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.

Summary

```
No: Chain Z rmsd lali nres %id PDB Description \Box 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 Query ident	LEELLLL1111LLLL-LLLL111EELLLEELAYTNSFTrgvyYPDK-VFRSsv1HSTQDLFL	30
	yvdvgpdsvksacievdiqqtffdktWPRPIDVskadgiiYPQGrTYSN-itITYQGLFP llllllllllllllllleellhhhhlllLLLLLLllllllll	59
DSSP Query ident	LLLLLEELLLLL111111LLLLL1111EELLLLEEEEE-EELLL	73
	YQGDHGDMYVYSaghatgttpQKLFVanysqdvKQFANGFVVRIgAAANStgtviispst LLLLLLEEELLEelleelleeLLEELlllllllEELLLLEEEEELLLLLeeeeelleeee	119
DSSP Query ident	lEEEEEEELlllLLLeeeeeelll iIRGWIFGTtldSKTQsllivnnat	98
	satirkIYPAFMLGssvgnfsdgkmgrffnhtlvllpdgcgtllrafYCILeprs eeelllLLLLEEEEeeeelllllllleeeeeeeeeeehhhleeeeeEEEEeell	174
DSSP Query ident	leeeelllllllLLLLLllllLLHH-hHLLLllllllllllllll	1 57
	gnhcpagnshtsFATYHtpaTDCSDGNYNRnaSLNSfkeyfnlrnctfmytyni 111111111111LLEEE111LLEELLEELL1hHHHHhhhheeeeeeeeeeee	228
DSSP Query ident	<pre>111EEEEEE-eeeEELL-EEEEEEIleeelllllllllllllEEEELLLLLllLEEE gnfKNLREF-vfkNIDG-YFKIYSkhtpinlvrdlpqgfsaLEPLVDlPIGIniTRFQ</pre>	213
	tedEILEWFgitqTAQGvHLFSSRyvdlyggNMFQFA-TLPVydtiKYYS	277
DSSP Query ident	EEelllllllLLLLllllllLLEEELLLEEELLLEEEellLLE-eeLLLLLLLLLL	272
	IIphsiRSIQsdrkAWAAFYVYKLQPLTFLLDfsvDGYIrraIDCGFN-DLSQ ELleeeLLLLllllLLLEEEEELEEEEEEEellLLLEeeeEELLLL-HHHH	329
ident	LLLLLLLLLLEEELLLLL11111111111111111111	332
Sbjct DSSP	LHĊSYEŚFDVĖSĠVŸSVŚSFE	350
ident	llllllhHHHHlllllleeeeelllllllllllllleeeeeeellllll	392
Sbjct DSSP	akpsgsvVEQA11111eeEELL	361
DSSP Query ident	hhhlllllllleeeeEEEELlllllLLLLeeeeeellllllll	452
	eGVECDfsPLLS	373
DSSP Query	lllllllllllllEEEEEllllllllLLLEEEpcngvegfncyfpLQSYGFqptngvgYQPYRV	484

ident Sbjct DSSP	gtppqvYNFKRLVFTNCNynltkllslfsvndftcsqispaaiasn lllllhHHLEEEEELLEEllhhhhhhhleeeeeeeelllhhhhhhll	419
DSSP Query ident Sbjct DSSP	cysslildyfsyplsmksdlsvssagpisqfnykqsfsnptclilatvphnlttitkplk lllleeeeeeeellhhhllllllllllhhhhhllllllll	484 479
DSSP Query ident Sbjct DSSP	ysyinkcsrllsddrtevpqlvnanqyspcvsivpstvwedgdyyrkqlsplegggwlva eeeeeeeeeellllllleeellllllllllllllll	484 539
DSSP Query ident Sbjct DSSP	eeeeellllllllllllllllllLLLllLLLllLLvvlsfellhapatvcgpkkstnlvKNKCvnFNFNgltGT sgstvamteqlqmgfgitvqygtdtnsvcpklefandtkiasQLGNCVEYslygvsGR eeeeeelllllleeeeeelllllllllllllllhhhHLLLEEEEeelleeEE	523 597
ident	LLLLLLLIIILLLLLLLLLLLLLLLLLLLLLLLLLLLL	582 653
ident	EEELLLLLHHHLL111111LLLL1111111LLLEEELLEEE	635 709
ident	LLLLLL-LEELLLLLLLLLLLLLLlllllllLEELLlLLLL-LLLLLLL CDIPIGA-GICASYQTqTNSPRRARSVasqsiIAYTMS1GAENS-VAYSNNS	685 762
DSSP Query ident Sbjct DSSP	EEELLEEEELLLLEEELHHHHHLLLLHHHHHHHHLLLHHHHHH	745 822
ident	HHHHHHHHHLLLLLLLLLLLLLLLLLLLLLLLLLLL	800 881
ident	LL111LLLL111111LLLLLLL1LLLLLLEEELLLLLHHHHHHHHHH	853 936
ident	HHHhLLL-11LLLLLLHHHHHHHHHHHHLLLLLHHHHHHHHHH	912 995
ident	hhlllLHHHHHHHHHHHHHHHHHHHHLLLLLLLLLHHHHHHHLLHHHH	970 1053
ident Sbjct	HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHLLLLLL	
Query ident Sbjct	LLEEEEEEEEEELLEEELLLLEEELLEEEEELLLEEELLL PHGVVFLHVTYVPAQEKNFTTAPAICHDGKAHFPREGVFVSNGTHWFVTQRN	
Query ident	LLLLEELLLLLEEEEILLLIILLLLLLL FYEPQIITTDNTFVSgNCDVviGIVNNTVY 1112	