Phyre^2

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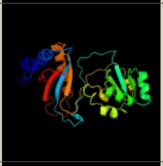
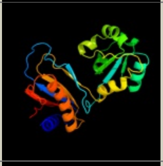
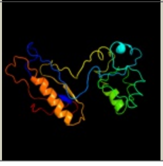
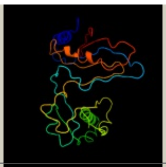
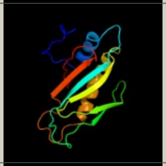
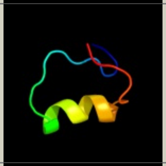
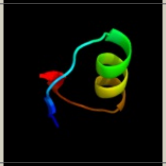
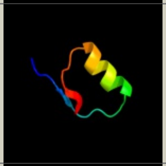
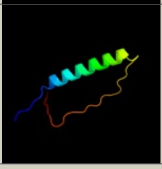
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qoyA_	Alignment		100.0	45	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**50s ribosomal protein l1; **PDBTitle:** crystal structure of ribosomal protein l1 from aquifex aeolicus
2	d1ad2a_	Alignment		100.0	50	**Fold:**Ribosomal protein L1 **Superfamily:**Ribosomal protein L1 **Family:**Ribosomal protein L1
3	c3bboD_	Alignment		100.0	45	**PDB header:**ribosome **Chain:** D: **PDB Molecule:**ribosomal protein l1; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
4	c2gyc2_	Alignment		100.0	100	**PDB header:**ribosome **Chain:** 2: **PDB Molecule:**50s ribosomal protein l1; **PDBTitle:** structure of the 50s subunit of a secm-stalled e. coli2 ribosome complex obtained by fitting atomic models for rna3 and protein components into cryo-em map emd-1143
5	d1mzpa_	Alignment		100.0	26	**Fold:**Ribosomal protein L1 **Superfamily:**Ribosomal protein L1 **Family:**Ribosomal protein L1
6	d1dwua_	Alignment		100.0	29	**Fold:**Ribosomal protein L1 **Superfamily:**Ribosomal protein L1 **Family:**Ribosomal protein L1
7	d1i2aa_	Alignment		100.0	29	**Fold:**Ribosomal protein L1 **Superfamily:**Ribosomal protein L1 **Family:**Ribosomal protein L1
8	c2zkr5_	Alignment		100.0	31	**PDB header:**ribosomal protein/rna **Chain:** 5: **PDB Molecule:**60s ribosomal protein l10a; **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	c1s1iA_	Alignment		100.0	18	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**60s ribosomal protein l1; **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.
10	c3iz5A_	Alignment		100.0	22	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**60s ribosomal protein l1 (l1p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
11	c2ftcA_	Alignment		100.0	20	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**mitochondrial ribosomal protein l1; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome

12	d2j01c1	Alignment		100.0	49	**Fold:**Ribosomal protein L1 **Superfamily:**Ribosomal protein L1 **Family:**Ribosomal protein L1
13	c2ov7C_	Alignment		100.0	59	**PDB header:**ribosomal protein **Chain:** C: **PDB Molecule:**50s ribosomal protein l1; **PDBTitle:** the first domain of the ribosomal protein l1 from thermus2 thermophilus
14	c2kzhA_	Alignment		57.6	37	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**tryptophan biosynthesis protein trpcf; **PDBTitle:** three-dimensional structure of a truncated phosphoribosylanthranilate2 isomerase (residues 255-384) from escherichia coli
15	d1piia1	Alignment		56.9	40	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
16	d1v5xa_	Alignment		48.6	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
17	d1nsja_	Alignment		43.2	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
18	d2i4ra1	Alignment		42.7	18	**Fold:**AtpF-like **Superfamily:**AtpF-like **Family:**AtpF-like
19	c1piiA_	Alignment		42.2	38	**PDB header:**bifunctional(isomerase and synthase) **Chain:** A: **PDB Molecule:**n-(5'phosphoribosyl)anthranilate isomerase; **PDBTitle:** three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
20	c2w40C_	Alignment		37.5	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glycerol kinase, putative; **PDBTitle:** crystal structure of plasmodium falciparum glycerol kinase2 with bound glycerol
21	c3nbmA_	Alignment	not modelled	33.2	15	**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.
