

## 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: A257263      Length= 338
Structure2: B257263      Length= 338 (by which all scores are normalized)
Number of residues in common= 338
RMSD of the common residues= 31.545
```

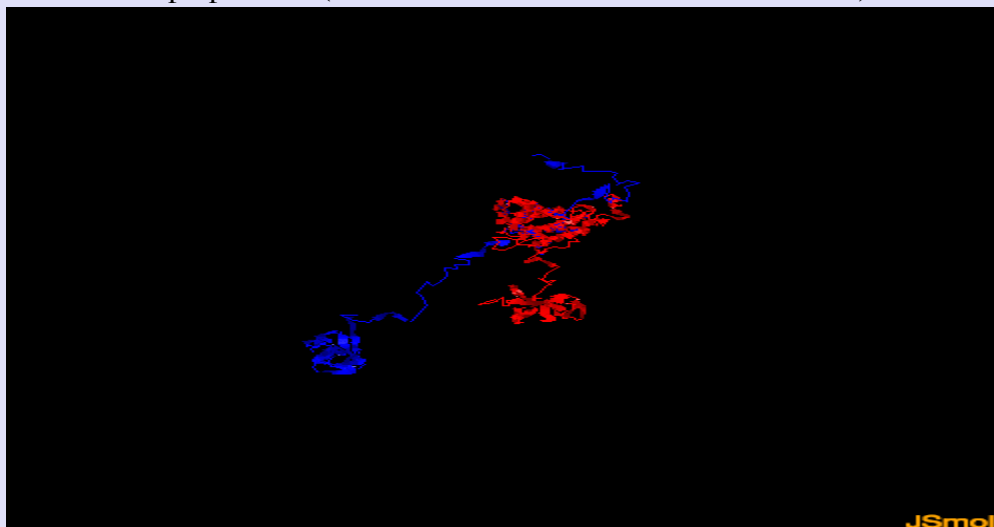
```
TM-score = 0.5577 (d0= 6.71)
MaxSub-score= 0.5385 (d0= 3.50)
GDT-TS-score= 0.5459 %(d<1)=0.5385 %(d<2)=0.5385 %(d<4)=0.5444 %(d<8)=0.5621
GDT-HA-score= 0.5399 %(d<0.5)=0.5385 %(d<1)=0.5385 %(d<2)=0.5385 %(d<4)=0.5444
```

```
----- rotation matrix to rotate Chain-1 to Chain-2 -----
i      t(i)      u(i,1)      u(i,2)      u(i,3)
1    -93.5760777162    0.9813763776   -0.0140938638    0.1915770564
2     16.5365935509    0.0257436577    0.9979579015   -0.0584575992
3     11.5065495267   -0.1903619438    0.0623008011    0.9797351380
```

```
Superposition in the TM-score: Length(d<5.0)=183 RMSD= 0.33
(":" denotes the residue pairs of distance < 5.0 Angstrom)
GPLGMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSQGQEARPEEIGWLNQYNETTGERGDFPGTYVEYI
GPLGMSAEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSQGQEARPEEIGWLNQYNETTGERGDFPGTYVEYI
1234567890123456789012345678901234567890123456789012345678901234567890123456789012
```

## Visualization

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



## Document downloads

- Click [A257263.pdb](#) to download the first structure that you submitted.
- Click [B257263.pdb](#) to download the second structure that you submitted.
- Click [C257263.pdb](#) to download the superposed structure in C-alpha trace (This file is in a Rasmol script format, you can run 'rasmol -script C257263.pdb' to view the structure).
- Click [D257263.pdb](#) to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D257263.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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