



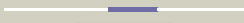


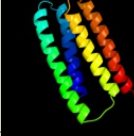

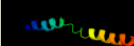





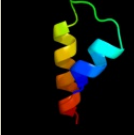



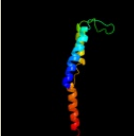


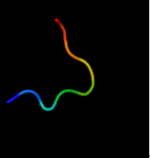


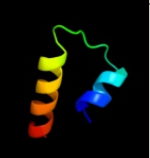
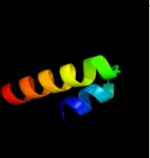
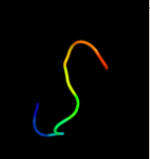


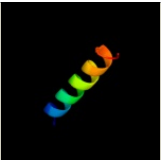
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3my2A_	 Alignment		50.9	12	PDB header: transport protein Chain: A: PDB Molecule: lipopolysaccharide export system protein lptc; PDBTitle: crystal structure of lptc
2	c2rdcA_	 Alignment		14.4	42	PDB header: lipid binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative lipid binding protein (gsu0061) from2 geobacter sulfurreducens pca at 1.80 a resolution
3	dlutca2	 Alignment		12.6	17	Fold: 7-bladed beta-propeller Superfamily: Clathrin heavy-chain terminal domain Family: Clathrin heavy-chain terminal domain
4	dlloedA_	 Alignment		10.3	7	Fold: Neurotransmitter-gated ion-channel transmembrane pore Superfamily: Neurotransmitter-gated ion-channel transmembrane pore Family: Neurotransmitter-gated ion-channel transmembrane pore
5	c2voyH_	 Alignment		8.8	14	PDB header: hydrolase Chain: H: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
6	c1c9lA_	 Alignment		8.6	15	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: clathrin; PDBTitle: peptide-in-groove interactions link target proteins to the2 b-propeller of clathrin
7	c1bpoA_	 Alignment		8.5	17	PDB header: membrane protein Chain: A: PDB Molecule: protein (clathrin); PDBTitle: clathrin heavy-chain terminal domain and linker
8	dlf5qb1	 Alignment		8.0	19	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
9	dlj1ua_	 Alignment		7.0	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
10	c1mhsA_	 Alignment		7.0	16	PDB header: membrane protein, proton transport Chain: A: PDB Molecule: plasma membrane atpase; PDBTitle: model of neurospora crassa proton atpase
11	c1ciiA_	 Alignment		6.8	9	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia

12	d1rubx1	Alignment		5.8	22	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
13	c3h3hA_	Alignment		5.8	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized snoal-like protein; PDBTitle: crystal structure of a snoal-like protein of unknown function2 (bth_ji0226) from burkholderia thailandensis e264 at 1.60 a3 resolution
14	c2rddb_	Alignment		5.6	25	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
15	d1g3nc1	Alignment		5.4	16	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
16	d2cchb1	Alignment		5.3	16	Fold: Cyclin-like Superfamily: Cyclin-like Family: Cyclin
17	d1b0na1	Alignment		5.3	30	Fold: Dimerisation interlock Superfamily: SinR repressor dimerisation domain-like Family: SinR repressor dimerisation domain-like

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[c3jvoA](#)

Alignment



5.2

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PDB header:viral protein
Chain: A: **PDB Molecule:**gp6;
PDBTitle: crystal structure of bacteriophage hk97 gp6