

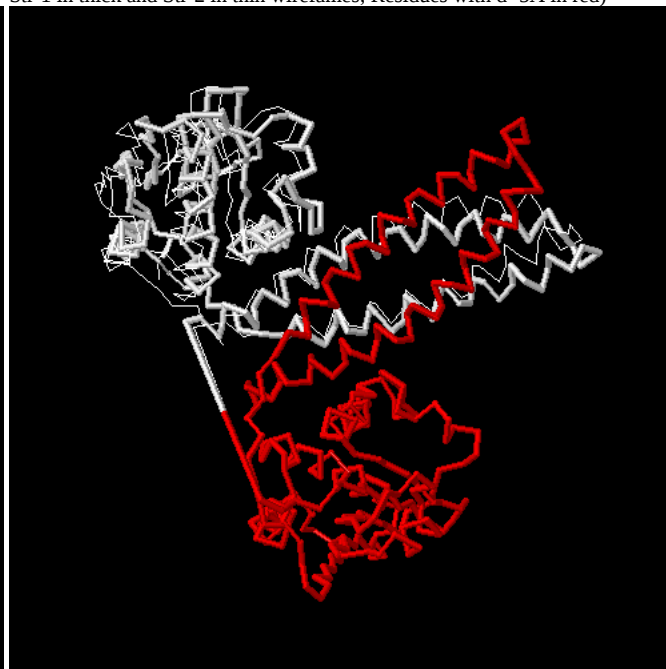
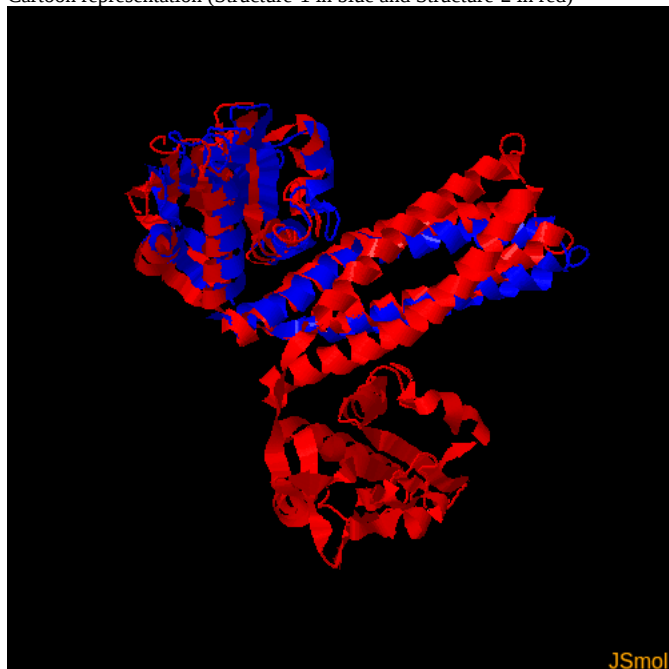
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*****
*                                     TM-SCORE                                     *
* A scoring function to assess the similarity of protein structures                *
* Based on statistics:                                                           *
*   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                               *
*****
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----- 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

```

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

 $\frac{1}{2}$

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