22	d1qapa1	Alignment	not modelled	25.6	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
23	c2ov6A_	Alignment	not modelled	22.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**v-type atp synthase subunit f; **PDBTitle:** the nmr structure of subunit f of the methanogenic a1ao atp synthase2 and its interaction with the nucleotide-binding subunit b
24	d1o4ua1	Alignment	not modelled	21.5	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
25	c2nqqA_	Alignment	not modelled	21.1	28	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
26	c2vqpA_	Alignment	not modelled	19.6	31	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**matrix protein; **PDBTitle:** structure of the matrix protein from human respiratory2 syncytial virus
27	c3hz6A_	Alignment	not modelled	19.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulokinase; **PDBTitle:** crystal structure of xylulokinase from chromobacterium violaceum
						PDB header:transferase

28	c2l2qA_	Alignment	not modelled	18.7	17	**Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
29	c2vhml_	Alignment	not modelled	16.8	12	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**50s ribosomal protein l11; **PDBTitle:** structure of pdf binding helix in complex with the ribosome2 (part 1 of 4)
30	c3g25B_	Alignment	not modelled	16.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** 1.9 angstrom crystal structure of glycerol kinase (glpk) from2 staphylococcus aureus in complex with glycerol.
31	c3gbtA_	Alignment	not modelled	16.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gluconate kinase; **PDBTitle:** crystal structure of gluconate kinase from lactobacillus acidophilus
32	c1xupO_	Alignment	not modelled	15.4	15	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** enterococcus casseliflavus glycerol kinase complexed with glycerol
33	c2d4wA_	Alignment	not modelled	13.3	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of glycerol kinase from cellulomonas sp.2 nt3060
34	c2dpnB_	Alignment	not modelled	13.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the glycerol kinase from thermus2 thermophilus hb8
35	c2nlxA_	Alignment	not modelled	12.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xylulose kinase; **PDBTitle:** crystal structure of the apo e. coli xylulose kinase
36	c3flcX_	Alignment	not modelled	12.7	15	**PDB header:**transferase **Chain:** X: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of the his-tagged h232r mutant of glycerol kinase2 from enterococcus casseliflavus with glycerol
37	d2azeb1	Alignment	not modelled	12.5	20	**Fold:**E2F-DP heterodimerization region **Superfamily:**E2F-DP heterodimerization region **Family:**E2F dimerization segment
38	c2zf5O_	Alignment	not modelled	12.0	8	**PDB header:**transferase **Chain:** O: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of highly thermostable glycerol kinase from a2 hyperthermophilic archaeon
39	d1qpoa1	Alignment	not modelled	11.6	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Nicotinate/Quinolinate PRTase C-terminal domain-like **Family:**NadC C-terminal domain-like
40	c3ifrB_	Alignment	not modelled	11.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carbohydrate kinase, fggy; **PDBTitle:** the crystal structure of xylulose kinase from rhodospirillum rubrum
41	c2ftcG_	Alignment	not modelled	10.5	39	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**39s ribosomal protein l11, mitochondrial; **PDBTitle:** structural model for the large subunit of the mammalian mitochondrial2 ribosome
42	c3bboK_	Alignment	not modelled	10.2	15	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**ribosomal protein l11; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
43	d1k1ga_	Alignment	not modelled	10.0	33	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
44	d1iiba_	Alignment	not modelled	9.9	14	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
45	d2p3ra1	Alignment	not modelled	9.9	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
46	d2nqra3	Alignment	not modelled	9.5	28	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
47	c3jvpA_	Alignment	not modelled	9.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribulokinase; **PDBTitle:** crystal structure of ribulokinase from bacillus halodurans
48	c3iz5J_	Alignment	not modelled	9.1	43	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l12 (l11p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
49	c3enpA_	Alignment	not modelled	8.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tp53rk-binding protein; **PDBTitle:** crystal structure of human cgi121
50	d3cjsb1	Alignment	not modelled	8.2	36	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
51	c3cjtP_	Alignment	not modelled	7.9	36	**PDB header:**transferase/ribosomal protein **Chain:** P: **PDB Molecule:**50s ribosomal protein l11; **PDBTitle:** ribosomal protein l11 methyltransferase (prma) in complex with2 dimethylated ribosomal protein l11
52	d2d00a1	Alignment	not modelled	7.6	17	**Fold:**AtpF-like **Superfamily:**AtpF-like **Family:**AtpF-like
53	c1glbG_	Alignment	not modelled	7.5	15	**PDB header:**phosphotransferase **Chain:** G: **PDB Molecule:**glycerol kinase; **PDBTitle:** structure of the regulatory complex of escherichia coli iiiglc with2 glycerol kinase

54	c2i4rA_	Alignment	not modelled	7.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**v-type atp synthase subunit f; **PDBTitle:** crystal structure of the v-type atp synthase subunit f from2 archaeoglobus fulgidus. nesg target gr52a.
