Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AG55
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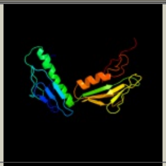
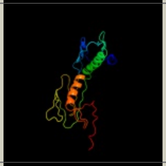
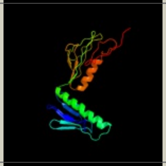
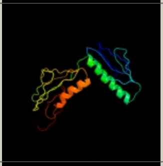
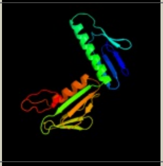
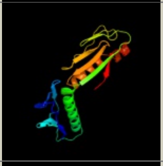
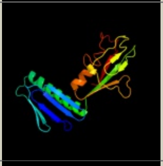
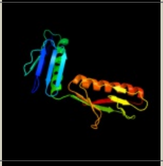
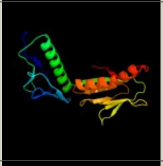
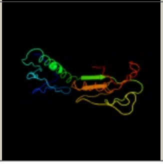
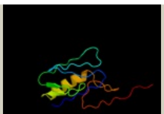
Unique Job ID	75607cdf1ab91700

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bbol_	Alignment		100.0	45	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**ribosomal protein l6; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
2	c2i2vG_	Alignment		100.0	100	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l6; **PDBTitle:** crystal structure of ribosome with messenger rna and the2 anticodon stem-loop of p-site trna. this file contains the3 50s subunit of one 70s ribosome. the entire crystal4 structure contains two 70s ribosomes and is described in5 remark 400.
3	c2hguH_	Alignment		100.0	38	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**50s ribosomal protein l6; **PDBTitle:** 70s t.th. ribosome functional complex with mrna and e- and p-site2 trnas at 4.5a. this entry 2hgu contains 50s ribosomal subunit. the3 30s ribosomal subunit can be found in pdb entry 2hgr.
4	c1sm1E_	Alignment		100.0	39	**PDB header:**ribosome/antibiotic **Chain:** E: **PDB Molecule:**50s ribosomal protein l6; **PDBTitle:** complex of the large ribosomal subunit from deinococcus radiodurans2 with quinupristin and dalfopristin
5	c487dJ_	Alignment		100.0	48	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**protein (50s l6 ribosomal protein); **PDBTitle:** seven ribosomal proteins fitted to a cryo-electron2 microscopic map of the large 50s subunit at 7.5 angstroms3 resolution
6	c1pnuE_	Alignment		100.0	39	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**50s ribosomal protein l6; **PDBTitle:** crystal structure of a streptomycin dependent ribosome from2 escherichia coli, 50s subunit of 70s ribosome. this file,3 1pnu, contains only molecules of the 50s ribosomal4 subunit. the 30s subunit, mrna, p-site trna, and a-site5 trna are in the pdb file 1pns.
7	c3ccmE_	Alignment		100.0	25	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**50s ribosomal protein l6p; **PDBTitle:** structure of anisomycin resistant 50s ribosomal subunit: 23s rrna2 mutation g2611u
8	c2zkre_	Alignment		100.0	25	**PDB header:**ribosomal protein/rna **Chain:** E: **PDB Molecule:**rna expansion segment es7 part ii; **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
9	c4a1eE_	Alignment		100.0	21	**PDB header:**ribosome **Chain:** E: **PDB Molecule:**60s ribosomal protein l9; **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
10	c3iz5F_	Alignment		100.0	24	**PDB header:**ribosome **Chain:** F: **PDB Molecule:**60s ribosomal protein l9 (l6p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
11	c1s1iH_	Alignment		100.0	26	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**60s ribosomal protein l9-a; **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.

12	d2qamg2	Alignment		100.0	100	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
13	d1rl6a2	Alignment		100.0	55	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
14	d2zjre1	Alignment		100.0	46	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
15	d2j01h2	Alignment		100.0	49	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
16	d2qamg1	Alignment		99.9	100	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
17	d1rl6a1	Alignment		99.9	40	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
18	d1vqoe1	Alignment		99.9	29	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
19	d2zjre2	Alignment		99.9	32	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
20	d2cqla1	Alignment		99.9	26	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
21	d2j01h1	Alignment	not modelled	99.8	25	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
22	d1vqoe2	Alignment	not modelled	99.7	22	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
23	d1a0ia1	Alignment	not modelled	38.5	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
24	c3q9qB_	Alignment	not modelled	35.6	35	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**heat shock protein beta-1; **PDBTitle:** hspb1 fragment second crystal form
25	c2wj7D_	Alignment	not modelled	34.5	41	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**alpha-crystallin b chain; **PDBTitle:** human alphab crystallin
26	c2bolA_	Alignment	not modelled	31.4	13	**PDB header:**heat shock protein **Chain:** A: **PDB Molecule:**small heat shock protein; **PDBTitle:** crystal structure and assembly of tsp36, a metazoan small2 heat shock protein
27	c3kd4A_	Alignment	not modelled	30.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative protease; **PDBTitle:** crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
28	c2jugB_	Alignment	not modelled	24.7	24	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**tubc protein; **PDBTitle:** multienzyme docking in hybrid megasynthetases
29	c2klrA	Alignment	not modelled	22.1	32	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**alpha-crystallin b chain;

