
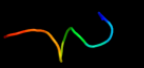






















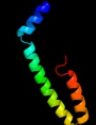
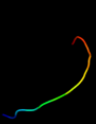

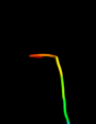
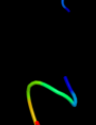


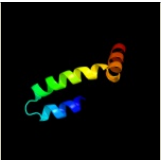
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2knuA_	 Alignment		47.3	50	PDB header: membrane protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: solution structure of the transmembrane proximal region of2 the hepatitis c virus e1 glycoprotein
2	c1lj2B_	 Alignment		32.4	27	PDB header: viral protein/ translation Chain: B: PDB Molecule: nonstructural rna-binding protein 34; PDBTitle: recognition of eif4g by rotavirus nsp3 reveals a basis for2 mrna circularization
3	c2jtvA_	 Alignment		14.4	25	PDB header: structural genomics Chain: A: PDB Molecule: protein of unknown function; PDBTitle: solution structure of protein rpa3401, northeast structural genomics2 consortium target rpt7, ontario center for structural proteomics3 target rp3384
4	c2ekwC_	 Alignment		12.9	22	PDB header: contractile protein Chain: C: PDB Molecule: myosin catalytic light chain lc-1, mantle muscle; PDBTitle: the crystal structure of squid myosin s1 in the presence of2 so4 2-
5	d1wwia1	 Alignment		12.9	26	Fold: Histone-fold Superfamily: Histone-fold Family: Bacterial histone-fold protein
6	c1dipA_	 Alignment		11.0	35	PDB header: acetylation Chain: A: PDB Molecule: delta-sleep-inducing peptide immunoreactive PDBTitle: the solution structure of porcine delta-sleep-inducing2 peptide immunoreactive peptide, nmr, 10 structures
7	d1r4va_	 Alignment		9.5	18	Fold: Histone-fold Superfamily: Histone-fold Family: Bacterial histone-fold protein
8	d1sl7a_	 Alignment		9.0	26	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
9	d1fxka_	 Alignment		8.4	35	Fold: Long alpha-hairpin Superfamily: Prefoldin Family: Prefoldin
10	d1sfua_	 Alignment		8.0	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
11	d2fm9a1	 Alignment		7.6	15	Fold: SipA N-terminal domain-like Superfamily: SipA N-terminal domain-like Family: SipA N-terminal domain-like

12	d1d1da2	Alignment		6.6	26	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
13	c2gffB_	Alignment		5.9	12	PDB header: sugar binding protein Chain: B: PDB Molecule: Isrg protein; PDBTitle: crystal structure of yersinia pestis Isrg
14	c2ogdB_	Alignment		5.9	12	PDB header: transferase Chain: B: PDB Molecule: farnesyl pyrophosphate synthase; PDBTitle: t. brucei farnesyl diphosphate synthase complexed with bisphosphonate2 bph-527
15	c1z8yF_	Alignment		5.8	50	PDB header: virus Chain: F: PDB Molecule: spike glycoprotein e1; PDBTitle: mapping the e2 glycoprotein of alphaviruses
16	d1rj9a1	Alignment		5.7	39	Fold: Four-helical up-and-down bundle Superfamily: Domain of the SRP/SRP receptor G-proteins Family: Domain of the SRP/SRP receptor G-proteins
17	d2v33a1	Alignment		5.4	56	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
18	d2qyc31	Alignment		5.4	57	Fold: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Superfamily: Ribosomal protein L7/12, oligomerisation (N-terminal) domain Family: Ribosomal protein L7/12, oligomerisation (N-terminal) domain

19

[d1uiya_](#)

Alignment



5.3

29

Fold: ClpP/crotonase
Superfamily: ClpP/crotonase
Family: Crotonase-like