Phyre^2

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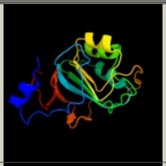
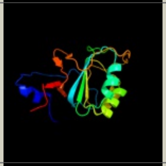
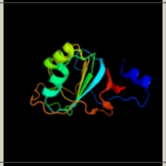
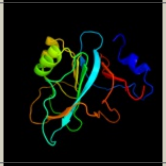
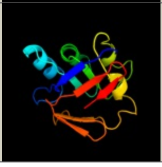
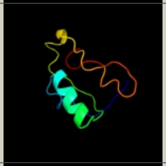
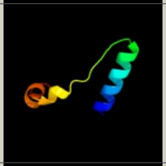
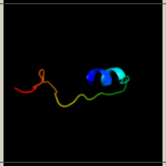
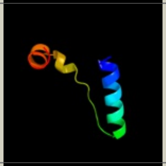
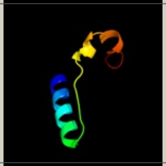
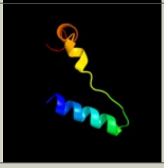
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1q5xa_	Alignment		100.0	100	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
2	c3c8oB_	Alignment		100.0	55	**PDB header:**hydrolase regulator **Chain:** B: **PDB Molecule:**regulator of ribonuclease activity a; **PDBTitle:** the crystal structure of rraa from pao1
3	c2pcnA_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:2-demethylmenaquinone **PDBTitle:** crystal structure of s-adenosylmethionine: 2-dimethylmenaquinone2 methyltransferase (gk_1813) from geobacillus kaustophilus hta426
4	d1vi4a_	Alignment		100.0	44	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
5	d1j3la_	Alignment		100.0	44	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
6	d1nxja_	Alignment		100.0	45	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**RraA-like **Family:**RraA-like
7	c1nxjA_	Alignment		100.0	45	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**probable s-adenosylmethionine:2- **PDBTitle:** structure of rv3853 from mycobacterium tuberculosis
8	c3nojA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate **PDBTitle:** the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
9	c3k4iC_	Alignment		100.0	19	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
10	c2c5qE_	Alignment		100.0	19	**PDB header:**structural genomics,unknown function **Chain:** E: **PDB Molecule:**rraa-like protein yer010c; **PDBTitle:** crystal structure of yeast yer010cp
11	d1vbga2	Alignment		76.9	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain

12	d1kbla2	Alignment		75.0	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
13	d2gp4a1	Alignment		60.6	20	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**IlvD/EDD C-terminal domain-like
14	d1f5va_	Alignment		55.4	18	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
15	d1e8ca2	Alignment		55.2	20	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
16	c3n2sD_	Alignment		53.4	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadph-dependent nitro/flavin reductase; **PDBTitle:** structure of nfra1 nitroreductase from b. subtilis
17	d1zcha1	Alignment		49.8	15	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
18	c2gp4A_	Alignment		47.1	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydratase; **PDBTitle:** structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
19	c3eofB_	Alignment		43.7	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase (yp_213212.1) from2 bacteroides fragilis nctc 9343 at 1.99 a resolution
20	d1bkja_	Alignment		42.7	18	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
21	c1vfgB_	Alignment	not modelled	42.6	17	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**poly a polymerase; **PDBTitle:** crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog
22	c1ou5A_	Alignment	not modelled	40.9	36	**PDB header:**translation, transferase **Chain:** A: **PDB Molecule:**trna cca-adding enzyme; **PDBTitle:** crystal structure of human cca-adding enzyme
23	d1vfga2	Alignment	not modelled	37.7	17	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
24	d1ou5a2	Alignment	not modelled	33.3	36	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
25	c1dbgA_	Alignment	not modelled	33.1	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**chondroitinase b; **PDBTitle:** crystal structure of chondroitinase b
26	c2vpiA_	Alignment	not modelled	31.2	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
27	d1ofla_	Alignment	not modelled	30.1	22	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Pectin lyase-like **Family:**Chondroitinase B
28	c1e8cB_	Alignment	not modelled	27.4	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**udp-n-acetylmuramoylalanyl-d-glutamate--2,6- **PDBTitle:** structure of mure the udp-n-acetylmuramyl tripeptide2 synthetase from e. coli
						Fold: Nucleotidyltransferase