29	c2klrA_	Alignment	not modelled	22.1	32	**PDBTitle:** solid-state nmr structure of the alpha-crystallin domain in alphab-2 crystallin oligomers
30	c2wj5A_	Alignment	not modelled	20.5	25	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**heat shock protein beta-6; **PDBTitle:** rat alpha crystallin domain
31	c3pgeA_	Alignment	not modelled	17.2	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**sumo-modified proliferating cell nuclear antigen; **PDBTitle:** structure of sumoylated pcna
32	d1j5pa3	Alignment	not modelled	14.4	21	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
33	c2gh8B_	Alignment	not modelled	14.0	11	**PDB header:**virus **Chain:** B: **PDB Molecule:**capsid protein; **PDBTitle:** x-ray structure of a native calicivirus
34	c3nicA_	Alignment	not modelled	13.2	31	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**eco29kir; **PDBTitle:** dna binding and cleavage by the giy-yig endonuclease r.eco29ki2 inactive variant y49f
35	c3l1eA_	Alignment	not modelled	12.8	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**alpha-crystallin a chain; **PDBTitle:** bovine alphaa crystallin zinc bound
36	c2ktsA_	Alignment	not modelled	12.3	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**heat shock protein hslj; **PDBTitle:** nmr structure of the protein np_415897.1
37	d1ev13_	Alignment	not modelled	12.1	11	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
38	d1oopc_	Alignment	not modelled	11.8	9	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
39	d2mev3_	Alignment	not modelled	11.1	16	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
40	c2gjhA_	Alignment	not modelled	11.0	22	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein; **PDBTitle:** nmr structure of cfr (c-terminal fragment of2 computationally designed novel-topology protein top7)
41	c2xseA_	Alignment	not modelled	10.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thymine dioxygenase jbp1; **PDBTitle:** the structural basis for recognition of j-base containing2 dna by a novel dna-binding domain in jbp1
42	c2d2fA_	Alignment	not modelled	10.7	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sufc protein; **PDBTitle:** crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
43	c3i38C_	Alignment	not modelled	10.4	37	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
44	c3i38E_	Alignment	not modelled	10.4	37	**PDB header:**chaperone **Chain:** E: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
45	d1v5ma_	Alignment	not modelled	9.9	18	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
46	d2gv8a2	Alignment	not modelled	9.8	28	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
47	c2wff3_	Alignment	not modelled	9.2	18	**PDB header:**virus **Chain:** 3: **PDB Molecule:**p1; **PDB Fragment:**capsid protein vp3, residues 311-536; **PDBTitle:** equine rhinitis a virus
48	d1cov3_	Alignment	not modelled	8.5	11	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
49	c2wzr3_	Alignment	not modelled	8.4	11	**PDB header:**virus **Chain:** 3: **PDB Molecule:**polyprotein; **PDB Fragment:**residues 285-503; **PDBTitle:** the structure of foot and mouth disease virus serotype sat1
50	d1ncqc_	Alignment	not modelled	7.0	10	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
51	d1fpn3_	Alignment	not modelled	6.3	16	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
52	c3cjiB_	Alignment	not modelled	6.2	11	**PDB header:**virus **Chain:** B: **PDB Molecule:**polyprotein; **PDBTitle:** structure of seneca valley virus-001
53	d1eah3_	Alignment	not modelled	6.1	10	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
54	d1ejxb_	Alignment	not modelled	5.9	16	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
55	d1h1oa1	Alignment	not modelled	5.9	28	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Two-domain cytochrome c
						Fold: Non-globular all-alpha subunits of globular proteins

56	d1xhmb1	Alignment	not modelled	5.9	41	**Superfamily:**Transducin (heterotrimeric G protein), gamma chain **Family:**Transducin (heterotrimeric G protein), gamma chain
57	d4ubpb_	Alignment	not modelled	5.7	13	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
58	c1xhmB_	Alignment	not modelled	5.7	41	**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
59	d1aym3_	Alignment	not modelled	5.6	16	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Picornaviridae-like VP (VP1, VP2, VP3 and VP4)
60	d1e9ya1	Alignment	not modelled	5.5	9	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
61	d1cuka3	Alignment	not modelled	5.4	27	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA helicase RuvA subunit, N-terminal domain
62	d1qfja1	Alignment	not modelled	5.3	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
63	c2latA_	Alignment	not modelled	5.2	40	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide--protein **PDBTitle:** solution structure of a human minimembrane protein ost4
64	d1h3fa2	Alignment	not modelled	5.0	30	**Fold:**Alpha-L RNA-binding motif **Superfamily:**Alpha-L RNA-binding motif **Family:**Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain