Phyre^2

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Description	P0ABM5
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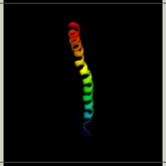
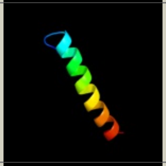
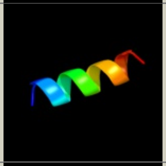
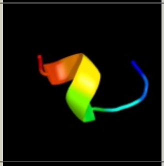
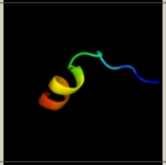
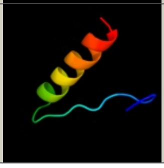
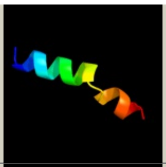
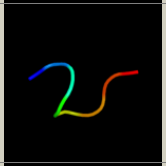
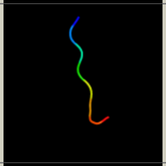
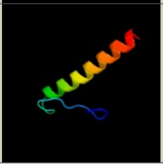
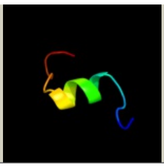
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1e8oa_	Alignment		36.4	36	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
2	c2kncB_	Alignment		18.0	19	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
3	c1q88B_	Alignment		15.2	33	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**39 kda initiator binding protein; **PDBTitle:** crystal structure of the c-domain of the t.vaginalis inr2 binding protein, ibp39 (monoclinic form)
4	d1q88a_	Alignment		13.1	36	**Fold:**39 kda initiator binding protein, IBP39, C-terminal domains **Superfamily:**39 kda initiator binding protein, IBP39, C-terminal domains **Family:**39 kda initiator binding protein, IBP39, C-terminal domains
5	c2fv2A_	Alignment		12.2	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rcd1 required for cell differentiation1 homolog; **PDBTitle:** crystal structure analysis of human rcd-1 conserved region
6	d1nekd_	Alignment		12.1	25	**Fold:**Heme-binding four-helical bundle **Superfamily:**Fumarate reductase respiratory complex transmembrane subunits **Family:**Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
7	c3hlzA_	Alignment		10.1	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bt_1490; **PDBTitle:** crystal structure of bt_1490 (np_810393.1) from bacteroides2 thetaiotaomicron vpi-5482 at 1.50 a resolution
8	d1914a1	Alignment		9.3	44	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
9	c1s5rA_	Alignment		8.5	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**high mobility group box transcription factor 1; **PDBTitle:** solution structure of hbp1 sid-msin3a pah2 complex
10	c1914A_	Alignment		8.1	44	**PDB header:**alu domain **Chain:** A: **PDB Molecule:**signal recognition particle 9/14 fusion protein; **PDBTitle:** signal recognition particle alu rna binding heterodimer, srp9/14
11	c3m4rA_	Alignment		8.0	3	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of the n-terminal class ii aldolase domain of a conserved2 protein from thermoplasma acidophilum

12	c3s8mA_	Alignment		7.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acp reductase; **PDBTitle:** the crystal structure of fabv
13	c2cq8A_	Alignment		6.4	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**10-formyltetrahydrofolate dehydrogenase; **PDBTitle:** solution structure of rsgi ruh-033, a pp-binding domain of2 10-fthfdh from human cdna
14	d2je6i2	Alignment		5.9	0	**Fold:**Barrel-sandwich hybrid **Superfamily:**Ribosomal L27 protein-like **Family:**ECR1 N-terminal domain-like
15	c2fk5B_	Alignment		5.7	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from thermus2 thermophilus hb8

16	d1sgga_	Alignment		5.6	11	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**SAM (sterile alpha motif) domain