Phyre²

Email	l.a.kelley@imperial.ac.uk
Description	P09372
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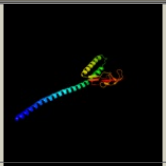
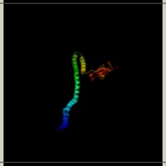
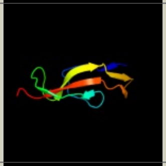
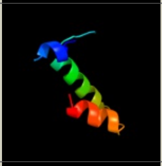
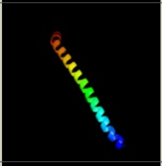
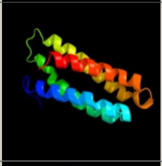
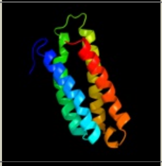
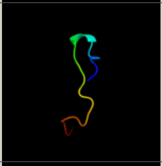
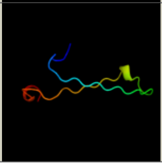
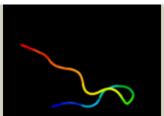
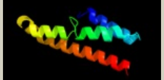
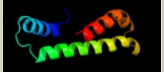
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1dkgB_	Alignment		100.0	99	**PDB header:**complex (hsp24/hsp70) **Chain:** B: **PDB Molecule:**nucleotide exchange factor grpe; **PDBTitle:** crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
2	c3a6mB_	Alignment		100.0	27	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**protein grpe; **PDBTitle:** crystal structure of grpe from thermus thermophilus hb8
3	d1dkga1	Alignment		99.8	100	**Fold:**Head domain of nucleotide exchange factor GrpE **Superfamily:**Head domain of nucleotide exchange factor GrpE **Family:**Head domain of nucleotide exchange factor GrpE
4	c3hl6B_	Alignment		27.8	22	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pathogenicity island protein; **PDBTitle:** staphylococcus aureus pathogenicity island 3 orf9 protein
5	c3swfA_	Alignment		21.8	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1; **PDBTitle:** cnga1 621-690 containing clz domain
6	d1rsoa_	Alignment		19.6	14	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
7	d1nzea_	Alignment		18.8	18	**Fold:**Four-helical up-and-down bundle **Superfamily:**Oxygen-evolving enhancer protein 3, **Family:**Oxygen-evolving enhancer protein 3,
8	c1nzeA_	Alignment		18.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxygen-evolving enhancer protein 3; **PDBTitle:** crystal structure of psbq polypeptide of photosystem ii2 from higher plants
9	d1x5ta1	Alignment		16.4	19	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
10	c2jvoA_	Alignment		15.0	22	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nucleolar protein 3; **PDBTitle:** segmental isotope labeling of npl3
11	c1w5fA_	Alignment		14.9	5	**PDB header:**cell division **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz, t7 mutated, domain swapped (t. maritima)

12	d2cpia1	Alignment		14.4	33	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
13	c3e7lD_	Alignment		14.2	15	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
14	c3mkxC_	Alignment		14.1	21	**PDB header:**antiviral protein **Chain:** C: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** crystal structure of bst2/tetherin
15	d1fnxh1	Alignment		14.0	14	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
16	d2cbia1	Alignment		13.5	16	**Fold:**Hyaluronidase domain-like **Superfamily:**Hyaluronidase post-catalytic domain-like **Family:**Hyaluronidase post-catalytic domain-like
17	d1rk8a_	Alignment		13.4	15	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
18	d1wi8a_	Alignment		13.1	17	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
19	d1etxa_	Alignment		12.6	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
20	d2choa1	Alignment		12.6	10	**Fold:**Hyaluronidase domain-like **Superfamily:**Hyaluronidase post-catalytic domain-like **Family:**Hyaluronidase post-catalytic domain-like
21	d2qeec1	Alignment	not modelled	11.6	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Uronate isomerase-like
22	d1w5fa2	Alignment	not modelled	11.3	5	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
23	d1ntca_	Alignment	not modelled	11.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
24	d1ttea1	Alignment	not modelled	10.7	22	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
25	c3bs9A_	Alignment	not modelled	10.6	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**nucleolysin tia-1 isoform p40; **PDBTitle:** x-ray structure of human tia-1 rrm2
26	d2j01s1	Alignment	not modelled	9.8	30	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
27	c3lraA_	Alignment	not modelled	9.5	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**disks large homolog 1, maguk p55 subfamily member 7, **PDBTitle:** structural basis for assembling a human tripartite complex dlg1-mpp7-2 mals3
28	d2cqca1	Alignment	not modelled	9.5	21	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
						Fold: Heme oxygenase-like

