Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AE95
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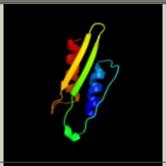
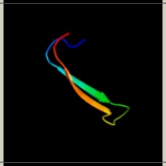
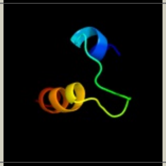
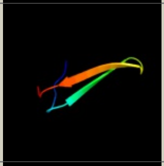
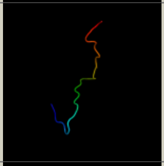
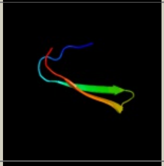
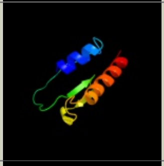
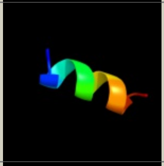
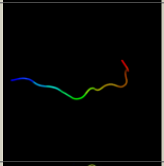
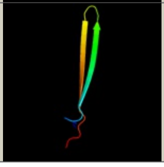
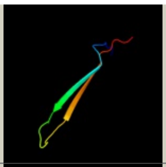
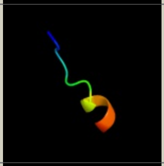
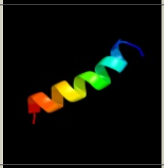
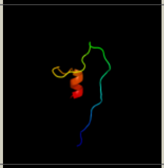
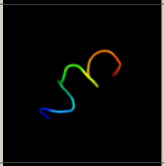
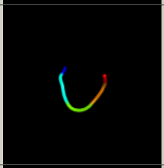
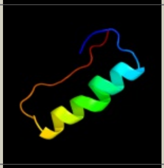
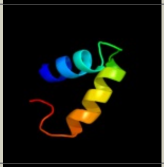
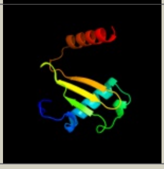
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qmha1	Alignment		78.0	3	**Fold:**Thioredoxin fold **Superfamily:**RNA 3'-terminal phosphate cyclase, RPTC, insert domain **Family:**RNA 3'-terminal phosphate cyclase, RPTC, insert domain
2	c3fcgB_	Alignment		54.2	8	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**f1 capsule-anchoring protein; **PDBTitle:** crystal structure analysis of the middle domain of the2 caf1a usher
3	d1ixca1	Alignment		17.3	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LysR-like transcriptional regulators
4	c3ohnA_	Alignment		17.0	26	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane usher protein fimd; **PDBTitle:** crystal structure of the fimd translocation domain
5	c2vqiA_	Alignment		16.7	7	**PDB header:**transport **Chain:** A: **PDB Molecule:**outer membrane usher protein papc; **PDBTitle:** structure of the p pilus usher (papc) translocation pore
6	c2lf0A_	Alignment		15.2	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yibl; **PDBTitle:** solution structure of sf3636, a two-domain unknown function protein2 from shigella flexneri 2a, determined by joint refinement of nmr,3 residual dipolar couplings and small-angle x-ray scatting, nesg4 target sfr339/ocsp target sf3636
7	c3rfzB_	Alignment		13.3	26	**PDB header:**cell adhesion/transport/chaperone **Chain:** B: **PDB Molecule:**outer membrane usher protein, type 1 fimbrial synthesis; **PDBTitle:** crystal structure of the fimd usher bound to its cognate fimc:fimh2 substrate
8	c2npbA_	Alignment		12.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**selenoprotein w; **PDBTitle:** nmr solution structure of mouse selw
9	c1vytE_	Alignment		10.8	58	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**voltage-dependent l-type calcium channel **PDBTitle:** beta3 subunit complexed with aid
10	c2enyA_	Alignment		10.3	31	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**obscurin; **PDBTitle:** solution structure of the ig-like domain (2735-2825) of2 human obscurin
11	c1bw8A_	Alignment		8.5	26	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**protein (mu2 adaptin subunit); **PDBTitle:** mu2 adaptin subunit (ap50) of ap2 adaptor (second domain),2 complexed with egfr internalization peptide fyralm

12	d2pr9a1	Alignment		7.4	26	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor **Family:**Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor
13	c1vytF_	Alignment		7.3	50	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel **PDBTitle:** beta3 subunit complexed with aid
14	c2wtgA_	Alignment		6.4	30	**PDB header:**oxygen transport **Chain:** A: **PDB Molecule:**globin-like protein; **PDBTitle:** high resolution 3d structure of c.elegans globin-like2 protein glb-1
15	c3q13A_	Alignment		6.1	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**spondin-1; **PDBTitle:** the structure of the ca2+-binding, glycosylated f-spondin domain of f-2 spondin, a c2-domain variant from extracellular matrix
16	d1zh5a1	Alignment		5.8	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**La domain
17	d1wu9a1	Alignment		5.8	60	**Fold:**EB1 dimerisation domain-like **Superfamily:**EB1 dimerisation domain-like **Family:**EB1 dimerisation domain-like
18	c3gr1A_	Alignment		5.3	17	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplamic domain of the t3ss inner membrane protein prgh2 from s.typhimurium (fragment 170-392)
19	c2dagA_	Alignment		5.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 5; **PDBTitle:** solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
20	c1nw1A_	Alignment		5.1	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**choline kinase (49.2 kd); **PDBTitle:** crystal structure of choline kinase
21	d1nw1a_	Alignment	not modelled	5.1	9	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**Choline kinase