29	d1miwa2	Alignment	not modelled	24.8	23	**Superfamily:**Nucleotidyltransferase **Family:**Poly A polymerase head domain-like
30	c3mvnA_	Alignment	not modelled	23.7	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamayl-medo- **PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamayl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
31	c3h37B_	Alignment	not modelled	21.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna nucleotidyl transferase-related protein; **PDBTitle:** the structure of cca-adding enzyme apo form i
32	c3aqnA_	Alignment	not modelled	19.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly(a) polymerase; **PDBTitle:** complex structure of bacterial protein (apo form ii)
33	d1thfd_	Alignment	not modelled	18.7	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
34	c3l7oB_	Alignment	not modelled	18.4	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
35	c3k6hB_	Alignment	not modelled	18.1	5	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitroreductase family protein; **PDBTitle:** crystal structure of a nitroreductase family protein from2 agrobacterium tumefaciens str. c58
36	c3tbiB_	Alignment	not modelled	16.6	33	**PDB header:**transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
37	c2pjmA_	Alignment	not modelled	16.4	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
38	c3bm2B_	Alignment	not modelled	16.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein ydja; **PDBTitle:** crystal structure of a minimal nitroreductase ydja from escherichia2 coli k12 with and without fmn cofactor
39	c1fdvA_	Alignment	not modelled	16.4	19	**PDB header:**dehydrogenase **Chain:** A: **PDB Molecule:**17-beta-hydroxysteroid dehydrogenase; **PDBTitle:** human 17-beta-hydroxysteroid-dehydrogenase type 1 mutant2 h221l complexed with nad+
40	c2wzvB_	Alignment	not modelled	15.3	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nfnb protein; **PDBTitle:** crystal structure of the fmn-dependent nitroreductase nfnb2 from mycobacterium smegmatis
41	d1uj4a1	Alignment	not modelled	14.3	15	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
42	c1miyB_	Alignment	not modelled	12.5	25	**PDB header:**translation, transferase **Chain:** B: **PDB Molecule:**trna cca-adding enzyme; **PDBTitle:** crystal structure of bacillus stearothermophilus cca-adding enzyme in2 complex with ctp
43	d1jtva_	Alignment	not modelled	11.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
44	d1fcqa_	Alignment	not modelled	10.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Bee venom hyaluronidase
45	c3cioA_	Alignment	not modelled	9.7	35	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase etk; **PDBTitle:** the kinase domain of escherichia coli tyrosine kinase etk
46	c3bemA_	Alignment	not modelled	9.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nad(p)h nitroreductase ydfn; **PDBTitle:** crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution
47	c2atmA_	Alignment	not modelled	9.6	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure of the recombinant allergen ves v 2
48	c1skoA_	Alignment	not modelled	9.5	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**mitogen-activated protein kinase kinase 1 **PDBTitle:** mp1-p14 complex
49	c1fcuA_	Alignment	not modelled	9.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronoglucosaminidase; **PDBTitle:** crystal structure (trigonal) of bee venom hyaluronidase
50	c3emkA_	Alignment	not modelled	9.3	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glucose/ribitol dehydrogenase; **PDBTitle:** 2.5a crystal structure of glucose/ribitol dehydrogenase2 from brucella melitensis
51	d1h6za2	Alignment	not modelled	9.3	15	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Phosphohistidine domain **Family:**Pyruvate phosphate dikinase, central domain
52	c3mjjD_	Alignment	not modelled	9.3	36	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**predicted acetamidase/formamidase; **PDBTitle:** crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
53	d1tvca1	Alignment	not modelled	9.1	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
54	d1ka9f_	Alignment	not modelled	9.1	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes

