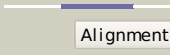
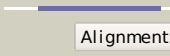
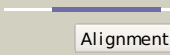
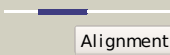
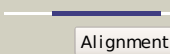
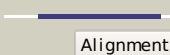
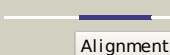
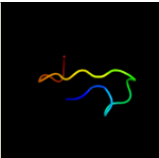
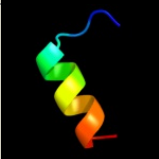
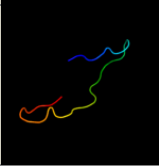


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1o51a_	 Alignment		18.4	23	Fold: Ferredoxin-like Superfamily: GlnB-like Family: DUF190/COG1993
2	c2dclB_	 Alignment		12.9	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical upf0166 protein ph1503; PDBTitle: structure of ph1503 protein from pyrococcus horikoshii ot3
3	d1bg2a_	 Alignment		11.1	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Motor proteins
4	d1qmya_	 Alignment		10.1	36	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: FMDV leader protease
5	d2dlka1	 Alignment		9.9	57	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
6	d1qola_	 Alignment		9.6	36	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: FMDV leader protease
7	c3b6vA_	 Alignment		7.4	17	PDB header: motor protein Chain: A: PDB Molecule: kinesin-like protein kif3c; PDBTitle: crystal structure of the motor domain of human kinesin family member2 3c in complex with adp
8	c3fbzA_	 Alignment		6.3	45	PDB header: structural protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of orf140 of the archaeal virus acidianus2 filamentous virus 1 (afv1)
9	d1zfda_	 Alignment		6.1	27	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
10	d3bexa1	 Alignment		5.6	50	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like
11	d2f9wa2	 Alignment		5.6	50	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: CoaX-like

12	d2dlka2	Alignment		5.6	35	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
13	c3fiaA_	Alignment		5.6	47	PDB header: protein binding Chain: A: PDB Molecule: intersectin-1; PDBTitle: crystal structure of the eh 1 domain from human intersectin-2 1 protein. northeast structural genomics consortium target3 hr3646e.
14	c3cguB_	Alignment		5.5	25	PDB header: hormone/signaling protein Chain: B: PDB Molecule: protein giant-lens; PDBTitle: crystal structure of unliganded argos

15

[c1mkjA](#)

Alignment



5.3

21

PDB header:transport protein
Chain: A: **PDB Molecule:**kinesin heavy chain;
PDBTitle: human kinesin motor domain with docked neck linker