913.pdb to download the first structure that you submitted.
- Click <u>B537913.pdb</u> to download the second structure that you submitted.
- Click <u>C537913.pdb</u> to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C537913.pdb' to view the structure).
- Click <u>D537913.pdb</u> to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D537913.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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