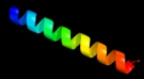
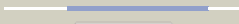
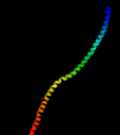
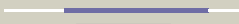
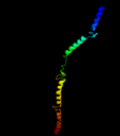
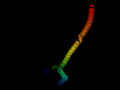
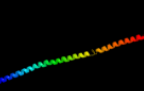
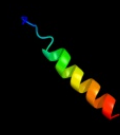
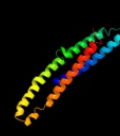
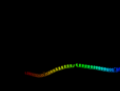
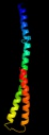
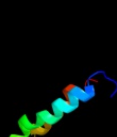


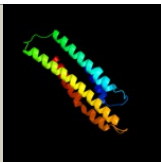
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2oszA_	 Alignment		57.0	33	PDB header: structural protein Chain: A: PDB Molecule: nucleoporin p58/p45; PDBTitle: structure of nup58/45 suggests flexible nuclear pore diameter by2 intermolecular sliding
2	c1ei3C_	 Alignment		27.9	10	PDB header: PDB COMPND:
3	c1degF_	 Alignment		17.6	9	PDB header: PDB COMPND:
4	c3ojaB_	 Alignment		17.0	16	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
5	c3u59C_	 Alignment		15.3	7	PDB header: contractile protein Chain: C: PDB Molecule: tropomyosin beta chain; PDBTitle: n-terminal 98-aa fragment of smooth muscle tropomyosin beta
6	c1degO_	 Alignment		14.4	11	PDB header: PDB COMPND:
7	c2wukD_	 Alignment		14.3	6	PDB header: cell cycle Chain: D: PDB Molecule: septum site-determining protein diviva; PDBTitle: diviva n-terminal domain, f17a mutant
8	c2xusA_	 Alignment		13.5	24	PDB header: protein binding Chain: A: PDB Molecule: breast cancer metastasis-suppressor 1; PDBTitle: crystal structure of the brms1 n-terminal region
9	d1k1fa_	 Alignment		13.0	21	Fold: Bcr-Abl oncoprotein oligomerization domain Superfamily: Bcr-Abl oncoprotein oligomerization domain Family: Bcr-Abl oncoprotein oligomerization domain
10	c3cwqA_	 Alignment		10.9	7	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
11	c2efrB_	 Alignment		10.3	11	PDB header: contractile protein Chain: B: PDB Molecule: general control protein gcn4 and tropomyosin 1 alpha chain; PDBTitle: crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution

12	c3pltB_	Alignment		10.2	14	PDB header: structural protein Chain: B: PDB Molecule: sphingolipid long chain base-responsive protein lsp1; PDBTitle: crystal structure of lsp1 from saccharomyces cerevisiae
13	c2gl2B_	Alignment		9.2	13	PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
14	d2gtsa1	Alignment		7.7	24	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
15	d1ykhb1	Alignment		6.2	13	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
16	c2x6pB_	Alignment		5.9	32	PDB header: de novo protein Chain: B: PDB Molecule: coil ser l19c; PDBTitle: crystal structure of coil ser l19c
17	c2x6pA_	Alignment		5.9	32	PDB header: de novo protein Chain: A: PDB Molecule: coil ser l19c; PDBTitle: crystal structure of coil ser l19c
18	d1sdia_	Alignment		5.7	9	Fold: YcfC-like Superfamily: YcfC-like Family: YcfC-like
19	c2x6pC_	Alignment		5.5	31	PDB header: de novo protein Chain: C: PDB Molecule: coil ser l19c; PDBTitle: crystal structure of coil ser l19c

20

[d1gs9a_](#)

Alignment



5.3

15

Fold:Four-helical up-and-down bundle
Superfamily:Apolipoprotein
Family:Apolipoprotein