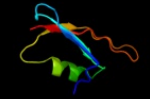
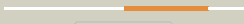
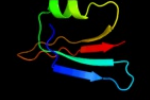
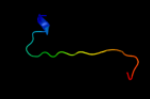
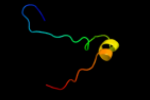
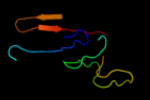
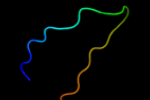
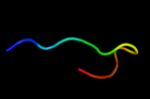
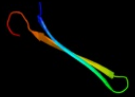
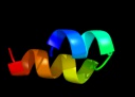
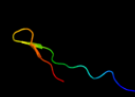


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1uv7A_	 Alignment		89.6	20	PDB header: transport Chain: A: PDB Molecule: general secretion pathway protein m; PDBTitle: periplasmic domain of epsm from vibrio cholerae
2	d1uv7a_	 Alignment		89.6	20	Fold: RRF/tRNA synthetase additional domain-like Superfamily: General secretion pathway protein M, EpsM Family: General secretion pathway protein M, EpsM
3	c2rjza_	 Alignment		70.3	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pilo protein; PDBTitle: crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
4	c2e26A_	 Alignment		16.2	23	PDB header: signaling protein Chain: A: PDB Molecule: reelin; PDBTitle: crystal structure of two repeat fragment of reelin
5	d1ikpa2	 Alignment		13.8	44	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: ADP-ribosylating toxins
6	c2htbB_	 Alignment		13.5	24	PDB header: isomerase Chain: B: PDB Molecule: putative enzyme related to aldose 1-epimerase; PDBTitle: crystal structure of a putative mutarotase (yeast) from2 salmonella typhimurium in monoclinic form
7	c3sbtB_	 Alignment		12.4	11	PDB header: splicing Chain: B: PDB Molecule: a1 cistron-splicing factor aar2; PDBTitle: crystal structure of a aar2-prp8 complex
8	d2et1a1	 Alignment		11.7	33	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
9	d2cssa1	 Alignment		9.6	50	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
10	d1fxza2	 Alignment		8.8	6	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
11	d1r89a3	 Alignment		8.6	12	Fold: Ferredoxin-like Superfamily: PAP/Archaeal CCA-adding enzyme, C-terminal domain Family: Archaeal tRNA CCA-adding enzyme

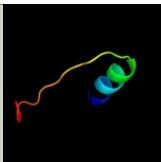
12	d1lc0a2	Alignment		8.4	32	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Biliverdin reductase
13	d1od5a2	Alignment		8.3	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: Germin/Seed storage 7S protein
14	c1lshB_	Alignment		8.0	20	PDB header: lipid binding protein Chain: B: PDB Molecule: lipovitellin (lv-2); PDBTitle: lipid-protein interactions in lipovitellin
15	d1lshb_	Alignment		8.0	20	Fold: Lipovitellin-phosvitin complex; beta-sheet shell regions Superfamily: Lipovitellin-phosvitin complex; beta-sheet shell regions Family: Lipovitellin-phosvitin complex; beta-sheet shell regions
16	c2xteH_	Alignment		7.1	27	PDB header: transcription Chain: H: PDB Molecule: f-box-like/wd repeat-containing protein tbl1x; PDBTitle: structure of the tbl1 tetramerisation domain
17	c2xtdB_	Alignment		7.0	27	PDB header: transcription Chain: B: PDB Molecule: tbl1 f-box-like/wd repeat-containing protein tbl1x; PDBTitle: structure of the tbl1 tetramerisation domain
18	d2p5ka1	Alignment		5.9	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
19	d2cspa1	Alignment		5.7	35	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III

20

[c3ktbD_](#)



Alignment



5.4

22

PDB header:transcription regulator
Chain: D: **PDB Molecule:**arsenical resistance operon trans-acting repressor;
PDBTitle: crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482