


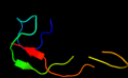

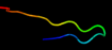

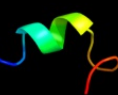

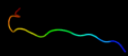





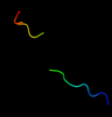





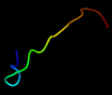

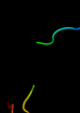
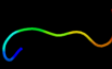

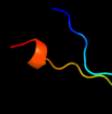


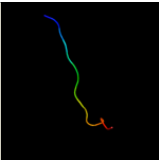


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k0ia2	 Alignment		24.5	36	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: PHBH-like
2	c3muwU	 Alignment		15.7	30	PDB header: virus Chain: U: PDB Molecule: structural polyprotein; PDBTitle: pseudo-atomic structure of the e2-e1 protein shell in sindbis virus
3	c2jqoA	 Alignment		13.0	38	PDB header: structural genomics Chain: A: PDB Molecule: hypothetical protein yoba; PDBTitle: nmr solution structure of bacillus subtilis yoba 21-120:2 northeast structural genomics consortium target sr547
4	c2ldjA	 Alignment		11.7	53	PDB header: de novo protein Chain: A: PDB Molecule: trp-cage mini-protein; PDBTitle: 1h chemical shift assignments and structure of trp-cage mini-protein2 with d-amino acid
5	d1czan3	 Alignment		9.7	40	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
6	c2ovfA	 Alignment		8.2	45	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: stal; PDBTitle: crystal structure of stal-pap complex
7	d1bg3a1	 Alignment		7.9	40	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
8	d1v4sa1	 Alignment		7.8	38	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
9	d1bg3a3	 Alignment		7.0	40	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
10	d1losya	 Alignment		6.5	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fungal immunomodulatory protein, FIP Family: Fungal immunomodulatory protein, FIP
11	d2j44a1	 Alignment		6.4	42	Fold: Prealbumin-like Superfamily: Starch-binding domain-like Family: PUD-like

12	c2h8kA_	Alignment		6.3	78	PDB header: transferase Chain: A: PDB Molecule: sult1c3 splice variant d; PDBTitle: human sulfotranferase sult1c3 in complex with pap
13	d1ig8a1	Alignment		6.3	40	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Hexokinase
14	c2bh7A_	Alignment		6.1	56	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylmuramoyl-l-alanine amidase; PDBTitle: crystal structure of a semet derivative of amid at 2.22 angstroms
15	d1q44a_	Alignment		5.8	56	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: PAPS sulfotransferase
16	c3f3hA_	Alignment		5.6	26	PDB header: antitumor protein Chain: A: PDB Molecule: immunomodulatory protein ling zhi-8; PDBTitle: crystal structure and anti-tumor activity of lz-8 from the fungus2 ganoderma lucidium
17	d1v58a2	Alignment		5.3	28	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
18	d1xcra1	Alignment		5.3	77	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: PTD012-like

19 [dlczan1](#)

Alignment



5.3

40

Fold:Ribonuclease H-like motif
Superfamily:Actin-like ATPase domain
Family:Hexokinase