55	c3gg4B_	Alignment	not modelled	6.9	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycerol kinase; **PDBTitle:** the crystal structure of glycerol kinase from yersinia2 pseudotuberculosis
56	d1r59o1	Alignment	not modelled	6.9	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Glycerol kinase
57	d1gtea2	Alignment	not modelled	6.9	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
58	d2bl5a1	Alignment	not modelled	6.8	25	**Fold:**Eukaryotic type KH-domain (KH-domain type I) **Superfamily:**Eukaryotic type KH-domain (KH-domain type I) **Family:**Eukaryotic type KH-domain (KH-domain type I)
59	c3ezwD_	Alignment	not modelled	6.7	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycerol kinase; **PDBTitle:** crystal structure of a hyperactive escherichia coli glycerol kinase2 mutant gly230 --> asp obtained using microfluidic crystallization3 devices
60	d1mmsa2	Alignment	not modelled	6.7	33	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
61	c1qapA_	Alignment	not modelled	6.6	24	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**quinolinic acid phosphoribosyltransferase; **PDBTitle:** quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
62	c3gk0H_	Alignment	not modelled	6.6	39	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
63	c1o4uA_	Alignment	not modelled	6.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**type ii quinolic acid phosphoribosyltransferase; **PDBTitle:** crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
64	c2hbpA_	Alignment	not modelled	6.5	13	**PDB header:**endocytosis, protein binding **Chain:** A: **PDB Molecule:**cytoskeleton assembly control protein sla1; **PDBTitle:** solution structure of sla1 homology domain 1
65	c2b7pA_	Alignment	not modelled	6.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
66	c3l0gD_	Alignment	not modelled	6.4	7	**PDB header:**transferase **Chain:** D: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
67	c1xtzA_	Alignment	not modelled	6.1	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
68	d2gycg2	Alignment	not modelled	6.0	33	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
69	d1xbpg2	Alignment	not modelled	5.8	33	**Fold:**Ribosomal L11/L12e N-terminal domain **Superfamily:**Ribosomal L11/L12e N-terminal domain **Family:**Ribosomal L11/L12e N-terminal domain
70	d1vjpa1	Alignment	not modelled	5.7	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
71	c1jqmA_	Alignment	not modelled	5.6	29	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**50s ribosomal protein l11; **PDBTitle:** fitting of l11 protein and elongation factor g (ef-g) in2 the cryo-em map of e. coli 70s ribosome bound with ef-g,3 gdp and fusidic acid
72	d1qk1a2	Alignment	not modelled	5.2	12	**Fold:**Glutamine synthetase/guanido kinase **Superfamily:**Glutamine synthetase/guanido kinase **Family:**Guanido kinase catalytic domain
73	c2jbmA_	Alignment	not modelled	5.2	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nicotinate-nucleotide pyrophosphorylase; **PDBTitle:** qprtase structure from human