

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: A297422      Length= 484
Structure2: B297422      Length= 484 (by which all scores are normalized)
Number of residues in common= 242
RMSD of the common residues= 0.000
```

```
TM-score   = 0.5000 (d0= 7.83)
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 -----
i      t(i)      u(i,1)      u(i,2)      u(i,3)
1      0.0000000000  1.0000000000  0.0000000000  0.0000000000
2      -0.0000000000  0.0000000000  1.0000000000  0.0000000000
3      0.0000000000  0.0000000000  0.0000000000  1.0000000000
```

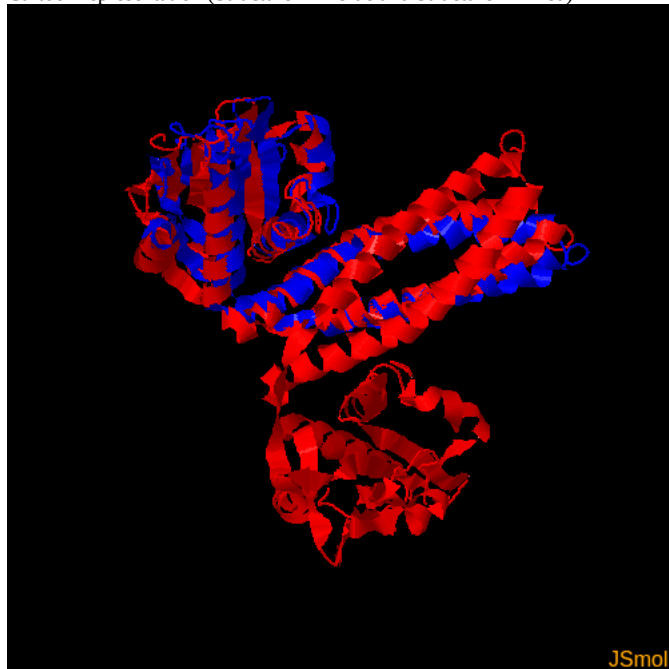
Superposition in the TM-score: Length(d<5.0)=242 RMSD= 0.00

(":" denotes the residue pairs of distance < 5.0 Angstrom)

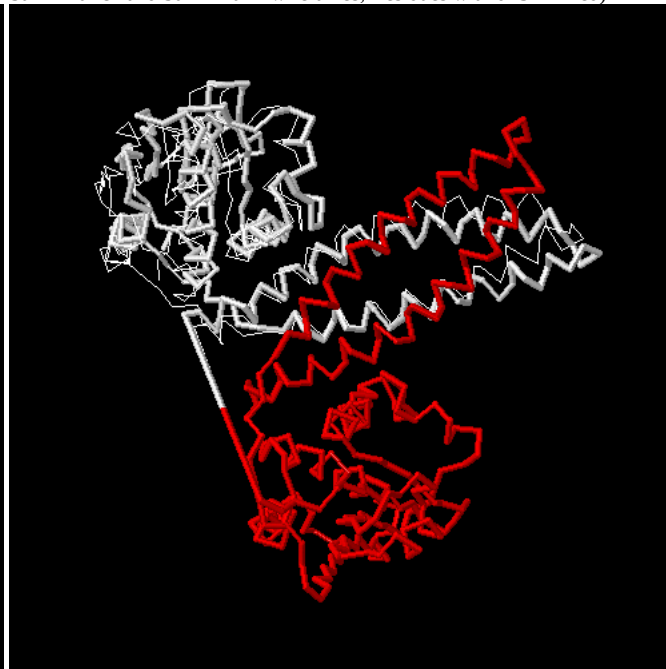
```
LSQAQKMQAIGQLAGGVAHDFNNLLTAIQLRLDQLLHRHPVGDPSEYGLNEIROGTGVRAADLVRKLLAFSRKQTVQREVLDLGELISEFEVLLRRLREDVKLITDYGRLDPQVRADKSQLETAVMNLAVNARDAV
::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
LSQAQKMQAIGQLAGGVAHDFNNLLTAIQLRLDQLLHRHPVGDPSEYGLNEIROGTGVRAADLVRKLLAFSRKQTVQREVLDLGELISEFEVLLRRLREDVKLITDYGRLDPQVRADKSQLETAVMNLAVNARDAV
1234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456
```

Visualization of TM-score superposition

Cartoon representation (Structure-1 in blue and Structure-2 in red)



Str-1 in thick and Str-2 in thin wireframes; Residues with d<5A in red



Document downloads

- Click [A297422.pdb](#) to download the first structure that you submitted.
- Click [B297422.pdb](#) to download the second structure that you submitted.
- Click [C297422.pdb](#) to download the superposed structure in C-alpha trace (This file is in a Rasmol script format, you can run 'rasmol -script C297422.pdb' to view the structure).
- Click [D297422.pdb](#) to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D297422.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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