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: A220475     Length=  212
Structure2: B220475     Length=  209 (by which all scores are normalized)
Number of residues in common=   74
RMSD of  the common residues=   11.897

TM-score    = 0.1022  (d0= 5.38)
MaxSub-score= 0.0441  (d0= 3.50)
GDT-TS-score= 0.0658 %(d<1)=0.0239 %(d<2)=0.0335 %(d<4)=0.0766 %(d<8)=0.1292
GDT-HA-score= 0.0383 %(d<0.5)=0.0191 %(d<1)=0.0239 %(d<2)=0.0335 %(d<4)=0.0766

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1    -46.4519540137  -0.2758608536   0.5023295515   0.8194911904
 2     21.6539349064  -0.8444908903   0.2805190795  -0.4562282129
 3     39.9245972342  -0.4590598279  -0.8179083492   0.3468284975

Superposition in the TM-score: Length(d<5.0)= 13  RMSD=  2.91
(":" denotes the residue pairs of distance < 5.0 Angstrom)
PVANADVVFDFQNYTAKAGDEVTVDVLVDSKNKPISADVKFKVDSPLTIEEIDKESLAFNTTVTNAILGANFKSLDDKGEPLVPKDGAAVFTLYVNVPANTPDGTYYVGFNGKNEVHKSNDGSQFTVASKNGAITV

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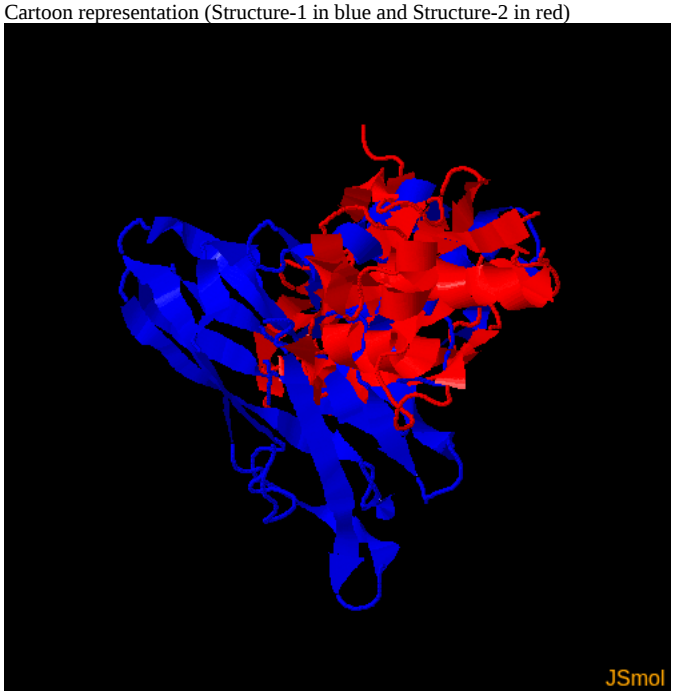
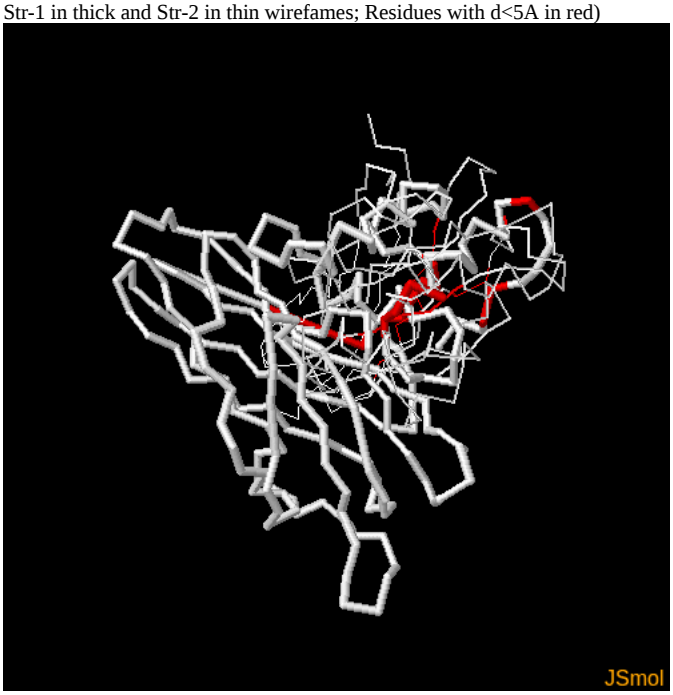
12345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456
```

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 wirefames; Residues with d<5A in red)



Document downloads

- Click A220475.pdb to download the first structure that you submitted.
- Click B220475.pdb to download the second structure that you submitted.
- Click C220475.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C220475.pdb' to view the structure).
- Click D220475.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D220475.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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