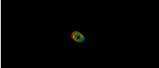


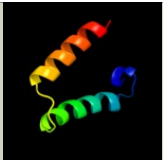
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w83C_	 Alignment		53.1	54	PDB header: protein transport Chain: C: PDB Molecule: c-jun-amino-terminal kinase-interacting protein PDBTitle: crystal structure of the arf6 gtpase in complex with a2 specific effector, jip4
2	c2xglB_	 Alignment		9.6	45	PDB header: antibiotic Chain: B: PDB Molecule: colicin-m immunity protein; PDBTitle: the x-ray structure of the escherichia coli colicin m immunity2 protein demonstrates the presence of a disulphide bridge, which is3 functionally essential
3	dltzza2	 Alignment		8.1	17	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
4	c1yrlD_	 Alignment		7.0	20	PDB header: oxidoreductase Chain: D: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: escherichia coli ketol-acid reductoisomerase
5	d1yeya2	 Alignment		6.3	12	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
6	c2kztA_	 Alignment		6.0	17	PDB header: apoptosis Chain: A: PDB Molecule: programmed cell death protein 4; PDBTitle: structure of the tandem ma-3 region of pdcd4
7	d2aqea1	 Alignment		5.7	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: SWIRM domain

8

[c2rg8A_](#)

Alignment



5.7

17

PDB header:apoptosis, translation
Chain: A: **PDB Molecule:**programmed cell death protein 4;
PDBTitle: crystal structure of programmed for cell death 4 middle
ma32 domain