Phyre^2

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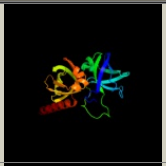
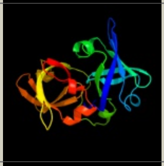
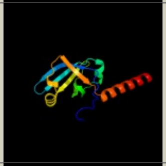
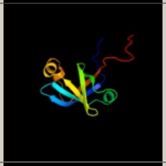
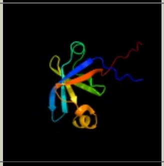
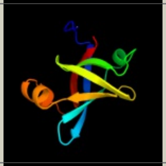
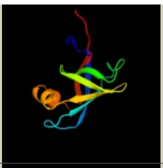
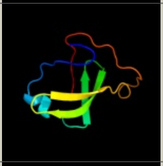
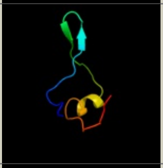
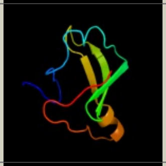
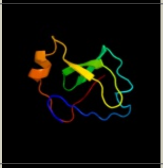
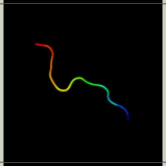
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1i8dB_	Alignment		100.0	100	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase; **PDBTitle:** crystal structure of riboflavin synthase
2	c1kzlA_	Alignment		100.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase; **PDBTitle:** riboflavin synthase from s.pombe bound to2 carboxyethyllumazine
3	c3a35B_	Alignment		100.0	31	**PDB header:**luminescent protein **Chain:** B: **PDB Molecule:**lumazine protein; **PDBTitle:** crystal structure of lump complexed with riboflavin
4	c3ddyA_	Alignment		100.0	32	**PDB header:**luminescent protein **Chain:** A: **PDB Molecule:**lumazine protein; **PDBTitle:** structure of lumazine protein, an optical transponder of luminescent2 bacteria
5	d1i8da2	Alignment		100.0	100	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Riboflavin synthase
6	d1kzla2	Alignment		100.0	33	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Riboflavin synthase
7	c1hzeB_	Alignment		100.0	100	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** solution structure of the n-terminal domain of riboflavin synthase2 from e. coli
8	c1i18B_	Alignment		100.0	100	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** solution structure of the n-terminal domain of riboflavin synthase2 from e. coli
9	d1i8da1	Alignment		100.0	100	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Riboflavin synthase
10	c1pkvA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** the n-terminal domain of riboflavin synthase in complex with2 riboflavin
11	c1pkvB_	Alignment		100.0	100	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin synthase alpha chain; **PDBTitle:** the n-terminal domain of riboflavin synthase in complex with2 riboflavin

12	d1kzla1	Alignment		100.0	38	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Riboflavin synthase
13	d2g50a1	Alignment		68.8	16	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
14	c3nrfA_	Alignment		64.0	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**apag protein; **PDBTitle:** crystal structure of an apag protein (pa1934) from pseudomonas2 aeruginosa pao1 at 1.50 a resolution
15	d1pkla1	Alignment		48.6	11	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
16	d1e0ta1	Alignment		46.2	31	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
17	d1liua1	Alignment		43.7	22	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
18	d1a3xa1	Alignment		34.7	15	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
19	c3o44G_	Alignment		33.8	36	**PDB header:**toxin **Chain:** G: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of the vibrio cholerae cytolysin (hlya) heptameric2 pore
20	d2hx0a1	Alignment		30.6	17	**Fold:**AF0104/ALDC/Ptd012-like **Superfamily:**AF0104/ALDC/Ptd012-like **Family:**AF0104-like
21	d1pkma1	Alignment	not modelled	29.2	20	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
22	c1xezA_	Alignment	not modelled	28.2	36	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of the vibrio cholerae cytolysin (hlya)2 pro-toxin with octylglucoside bound
23	c1hn0A_	Alignment	not modelled	27.4	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitin abc lyase i; **PDBTitle:** crystal structure of chondroitin abc lyase i from proteus2 vulgaris at 1.9 angstroms resolution
24	d1zbfa1	Alignment	not modelled	26.8	10	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Ribonuclease H
25	d3bzka4	Alignment	not modelled	25.2	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	d1hn0a3	Alignment	not modelled	23.5	11	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
27	c1v0eB_	Alignment	not modelled	20.2	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endo-alpha-sialidase; **PDBTitle:** endosialidase of bacteriophage k1f
28	d1zrua1	Alignment	not modelled	17.9	24	**Fold:**Virus attachment protein globular domain **Superfamily:**Virus attachment protein globular domain **Family:**Lactophage receptor-binding protein head domain
29	c2izpB	Alignment	not modelled	16.9	25	**PDB header:**toxin **Chain:** B: **PDB Molecule:**putative membrane antigen;

