Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	O14683
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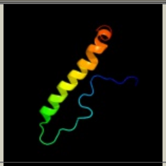
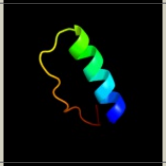
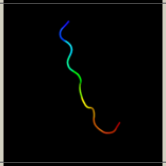
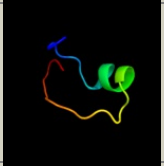
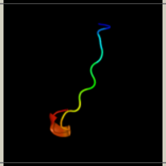
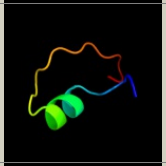
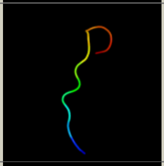
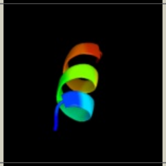
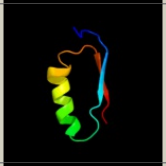
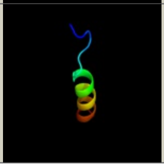
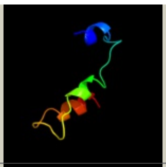
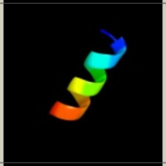
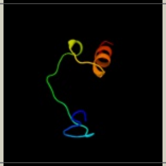
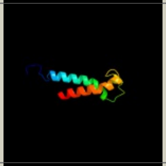
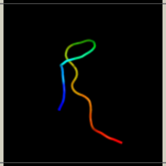
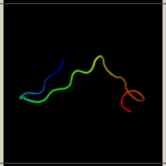
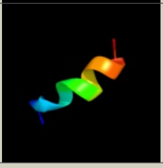
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hjnA_	Alignment		44.8	9	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**maintenance of ploidy protein mob1; **PDBTitle:** structural and functional analysis of saccharomyces2 cerevisiae mob1
2	c3nr5A_	Alignment		25.9	46	**PDB header:**transcription **Chain:** A: **PDB Molecule:**repressor of rna polymerase iii transcription maf1 homolog; **PDBTitle:** crystal structure of human maf1
3	c3qoqC_	Alignment		20.9	46	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**alginate and motility regulator z; **PDBTitle:** crystal structure of the transcription factor amrz in complex with the2 18 base pair amrz1 binding site
4	d1ixrc1	Alignment		15.2	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
5	c1u9pA_	Alignment		15.0	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
6	d1in4a1	Alignment		14.2	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
7	c1t0fC_	Alignment		14.1	24	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**transposon tn7 transposition protein tnsc; **PDBTitle:** crystal structure of the tnsa/tnsc(504-555) complex
8	d1mnta_	Alignment		13.3	31	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
9	c2v6xB_	Alignment		13.0	55	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**doa4-independent degradation protein 4; **PDBTitle:** stractural insight into the interaction between escrt-iii2 and vps4
10	c1kyqC_	Alignment		12.8	34	**PDB header:**oxidoreductase, lyase **Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8; **PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
11	d1rk8b_	Alignment		12.5	40	**Fold:**Mago nashi protein **Superfamily:**Mago nashi protein **Family:**Mago nashi protein

12	c3di3A_	Alignment		11.7	26	**PDB header:**cytokine/cytokine receptor **Chain:** A: **PDB Molecule:**interleukin-7; **PDBTitle:** crystal structure of the complex of human interleukin-7 with2 glycosylated human interleukin-7 receptor alpha ectodomain
13	c1yewF_	Alignment		11.1	15	**PDB header:**oxidoreductase, membrane protein **Chain:** F: **PDB Molecule:**particulate methane monooxygenase, a subunit; **PDBTitle:** crystal structure of particulate methane monooxygenase
14	c3izcS_	Alignment		11.1	26	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein rpl20 (l18ae); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
15	d1ixsb1	Alignment		9.9	32	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
16	d1kqfc_	Alignment		9.7	16	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Formate dehydrogenase N, cytochrome (gamma) subunit
17	c3o27B_	Alignment		9.5	29	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of c68 from the hybrid virus-plasmid pssvx
18	c3chxF_	Alignment		9.4	15	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**pmoa; **PDBTitle:** crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)
19	c3izci_	Alignment		9.3	29	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein rpl10 (l10e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
20	c3tweA_	Alignment		8.8	67	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**alpha4h; **PDBTitle:** crystal structure of the de novo designed peptide alpha4h
21	c3tweB_	Alignment	not modelled	8.6	67	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**alpha4h; **PDBTitle:** crystal structure of the de novo designed peptide alpha4h
22	c2islB_	Alignment	not modelled	8.1	32	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**blub; **PDBTitle:** blub bound to reduced flavin (fmnh2) and molecular oxygen.2 (clear crystal form)
23	c4a19X_	Alignment	not modelled	8.1	15	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**rpl18a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
24	c2bbdA_	Alignment	not modelled	7.9	40	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**coat protein; **PDBTitle:** crystal structure of the stiv mcp
25	d1czan4	Alignment	not modelled	7.9	30	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Hexokinase
26	c3iz5i_	Alignment	not modelled	7.7	30	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l10 (l10e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
27	d2j0sc1	Alignment	not modelled	7.6	45	**Fold:**Mago nashi protein **Superfamily:**Mago nashi protein **Family:**Mago nashi protein
28	c3lw6A_	Alignment	not modelled	7.3	63	**PDB header:**transferase **Chain:** A: **PDB Molecule:**beta-4-galactosyltransferase 7; **PDBTitle:** crystal structure of drosophila beta1,4-galactosyltransferase-7

29	c3ge5A_	Alignment	not modelled	7.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nad(p)h:fmn oxidoreductase; **PDBTitle:** crystal structure of a putative nad(p)h:fmn oxidoreductase (pg0310)2 from porphyromonas gingivalis w83 at 1.70 a resolution
30	c1nybA_	Alignment	not modelled	6.9	36	**PDB header:**transcription/rna **Chain:** A: **PDB Molecule:**probable regulatory protein n; **PDBTitle:** solution structure of the bacteriophage phi21 n peptide-boxb2 rna complex
31	d1kyqa1	Alignment	not modelled	6.6	34	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
32	d2gaxa1	Alignment	not modelled	6.6	25	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
33	c1ho7A_	Alignment	not modelled	6.3	47	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**voltage-gated potassium channel protein; **PDBTitle:** nmr structure of the potassium channel fragment l45 in tfe
34	c1ho2A_	Alignment	not modelled	6.3	47	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**voltage-gated potassium channel protein; **PDBTitle:** nmr structure of the potassium channel fragment l45 in2 micelles
35	d2frea1	Alignment	not modelled	6.1	21	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
36	d1b9ha_	Alignment	not modelled	5.8	16	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
37	c3jtgA_	Alignment	not modelled	5.7	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ets-related transcription factor elf-3; **PDBTitle:** crystal structure of mouse elf3 c-terminal dna-binding domain in2 complex with type ii tgf-beta receptor promoter dna
38	c3bemA_	Alignment	not modelled	5.7	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nad(p)h nitroreductase ydfn; **PDBTitle:** crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution
39	d3cx5d2	Alignment	not modelled	5.5	50	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
40	d1oe4a_	Alignment	not modelled	5.5	26	**Fold:**Uracil-DNA glycosylase-like **Superfamily:**Uracil-DNA glycosylase-like **Family:**Single-strand selective monofunctional uracil-DNA glycosylase SMUG1
41	d1pv0a_	Alignment	not modelled	5.4	27	**Fold:**Long alpha-hairpin **Superfamily:**Sporulation inhibitor Sda **Family:**Sporulation inhibitor Sda
42	d1ppjd2	Alignment	not modelled	5.4	63	**Fold:**Single transmembrane helix **Superfamily:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor **Family:**Cytochrome c1 subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase), transmembrane anchor
43	c4a19L_	Alignment	not modelled	5.4	29	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**rpl34; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
44	c1ckkB_	Alignment	not modelled	5.4	25	**PDB header:**calmodulin-peptide complex **Chain:** B: **PDB Molecule:**protein (rat ca2+/calmodulin dependent protein **PDBTitle:** calmodulin/rat ca2+/calmodulin dependent protein kinase2 fragment
45	c2zkrq_	Alignment	not modelled	5.3	20	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 part ii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
46	c1q2iA_	Alignment	not modelled	5.2	40	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**pnc27; **PDBTitle:** nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
47	d1dp7p_	Alignment	not modelled	5.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**P4 origin-binding domain-like