Phyre^2

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Description	P33668
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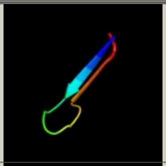
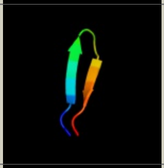
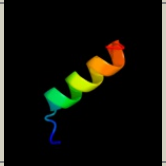
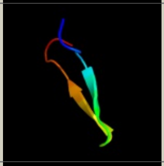
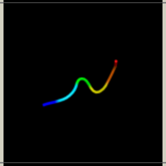
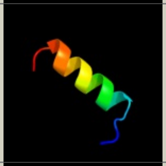
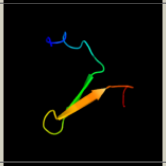
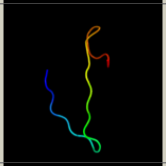
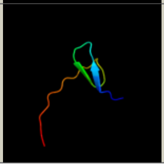
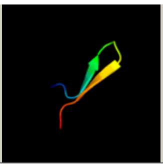
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1f0cB_	Alignment		12.4	28	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**ice inhibitor; **PDBTitle:** structure of the viral serpin crma
2	d3c0na1	Alignment		11.2	33	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**Aerolysin/Pertussis toxin (APT) domain
3	c2vp7B_	Alignment		10.6	26	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**b-cell cll/lymphoma 9 protein; **PDBTitle:** decoding of methylated histone h3 tail by the pygo-bcl9 wnt2 signaling complex
4	d2oaia1	Alignment		10.3	21	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
5	c2yrmA_	Alignment		10.1	67	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**b-cell lymphoma 6 protein; **PDBTitle:** solution structure of the 1st zf-c2h2 domain from human b-2 cell lymphoma 6 protein
6	c2vpdB_	Alignment		10.0	26	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**b-cell cll/lymphoma 9 protein; **PDBTitle:** decoding of methylated histone h3 tail by the pygo-bcl9 wnt2 signaling complex
7	c1eptA_	Alignment		9.2	19	**PDB header:**hydrolase (serine protease) **Chain:** A: **PDB Molecule:**porcine e-trypsin; **PDBTitle:** refined 1.8 angstroms resolution crystal structure of2 porcine epsilon-trypsin
8	c2vpdD_	Alignment		9.0	26	**PDB header:**gene regulation **Chain:** D: **PDB Molecule:**b-cell cll/lymphoma 9 protein; **PDBTitle:** decoding of methylated histone h3 tail by the pygo-bcl9 wnt2 signaling complex
9	d2fa8a1	Alignment		8.5	32	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Selenoprotein W-related
10	c2obkE_	Alignment		7.8	32	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**selt/selw/selh selenoprotein domain; **PDBTitle:** x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.
11	c3thdD_	Alignment		7.6	21	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**beta-galactosidase; **PDBTitle:** crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin

12	d2p13a1	Alignment		7.2	22	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like

13	c2npbA_	Alignment		6.4	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**selenoprotein w; **PDBTitle:** nmr solution structure of mouse selw