						PDBTitle: bipd - an invasion prtein associated with the type-iii2 secretion system of burkholderia pseudomallei.
30	d2izpa1	Alignment	not modelled	15.4	25	**Fold:**IpaD-like **Superfamily:**IpaD-like **Family:**IpaD-like
31	d1vqoq1	Alignment	not modelled	15.2	24	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
32	c3da0C_	Alignment	not modelled	13.8	24	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**cleaved chimeric receptor binding protein from **PDBTitle:** crystal structure of a cleaved form of a chimeric receptor binding2 protein from lactococcal phages subspecies tp901-1 and p2
33	c2khiA_	Alignment	not modelled	13.7	10	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 4 of the e. coli ribosomal2 protein s1
34	c3h43F_	Alignment	not modelled	13.2	20	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii
35	c2zkrq_	Alignment	not modelled	12.8	29	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:**rna expansion segment es31 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
36	d1qfja1	Alignment	not modelled	12.8	7	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
37	d1xpna_	Alignment	not modelled	12.7	25	**Fold:**Prealbumin-like **Superfamily:**Hypothetical protein PA1324 **Family:**Hypothetical protein PA1324
38	c2jz2A_	Alignment	not modelled	12.4	44	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
39	d1xsza2	Alignment	not modelled	11.9	25	**Fold:**TBP-like **Superfamily:**RalF, C-terminal domain **Family:**RalF, C-terminal domain
40	d1yq2a3	Alignment	not modelled	11.6	21	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**beta-Galactosidase/glucuronidase, N-terminal domain
41	c3kf8D_	Alignment	not modelled	11.4	27	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**protein ten1; **PDBTitle:** crystal structure of c. tropicalis stn1-ten1 complex
42	c1s1iQ_	Alignment	not modelled	11.2	35	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**60s ribosomal protein l21-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.
43	c2dycA_	Alignment	not modelled	11.1	20	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**galectin-4; **PDBTitle:** crystal structure of the n-terminal domain of mouse galectin-4
44	d1ulea_	Alignment	not modelled	10.9	12	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**Galectin (animal S-lectin)
45	d2f0ca1	Alignment	not modelled	10.6	20	**Fold:**Virus attachment protein globular domain **Superfamily:**Virus attachment protein globular domain **Family:**Lactophage receptor-binding protein head domain
46	c3d8mA_	Alignment	not modelled	10.4	24	**PDB header:**virus/viral protein **Chain:** A: **PDB Molecule:**baseplate protein, receptor binding protein; **PDBTitle:** crystal structure of a chimeric receptor binding protein from2 lactococcal phages subspecies tp901-1 and p2
47	d1s04a_	Alignment	not modelled	10.2	22	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ProFAR isomerase associated domain
48	c3iz5U_	Alignment	not modelled	9.4	29	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein l21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
49	d1r9fa_	Alignment	not modelled	9.4	36	**Fold:**Tombusvirus P19 core protein, VP19 **Superfamily:**Tombusvirus P19 core protein, VP19 **Family:**Tombusvirus P19 core protein, VP19
50	c2p6yA_	Alignment	not modelled	9.3	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein vca0587; **PDBTitle:** x-ray structure of the protein q9km02_vibch from vibrio cholerae at2 the resolution 1.63 a. northeast structural genomics consortium3 target vcr80.
51	c2r7fA_	Alignment	not modelled	9.3	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease ii family protein; **PDBTitle:** crystal structure of ribonuclease ii family protein from deinococcus2 radiodurans, hexagonal crystal form. northeast structural genomics3 target drr63
52	c3izcU_	Alignment	not modelled	9.2	35	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**60s ribosomal protein rpl21 (l21e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
						PDB header:ribosome **Chain:** P: **PDB Molecule:**60s ribosomal protein l21;