55	c1vdzA_	Alignment	not modelled	8.4	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**a-type atpase subunit a; **PDBTitle:** crystal structure of a-type atpase catalytic subunit a from2 pyrococcus horikoshii ot3
56	c2pe4A_	Alignment	not modelled	8.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hyaluronidase-1; **PDBTitle:** structure of human hyaluronidase 1, a hyaluronan hydrolyzing enzyme2 involved in tumor growth and angiogenesis
57	d2f4la1	Alignment	not modelled	8.4	21	**Fold:**CUB-like **Superfamily:**Acetamidase/Formamidase-like **Family:**Acetamidase/Formamidase-like
58	d1i1qb_	Alignment	not modelled	8.4	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
59	c2xrfA_	Alignment	not modelled	8.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridine phosphorylase 2; **PDBTitle:** crystal structure of human uridine phosphorylase 2
60	c3eo7A_	Alignment	not modelled	8.3	24	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative nitroreductase; **PDBTitle:** crystal structure of a putative nitroreductase (ava_2154) from2 anabaena variabilis atcc 29413 at 1.80 a resolution
61	c3pbiA_	Alignment	not modelled	8.2	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**invasion protein; **PDBTitle:** structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
62	d1h5ya_	Alignment	not modelled	8.2	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
63	c3hj9A_	Alignment	not modelled	8.2	8	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of a putative nitroreductase (reut_a1228) from2 ralstonia eutropha jmp134 at 2.00 a resolution
64	c3b9tD_	Alignment	not modelled	7.8	29	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**twin-arginine translocation pathway signal protein; **PDBTitle:** crystal structure of predicted acetamidase/formamidase (yp_546212.1)2 from methylobacillus flagellatus kt at 1.58 a resolution
65	c2xivA_	Alignment	not modelled	7.7	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of2 mycobacterium tuberculosis
66	c2r01A_	Alignment	not modelled	7.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitroreductase family protein; **PDBTitle:** crystal structure of a putative fmn-dependent nitroreductase (ct0345)2 from chlorobium tepidum tls at 1.15 a resolution
67	d2fsua1	Alignment	not modelled	7.0	10	**Fold:**PLP-dependent transferase-like **Superfamily:**PhnH-like **Family:**PhnH-like
68	c2fsuA_	Alignment	not modelled	7.0	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein phnh; **PDBTitle:** crystal structure of the phnh protein from escherichia coli
69	d1eara1	Alignment	not modelled	7.0	30	**Fold:**Urease metallochaperone UreE, N-terminal domain **Superfamily:**Urease metallochaperone UreE, N-terminal domain **Family:**Urease metallochaperone UreE, N-terminal domain
70	d1j5ya1	Alignment	not modelled	6.8	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
71	c2i7hE_	Alignment	not modelled	6.7	10	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitroreductase-like family protein; **PDBTitle:** crystal structure of the nitroreductase-like family protein from2 bacillus cereus
72	c2ii1A_	Alignment	not modelled	6.6	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**acetamidase; **PDBTitle:** crystal structure of acetamidase (10172637) from bacillus halodurans2 at 1.95 a resolution
73	c3gt2A_	Alignment	not modelled	6.6	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the p60 domain from m. avium2 paratuberculosis antigen map1272c
74	c3rkuC_	Alignment	not modelled	6.5	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase ymr226c; **PDBTitle:** substrate fingerprint and the structure of nadp+ dependent serine2 dehydrogenase from saccharomyces cerevisiae complexed with nadp+
75	c1vbhA_	Alignment	not modelled	6.5	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate,orthophosphate dikinase; **PDBTitle:** pyruvate phosphate dikinase with bound mg-pep from maize
76	d2cs7a1	Alignment	not modelled	6.3	21	**Fold:**IL8-like **Superfamily:**PhtA domain-like **Family:**PhtA domain-like
77	d1gph12	Alignment	not modelled	6.1	16	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Class II glutamine amidotransferases
78	c1y43B_	Alignment	not modelled	5.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**aspergillopepsin ii heavy chain; **PDBTitle:** crystal structure of aspergilloglutamic peptidase from2 aspergillus niger
79	c2kytA_	Alignment	not modelled	5.7	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**group xvi phospholipase a2; **PDBTitle:** solution struture of the h-rev107 n-terminal domain
						PDB header:immune system, rna binding protein **Chain:** D: **PDB Molecule:**mp18 rna editing complex protein;

80	c3k81D_	Alignment	not modelled	5.7	25	**PDBTitle:** structure of the central interaction protein from the trypanosoma2 brucei editosome in complex with single domain antibodies
81	d1vzwa1	Alignment	not modelled	5.7	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Histidine biosynthesis enzymes
82	d1p3da2	Alignment	not modelled	5.5	27	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**MurCDEF C-terminal domain
83	c3ny0D_	Alignment	not modelled	5.5	20	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**urease accessory protein uree; **PDBTitle:** crystal structure of uree from helicobacter pylori (ni2+ bound form)
84	c2wknE_	Alignment	not modelled	5.3	36	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**formamidase; **PDBTitle:** gamma lactamase from delftia acidovorans
85	d1vkya_	Alignment	not modelled	5.2	18	**Fold:**QueA-like **Superfamily:**QueA-like **Family:**QueA-like