29	d1we1a_	Alignment	not modelled	9.1	6	**Superfamily:**Heme oxygenase-like **Family:**Eukaryotic type heme oxygenase
30	c3he5A_	Alignment	not modelled	9.0	24	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**synzip1; **PDBTitle:** heterospecific coiled-coil pair synzip2:synzip1
31	c2x7aB_	Alignment	not modelled	8.8	21	**PDB header:**immune system **Chain:** B: **PDB Molecule:**bone marrow stromal antigen 2; **PDBTitle:** structural basis of hiv-1 tethering to membranes by the2 bst2-tetherin ectodomain
32	d1fxla1	Alignment	not modelled	8.6	13	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
33	d1pzqa_	Alignment	not modelled	8.6	25	**Fold:**Dimerisation interlock **Superfamily:**Docking domain A of the erythromycin polyketide synthase (DEBS) **Family:**Docking domain A of the erythromycin polyketide synthase (DEBS)
34	c1zvuA_	Alignment	not modelled	8.5	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**topoisomerase iv subunit a; **PDBTitle:** structure of the full-length e. coli parc subunit
35	c3movB_	Alignment	not modelled	7.8	17	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of human lamin-b1 coil 2 segment
36	c2jl8S_	Alignment	not modelled	7.8	30	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**50s ribosomal protein l18; **PDBTitle:** insights into translational termination from the structure2 of rf2 bound to the ribosome (part 4 of 4).3 this file contains the 50s subunit.
37	d2d6fa1	Alignment	not modelled	7.6	10	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
38	c3q9vB_	Alignment	not modelled	7.5	29	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding response regulator; **PDBTitle:** crystal structure of rra c-terminal domain(123-221) from deinococcus2 radiodurans
39	c3m9bK_	Alignment	not modelled	7.4	11	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
40	d1h2vz_	Alignment	not modelled	7.3	15	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
41	c3md1B_	Alignment	not modelled	7.1	13	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**nuclear and cytoplasmic polyadenylated rna-binding protein **PDBTitle:** crystal structure of the second rrm domain of yeast poly(u)-binding2 protein (pub1)
42	d1igub_	Alignment	not modelled	7.0	10	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
43	d1fipa_	Alignment	not modelled	6.9	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
44	d1tafa_	Alignment	not modelled	6.7	7	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
45	d2zjrl1	Alignment	not modelled	6.6	30	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
46	d1cvja1	Alignment	not modelled	6.5	11	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
47	d2otaa1	Alignment	not modelled	6.5	33	**Fold:**YejL-like **Superfamily:**YejL-like **Family:**YejL-like
48	c3swyB_	Alignment	not modelled	6.3	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cyclic nucleotide-gated cation channel alpha-3; **PDBTitle:** cnga3 626-672 containing clz domain
49	d1ovya_	Alignment	not modelled	6.2	40	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
50	c2kxyA_	Alignment	not modelled	6.1	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of sur18c from streptococcus thermophilus.2 northeast structural genomics consortium target sur18c
51	d2cqba1	Alignment	not modelled	6.0	22	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
52	c1qzuB_	Alignment	not modelled	5.9	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein mds018; **PDBTitle:** crystal structure of human phosphopantothenoylcysteine decarboxylase
53	d1igqa_	Alignment	not modelled	5.9	17	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
54	d1ov2a_	Alignment	not modelled	5.9	13	**Fold:**RAP domain-like **Superfamily:**RAP domain-like **Family:**RAP domain

55	c1xe1A_	Alignment	not modelled	5.8	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf0907; **PDBTitle:** hypothetical protein from pyrococcus furiosus pfu-880080-001
56	d1xe1a_	Alignment	not modelled	5.8	31	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
57	d1bv8a_	Alignment	not modelled	5.8	11	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Alpha-macroglobulin receptor domain **Family:**Alpha-macroglobulin receptor domain
58	d2j0sd1	Alignment	not modelled	5.6	15	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
59	c1m7lA_	Alignment	not modelled	5.5	11	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**pulmonary surfactant-associated protein d; **PDBTitle:** solution structure of the coiled-coil trimerization domain2 from lung surfactant protein d
60	d1kyza2	Alignment	not modelled	5.4	13	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Plant O-methyltransferase, C-terminal domain
61	d1jeyb1	Alignment	not modelled	5.3	8	**Fold:**SPOC domain-like **Superfamily:**SPOC domain-like **Family:**Ku80 subunit middle domain
62	d1huwa_	Alignment	not modelled	5.2	12	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
63	c3cxjB_	Alignment	not modelled	5.2	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein from2 methanothermobacter thermautotrophicus
64	c3nmdA_	Alignment	not modelled	5.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cgmp dependent protein kinase; **PDBTitle:** crystal structure of the leucine zipper domain of cgmp dependent2 protein kinase i beta
65	d1jeya1	Alignment	not modelled	5.2	17	**Fold:**SPOC domain-like **Superfamily:**SPOC domain-like **Family:**Ku70 subunit middle domain