53	c4a1aP_	Alignment	not modelled	9.0	35	**PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
54	d1cb8a2	Alignment	not modelled	8.8	13	**Fold:**Hyaluronate lyase-like, C-terminal domain **Superfamily:**Hyaluronate lyase-like, C-terminal domain **Family:**Hyaluronate lyase-like, C-terminal domain
55	d1fnda1	Alignment	not modelled	8.7	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
56	c2wg6L_	Alignment	not modelled	8.1	22	**PDB header:**transcription,hydrolase **Chain:** L: **PDB Molecule:**general control protein gcn4, **PDBTitle:** proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant
57	c3htnA_	Alignment	not modelled	7.9	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative dna binding protein; **PDBTitle:** crystal structure of a putative dna binding protein (bt_1116) from2 bacteroides thetaiotaomicron vpi-5482 at 1.50 a resolution
58	d1krha1	Alignment	not modelled	7.8	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
59	c2z14A_	Alignment	not modelled	7.7	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ef-hand domain-containing family member c2; **PDBTitle:** crystal structure of the n-terminal duf1126 in human ef-2 hand domain containing 2 protein
60	d1gawa1	Alignment	not modelled	7.6	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
61	c3ca9A_	Alignment	not modelled	7.5	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**deoxyuridine triphosphatase; **PDBTitle:** evolution of chlorella virus dutpase
62	d2plia1	Alignment	not modelled	7.5	21	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
63	d2c9aa2	Alignment	not modelled	7.4	23	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**MAM domain
64	d2oaia1	Alignment	not modelled	7.0	13	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
65	d1pk6a_	Alignment	not modelled	6.9	17	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
66	c1aqfB_	Alignment	not modelled	6.9	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
67	d2p13a1	Alignment	not modelled	6.7	14	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
68	c3ftjA_	Alignment	not modelled	6.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**macrolide export atp-binding/permease protein **PDBTitle:** crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans
69	c3m9bK_	Alignment	not modelled	6.7	25	**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
70	d1k8kg_	Alignment	not modelled	6.5	14	**Fold:**alpha-alpha superhelix **Superfamily:**Arp2/3 complex 16 kDa subunit ARPC5 **Family:**Arp2/3 complex 16 kDa subunit ARPC5
71	d1fdra1	Alignment	not modelled	6.4	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
72	c1t5aB_	Alignment	not modelled	6.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase, m2 isozyme; **PDBTitle:** human pyruvate kinase m2
73	c2khjA_	Alignment	not modelled	6.3	13	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
74	d1j8hd1	Alignment	not modelled	6.0	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
75	d2plsa1	Alignment	not modelled	6.0	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
76	c2k4vA_	Alignment	not modelled	5.9	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pa1076; **PDBTitle:** solution structure of uncharacterized protein pa1076 from2 pseudomonas aeruginosa. northeast structural genomics3 consortium (nesg) target pat3, ontario center for4 structural proteomics target pa1076 .
77	d1duna_	Alignment	not modelled	5.8	13	**Fold:**beta-clip **Superfamily:**dUTPase-like **Family:**dUTPase-like
78	c2l0dA_	Alignment	not modelled	5.8	12	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**cell surface protein; **PDBTitle:** solution nmr structure of putative cell surface protein

						ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
79	d1qfza1	Alignment	not modelled	5.6	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
80	c3lgjA_	Alignment	not modelled	5.4	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of single-stranded binding protein (ssb) from2 bartonella henselae
81	c2zzfA_	Alignment	not modelled	5.3	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**alanyl-trna synthetase; **PDBTitle:** crystal structure of alanyl-trna synthetase without2 oligomerization domain
82	c2aklA_	Alignment	not modelled	5.3	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phna-like protein pa0128; **PDBTitle:** solution structure for phn-a like protein pa0128 from2 pseudomonas aeruginosa
83	d3deda1	Alignment	not modelled	5.1	17	**Fold:**FAD-binding/transporter-associated domain-like **Superfamily:**FAD-binding/transporter-associated domain-like **Family:**CorC/HlyC domain-like
84	d1am2a_	Alignment	not modelled	5.0	19	**Fold:**Hedgehog/intein (Hint) domain **Superfamily:**Hedgehog/intein (Hint) domain **Family:**Intein (protein splicing domain)
85	c2vl6C_	Alignment	not modelled	5.0	27	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** structural analysis of the sulfolobus solfataricus mcm2 protein n-terminal domain