Phyre^2

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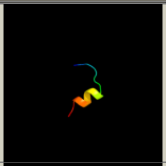
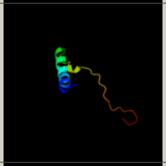
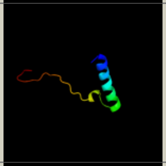
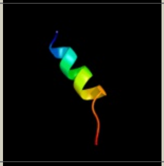
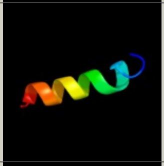
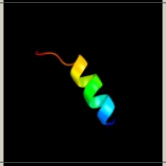
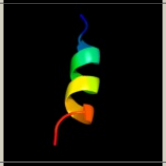
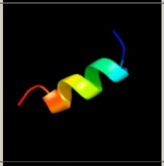
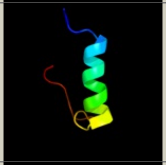
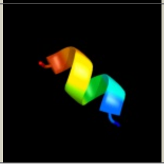
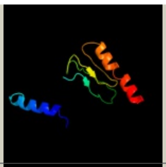
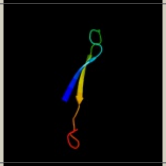
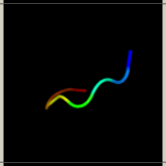
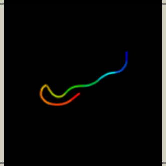
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f9jP_	Alignment		32.7	50	**PDB header:**rna binding protein **Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1; **PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
2	c3agjD_	Alignment		21.7	18	**PDB header:**translation/hydrolase **Chain:** D: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
3	c3agjB_	Alignment		21.7	18	**PDB header:**translation/hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
4	d2qi2a1	Alignment		16.5	25	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
5	c3lydA_	Alignment		14.3	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of putative uncharacterized protein from jonesia2 denitrificans
6	d2vgna1	Alignment		13.4	31	**Fold:**Sm-like fold **Superfamily:**Dom34/Pelota N-terminal domain-like **Family:**Dom34/Pelota N-terminal domain-like
7	c2qi2A_	Alignment		12.6	21	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein pelota related protein; **PDBTitle:** crystal structure of the thermoplasma acidophilum pelota2 protein
8	c3obyB_	Alignment		11.2	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
9	d1w6ga2	Alignment		10.5	17	**Fold:**Cystatin-like **Superfamily:**Amine oxidase N-terminal region **Family:**Amine oxidase N-terminal region
10	c3obwA_	Alignment		9.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein pelota homolog; **PDBTitle:** crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity
11	c2zkrx_	Alignment		9.3	56	**PDB header:**ribosomal protein/rna **Chain:** X: **PDB Molecule:**rna helices; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map

12	d1xl7a2	Alignment		9.3	15	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**Choline/Carnitine O-acyltransferase
13	c3jywW_	Alignment		9.0	44	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein l31(a); **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
14	c3kztB_	Alignment		8.9	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein of unknown function (np_812423.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
15	c3lg8B_	Alignment		8.7	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**a-type atp synthase subunit e; **PDBTitle:** crystal structure of the c-terminal part of subunit e (e101-206) from2 methanocaldococcus jannaschii of a1ao atp synthase
16	c4a1eW_	Alignment		8.5	44	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein l31; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
17	c2j376_	Alignment		8.4	67	**PDB header:**ribosome **Chain:** 6: **PDB Molecule:**ribosomal protein l31; **PDBTitle:** model of mammalian srp bound to 80s rncs
18	d1q7ea_	Alignment		8.1	24	**Fold:**CoA-transferase family III (CaiB/BaiF) **Superfamily:**CoA-transferase family III (CaiB/BaiF) **Family:**CoA-transferase family III (CaiB/BaiF)
19	c2fipA_	Alignment		7.8	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**late genes activator; **PDBTitle:** phage phi29 transcription regulator p4
20	d1vqox1	Alignment		7.8	44	**Fold:**Ribosomal protein L31e **Superfamily:**Ribosomal protein L31e **Family:**Ribosomal protein L31e
21	d1u5tb1	Alignment	not modelled	7.7	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
22	d1xhmb1	Alignment	not modelled	7.6	14	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
23	c3mcaB_	Alignment	not modelled	7.5	38	**PDB header:**translation regulation/hydrolase **Chain:** B: **PDB Molecule:**protein dom34; **PDBTitle:** structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
24	c1xhmB_	Alignment	not modelled	7.5	14	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein g(i)/g(s) **PDBTitle:** the crystal structure of a biologically active peptide2 (sigk) bound to a g protein beta:gamma heterodimer
25	c3hogA_	Alignment	not modelled	7.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**superoxide dismutase [cu-zn], chloroplastic; **PDBTitle:** metal-free tomato chloroplast superoxide dismutase
26	c3hxxA_	Alignment	not modelled	7.4	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
27	c1yfsB_	Alignment	not modelled	7.3	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
28	d1riqa2	Alignment	not modelled	7.2	21	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain

29	c2cv8A_	Alignment	not modelled	6.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**trna-splicing endonuclease; **PDBTitle:** crystal structure of trna-intron endonuclease from2 sulfolobus tokodaii
30	c3m9vA_	Alignment	not modelled	6.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent oxidoreductase; **PDBTitle:** x-ray structure of a kijd3 in complex with dtdp
31	d1whza_	Alignment	not modelled	6.4	21	**Fold:**dsRBD-like **Superfamily:**YcfA/nrd intein domain **Family:**YcfA-like
32	c1wqeA_	Alignment	not modelled	6.3	46	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omtx3; **PDBTitle:** an unusual fold for potassium channel blockers: nmr2 structure of three toxins from the scorpion opisthacanthus3 madagascariensis
33	c3nbmA_	Alignment	not modelled	6.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
34	c1e2vB_	Alignment	not modelled	6.0	67	**PDB header:**electron transport proteins **Chain:** B: **PDB Molecule:**cytochrome f; **PDBTitle:** n153q mutant of cytochrome f from chlamydomonas reinhardtii
35	d1ukua_	Alignment	not modelled	5.9	35	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
36	d1vf5c1	Alignment	not modelled	5.9	67	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
37	c1s1iW_	Alignment	not modelled	5.8	44	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein l31; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
38	d1ci3m1	Alignment	not modelled	5.8	67	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
39	d1e2wa1	Alignment	not modelled	5.8	67	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
40	d1gg2g_	Alignment	not modelled	5.8	16	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
41	c3phfX_	Alignment	not modelled	5.7	15	**PDB header:**viral protein **Chain:** X: **PDB Molecule:**envelope glycoprotein l; **PDBTitle:** crystal structure of the epstein-barr virus gh and gl complex
42	d1vhfa_	Alignment	not modelled	5.6	24	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
43	d1hcza1	Alignment	not modelled	5.5	67	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Cytochrome f, large domain **Family:**Cytochrome f, large domain
44	d2zfha1	Alignment	not modelled	5.4	35	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Divalent ion tolerance proteins CutA (CutA1)
45	c1xk8A_	Alignment	not modelled	5.4	35	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**divalent cation tolerant protein cuta; **PDBTitle:** divalent cation tolerant protein cuta from homo sapiens2 o60888
46	d1y1pa1	Alignment	not modelled	5.4	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
47	d1vkra_	Alignment	not modelled	5.4	22	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
48	c1vkrA_	Alignment	not modelled	5.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components; **PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii
49	c2ezvA_	Alignment	not modelled	5.3	18	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**type ii restriction enzyme sfii; **PDBTitle:** crystal structure of tetrameric restriction endonuclease2 sfii bound to cognate dna.
50	d1kx5b_	Alignment	not modelled	5.2	19	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones