

Results: s001A

Query: s001A

Select neighbours (check boxes) for viewing as multiple structural alignment or 3D superimposition. The list of neighbours is sorted by Z-score. Similarities with a Z-score lower than 2 are spurious. Each neighbour has links to pairwise structural alignment with the query structure, and to the PDB format coordinate file where the neighbour is superimposed onto the query structure.

☒ Expand gaps

Summary

No:	Chain	Z	rmsd	lali	nres	%id	PDB	Description
1:	t001-C	25.6	5.5	751	1207	30	PDB	

Pairwise Structural Alignments

Notation: three-state secondary structure definitions by DSSP (reduced to H=helix, E=sheet, L=coil) are shown above the amino acid sequence. Structurally equivalent residues are in uppercase, structurally non-equivalent residues (e.g. in loops) are in lowercase. Amino acid identities are marked by vertical bars.

No 1: Query=s001A Sbjct=t001C Z-score=25.6

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```
DSSP -----LEELL---l111LLL-LLLL11EELLEEEL
Query -----AYTNSFT--rgvyYDPK-VFRSsvLHSTQDLFL      30
ident                                     ||                               |
Sbjct yvdvgpdsvksacievdiqqtfddktWPRPIDVskadgiiYPQGrTYSN-itITYQGILFP    59
DSSP l111111111111leel1hhhhh11LLLLLL1111111111111111-eeEEEEEEEL
```

DSSP	LLLLLEELLLLL---111111LLLLL---1111EELLLEEEEE-EELLL-----	
Query	PFFSNVTWFHAI---hvsrgtGTRKF---dnvpLPFNDGVYFAS-TEKSN-----	73
ident		
Subjt	YQGDHGDMYVYSaghatgttPQKLfVanysqdvKQFANGFVVRIGAAANStgtviiispst	119
DSSP	LLLLLEEEELLLeelleelleLEEL111111EELLLEEEEEELLLLLLeeeelleeee	

```
DSSP   -----1EEEEEEEL-----11111111leeeeeelll
Query  -----iIRGWIFGT-----tldSKTQSlIivnnat    98
ident      |
Sbjct    satirkIYPAFMLGssvgnfsdkgmgrffnhtlvllpdgcgtllrafYCIL-----eprs    174
DSSP     eeell11111111EEEEEEEEeeell11111111leeeeeeeeeehhhleeeeeEEEE-----eell
```

[illegible]

```
DSSP    lllEEEEEE-eeeEELL-EEEEElleelllllllllllLEEEEllLLL--llLEEE
Query   gnfKNLREF-vfKNIDG-YFKIYSkhtpinlvrdlpqgfsaLEPLVDlPIGI--niTRFQ      213
ident   | | |
Sbjct   tedEILEWFfgitqTAQGvHLFSSR-----yvdllyggNMFQFA-TLPVydtkYYYS      277
DSSP    lllLLLLLEeeeeLLLeEEEEELL-----llllllllLEEEEE-EELLllllLEEE
```

[illegible]

DSSP	LLLLLLLLLLLLLEEEELLLLLLIIIIIIIIIIIIIIIIIIIIIIHHHHHIIIIIIIIIIeeel	
Query	TKCTLKSFVEKGIYQTSNFRvqptesivrfpnitnlcpfgevfnatrfasvyawnrkri	332
ident		
Sbjct	LHCSYESFDVESGVYSVSFFE-----	350
DSSP	HHHHHLLLLLLLLLEEEELLLLLL-----	

DSSP	111111hHHHH11111leeeee111111111111leeeeeee11111111111111h	
Query	sncvadySVLYnsasfstfkcycgvsptklndlcftnvadsfvirgdevrqiapgqtgki	392
ident		
Sbjct	akpsgsvVEQA-----	361
DSSP	1111leeEELL-----	

DSSP	hhhlllllllleeEEELllllLLLLleeeeeeellllllllllllllllllllllll	
Query	adynyklpddftgcvIAWNSnnldskVGGNynylr1frksnlkpferdisteiyyagst	452
ident		
Sbjct	-----eGVECD---fsPLLS-----	373
DSSP	-----llLLLL--llLLLL-----	

DSSP 111111111111LEEEEEE111111LLLEEE-----
Query pcngvegfcncyfpLQSYGFqptnvgvYQPYRV----- 484

```
ident
Sbjct  -----gtppqvYNFKRL-----VFTNCNynltklslfsvndftcsqispaaiasn  419
DSSP   -----11111hHHLEEE-----EELLEEl1hhhhhhhleeeeeeeel11hhhhh11
```

