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: A735896     Length=  215
Structure2: B735896     Length=  209 (by which all scores are normalized)
Number of residues in common=   69
RMSD of  the common residues=   11.878

TM-score    = 0.0961  (d0= 5.38)
MaxSub-score= 0.0430  (d0= 3.50)
GDT-TS-score= 0.0622 %(d<1)=0.0239 %(d<2)=0.0335 %(d<4)=0.0622 %(d<8)=0.1292
GDT-HA-score= 0.0359 %(d<0.5)=0.0239 %(d<1)=0.0239 %(d<2)=0.0335 %(d<4)=0.0622

 -------- rotation matrix to rotate Chain-1 to Chain-2 ------
 i          t(i)         u(i,1)         u(i,2)         u(i,3)
 1      7.7107086384   0.8105900163   0.0230008372  -0.5851621886
 2    -52.7555597529   0.3666185917   0.7592568600   0.5376986412
 3     13.7562278410   0.4566559248  -0.6503844878   0.6070134960

Superposition in the TM-score: Length(d<5.0)= 15  RMSD=  3.23
(":" denotes the residue pairs of distance < 5.0 Angstrom)
PVANADVVFDFQNYTAKAGDEVTVDVLVDSKNKPISAXDVKFKVDSPLTIEEIDKESLAFNTTVXTNXAILGANFKSLDDKGEPLVPKDGAAVFTLYVNVPANTPDGTYYVGFNGKNEVHKSNDGSQFTVASKNGA
      -----------------------------------------------------------------------------------------------------------------------------------------
123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345678901234567890123456789012345
```
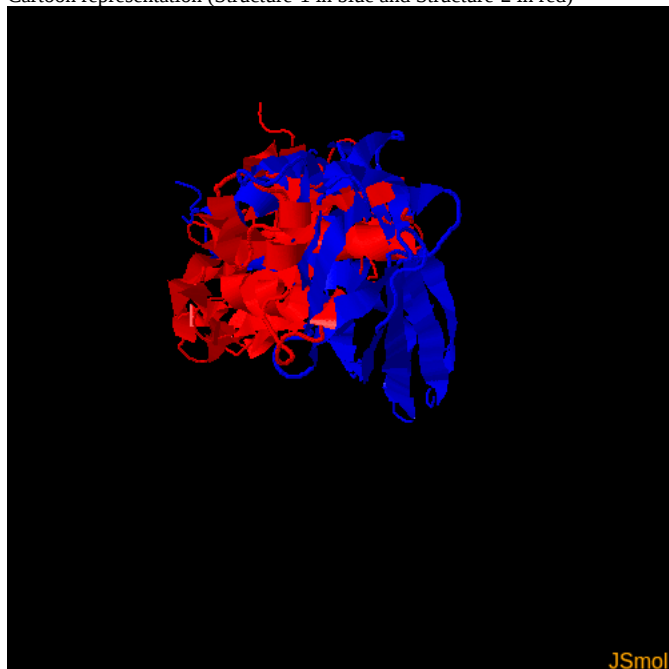
Visualization of TM-score superposition

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 A735896.pdb to download the first structure that you submitted.
- Click B735896.pdb to download the second structure that you submitted.
- Click C735896.pdb to download the superposed structure in C-alpah trace (This file is in a Rasmol script format, you can run 'rasmol -script C735896.pdb' to view the structure).
- Click D735896.pdb to download the superposed structure in full-atom (This file is in a Rasmol script format, you can run 'rasmol -script D735896.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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