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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: zhngh@umich.edu                             *
*****
```

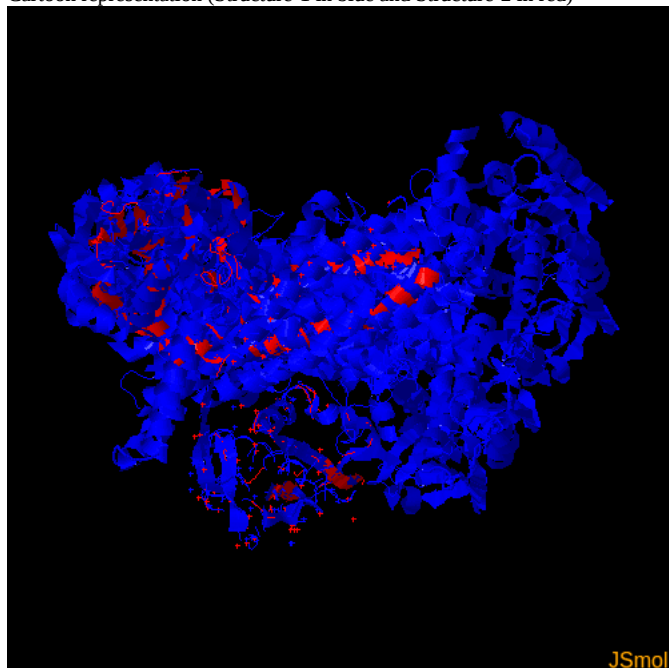
```

----- 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

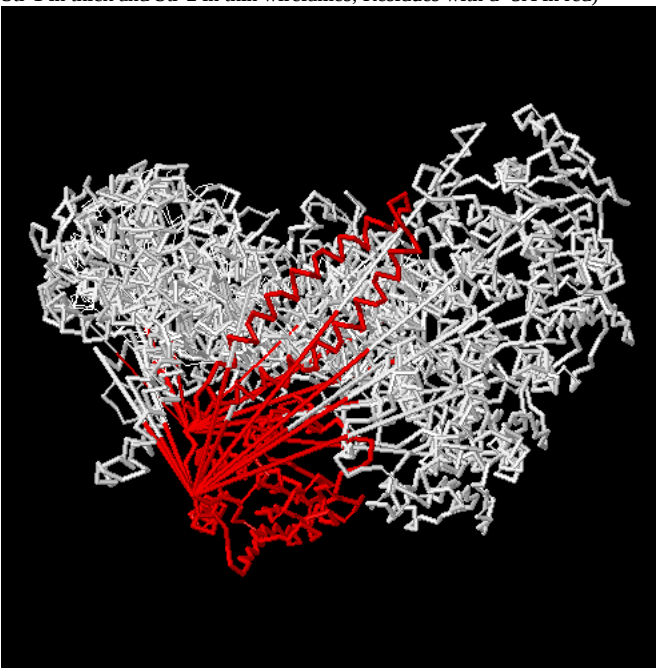
```

[illegible]

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



Str-1 in thick and Str-2 in thin wireframes; Residues with $d < 5\text{\AA}$ in red)



- Click [A695157.pdb](#) to download the first structure that you submitted.
- Click [B695157.pdb](#) to download the second structure that you submitted.
- Click [C695157.pdb](#) to download the superposed structure in C-alpha trace (This file is in a Rasmol script format, you can run 'rasmol -script C695157.pdb' to view the structure).

- Click [D695157.pdb](#) to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D695157.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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