Phyre^2

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Description	P33135
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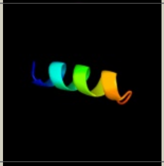
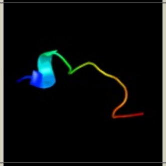
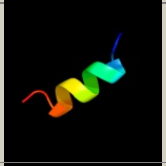
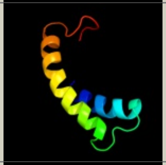
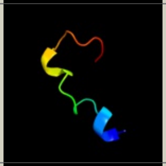
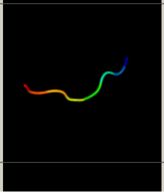
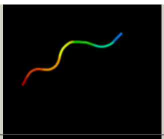
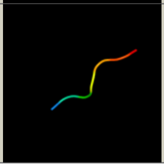
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1r7ma1	Alignment		15.7	40	**Fold:**Homing endonuclease-like **Superfamily:**Homing endonucleases **Family:**Group I mobile intron endonuclease
2	c2lkgA_	Alignment		10.2	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**acetylcholine receptor; **PDBTitle:** wsa major conformation
3	c3cm1C_	Alignment		9.2	31	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**ssga-like sporulation-specific cell division protein; **PDBTitle:** crystal structure of ssga-like sporulation-specific cell division2 protein (yp_290167.1) from thermobifida fusca yx-er1 at 2.60 a3 resolution
4	d1fn9a_	Alignment		7.6	12	**Fold:**Outer capsid protein sigma 3 **Superfamily:**Outer capsid protein sigma 3 **Family:**Outer capsid protein sigma 3
5	c2b3gB_	Alignment		7.5	14	**PDB header:**replication **Chain:** B: **PDB Molecule:**cellular tumor antigen p53; **PDBTitle:** p53n (fragment 33-60) bound to rpa70n
6	c2yvxD_	Alignment		6.6	24	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
7	c1qloA_	Alignment		6.3	14	**PDB header:**membrane proteins **Chain:** A: **PDB Molecule:**herpes simplex virus protein icp47; **PDBTitle:** structure of the active domain of the herpes simplex virus2 protein icp47 in water/sodium dodecyl sulfate solution3 determined by nuclear magnetic resonance spectroscopy
8	c1r7mA_	Alignment		6.2	40	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**intron-encoded endonuclease i-scei; **PDBTitle:** the homing endonuclease i-scei bound to its dna recognition2 region
9	c2kr6A_	Alignment		6.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**presenilin-1; **PDBTitle:** solution structure of presenilin-1 ctf subunit
10	c2zfdB_	Alignment		5.7	18	**PDB header:**signaling protein/transferase **Chain:** B: **PDB Molecule:**putative uncharacterized protein t20l15_90; **PDBTitle:** the crystal structure of plant specific calcium binding protein atcbl22 in complex with the regulatory domain of atcipk14
11	c2d10F_	Alignment		5.2	38	**PDB header:**cell adhesion **Chain:** F: **PDB Molecule:**ezrin-radixin-moesin binding phosphoprotein 50; **PDBTitle:** crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide

12	c2d10G_	Alignment		5.2	38	**PDB header:**cell adhesion **Chain:** G: **PDB Molecule:**ezrin-radixin-moesin binding phosphoprotein 50; **PDBTitle:** crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide
13	c2d10E_	Alignment		5.2	38	**PDB header:**cell adhesion **Chain:** E: **PDB Molecule:**ezrin-radixin-moesin binding phosphoprotein 50; **PDBTitle:** crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide

14	c2d10H_	Alignment		5.2	38	**PDB header:**cell adhesion **Chain:** H: **PDB Molecule:**ezrin-radixin-moesin binding phosphoprotein 50; **PDBTitle:** crystal structure of the radixin ferm domain complexed with2 the nherf-1 c-terminal tail peptide