














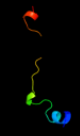


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2v5iA_	 Alignment		15.3	30	PDB header: viral protein Chain: A: PDB Molecule: salmonella typhimurium db7155 bacteriophage det7 PDBTitle: structure of the receptor-binding protein of bacteriophage2 det7: a podoviral tailspike in a myovirus
2	dluwwa_	 Alignment		12.1	71	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Family 28 carbohydrate binding module, CBM28
3	dltywa_	 Alignment		9.6	33	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: P22 tailspike protein
4	c3acgA_	 Alignment		8.6	57	PDB header: hydrolase Chain: A: PDB Molecule: beta-1,4-endoglucanase; PDBTitle: crystal structure of carbohydrate-binding module family 282 from clostridium josui cel5a in complex with cellobiose
5	c2dlaB_	 Alignment		8.2	69	PDB header: replication Chain: B: PDB Molecule: 397aa long hypothetical protein; PDBTitle: primase large subunit amino terminal domain from pyrococcus horikoshii
6	c2xc1A_	 Alignment		6.8	33	PDB header: hydrolase Chain: A: PDB Molecule: bifunctional tail protein; PDBTitle: full-length tailspike protein mutant y108w of bacteriophage2 p22
7	c3echC_	 Alignment		6.8	75	PDB header: transcription, transcription regulation Chain: C: PDB Molecule: 25-mer fragment of protein armr; PDBTitle: the marr-family repressor mexr in complex with its antirepressor armr
8	c2wg3C_	 Alignment		6.7	34	PDB header: signaling protein Chain: C: PDB Molecule: hedgehog-interacting protein; PDBTitle: crystal structure of the complex between human hedgehog-2 interacting protein hip and desert hedgehog without calcium

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[d1ed7a_](#)

Alignment



5.8

28

Fold: WW domain-like

Superfamily: Carbohydrate binding domain

Family: Carbohydrate binding domain