Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A7D7
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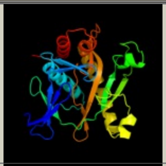
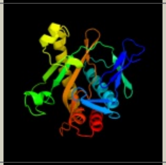
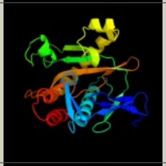
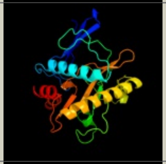
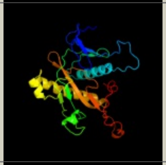
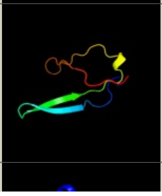
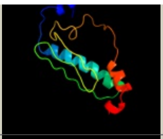
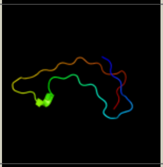
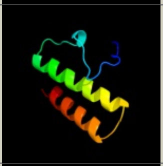
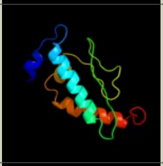
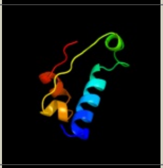
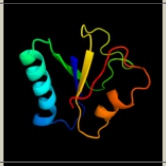
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gqsA_	Alignment		100.0	100	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide **PDBTitle:** saicar synthetase complexed with cair-mg2+ and adp
2	c2z02A_	Alignment		100.0	43	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide **PDBTitle:** crystal structure of2 phosphoribosylaminoimidazolesuccinocarboxamide synthase3 wit atp from methanocaldococcus jannaschii
3	c3kreA_	Alignment		100.0	41	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide synthase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from ehrlichia chaffeensis at 1.8a resolution
4	c3nuaB_	Alignment		100.0	42	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide synthase; **PDBTitle:** crystal structure of phosphoribosylaminoimidazole-succinocarboxamide2 synthase from clostridium perfringens
5	c2ywvB_	Alignment		100.0	44	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole succinocarboxamide synthetase; **PDBTitle:** crystal structure of saicar synthetase from geobacillus kaustophilus
6	d2cnqa1	Alignment		100.0	30	**Fold:**SAICAR synthase-like **Superfamily:**SAICAR synthase-like **Family:**SAICAR synthase
7	c3r9rA_	Alignment		100.0	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole-succinocarboxamide synthase; **PDBTitle:** structure of a phosphoribosylaminoimidazole-succinocarboxamide2 synthase from mycobacterium abscessus atcc 19977 / dsm 44196
8	d1kuta_	Alignment		100.0	39	**Fold:**SAICAR synthase-like **Superfamily:**SAICAR synthase-like **Family:**SAICAR synthase
9	c2h31A_	Alignment		100.0	32	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
10	c1zp9A_	Alignment		57.1	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rio1 kinase; **PDBTitle:** crystal structure of full-legnth a.fulgidus rio1 serine kinase bound2 to atp and mn2+ ions.
11	d2h3ka1	Alignment		36.5	14	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**NEAT domain-like **Family:**NEAT domain

12	c3nj2B_	Alignment		33.8	16	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**duf269-containing protein; **PDBTitle:** crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
13	d1kjqa3	Alignment		19.8	34	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
14	d2a5za1	Alignment		18.7	12	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**SO2946-like
15	d1i4ya_	Alignment		18.4	9	**Fold:**Four-helical up-and-down bundle **Superfamily:**Hemerythrin-like **Family:**Hemerythrin-like
16	c3g7pA_	Alignment		17.5	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**nitrogen fixation protein; **PDBTitle:** crystal structure of a nifx-associated protein of unknown function2 (afe_1514) from acidithiobacillus ferrooxidans atcc at 2.00 a3 resolution
17	c2pvpB_	Alignment		16.8	34	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
18	d1pmia_	Alignment		15.3	15	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Type I phosphomannose isomerase
19	c3lzcA_	Alignment		14.1	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**dph2; **PDBTitle:** crystal structure of dph2 from pyrococcus horikoshii
20	c2auwB_	Alignment		12.7	23	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
21	c3h1yA_	Alignment	not modelled	11.7	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mannose-6-phosphate isomerase; **PDBTitle:** crystal structure of mannose 6-phosphate isomerase from2 salmonella typhimurium bound to substrate (f6p)and metal3 atom (zn)
22	d1hrba_	Alignment	not modelled	11.4	9	**Fold:**Four-helical up-and-down bundle **Superfamily:**Hemerythrin-like **Family:**Hemerythrin-like
23	c3cegA_	Alignment	not modelled	11.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**baculoviral iap repeat-containing protein 6; **PDBTitle:** crystal structure of the ubc domain of baculoviral iap2 repeat-containing protein 6
24	c3eplA_	Alignment	not modelled	10.6	24	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna isopentenyltransferase; **PDBTitle:** crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
25	c3s6bA_	Alignment	not modelled	10.5	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150
26	c1tqmA_	Alignment	not modelled	10.3	13	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of a. fulgidus rio2 serine protein kinase bound to2 amppnp
27	c3exaD_	Alignment	not modelled	9.6	18	**PDB header:**transferase **Chain:** D: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of the full-length trna2 isopentenylpyrophosphate transferase (bh2366) from3 bacillus halodurans, northeast structural genomics4 consortium target bhr41.
						PDB header:ligase

28	c3r23B_	Alignment	not modelled	9.5	20	**Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
29	d1zara2	Alignment	not modelled	9.5	15	**Fold:**Protein kinase-like (PK-like) **Superfamily:**Protein kinase-like (PK-like) **Family:**RIO1-like kinases
30	c3idwA_	Alignment	not modelled	9.4	6	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
31	c2vd2A_	Alignment	not modelled	8.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp phosphoribosyltransferase; **PDBTitle:** the crystal structure of hisg from b. subtilis
32	c2qeaB_	Alignment	not modelled	8.3	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative general stress protein 26; **PDBTitle:** crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution
33	c1ylaB_	Alignment	not modelled	8.3	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ubiquitin-conjugating enzyme e2-25 kda; **PDBTitle:** ubiquitin-conjugating enzyme e2-25 kda (huntington interacting protein2 2)
34	d2hq7a1	Alignment	not modelled	8.3	7	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
35	d1a62a2	Alignment	not modelled	8.2	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
36	c3a8tA_	Alignment	not modelled	8.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate isopentenyltransferase; **PDBTitle:** plant adenylate isopentenyltransferase in complex with atp
37	c3d3qB_	Alignment	not modelled	7.8	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate **PDBTitle:** crystal structure of trna delta(2)-isopentenylpyrophosphate2 transferase (se0981) from staphylococcus epidermidis.3 northeast structural genomics consortium target ser100
38	d2cdqa3	Alignment	not modelled	7.6	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
39	c2dvzA_	Alignment	not modelled	7.6	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
40	c3dmbA_	Alignment	not modelled	7.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative general stress protein 26 with a pnp-oxidase like **PDBTitle:** crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
41	d2hmfa2	Alignment	not modelled	7.5	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Aspartokinase allosteric domain-like
42	d1rz4a1	Alignment	not modelled	7.5	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Eukaryotic translation initiation factor 3 subunit 12, eIF3k, C-terminal domain
43	d2d6fa1	Alignment	not modelled	7.5	30	**Fold:**Sm-like fold **Superfamily:**GatD N-terminal domain-like **Family:**GatD N-terminal domain-like
44	d1tf5a1	Alignment	not modelled	6.9	42	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
45	d1nkta1	Alignment	not modelled	6.9	50	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
46	d2r7ka2	Alignment	not modelled	6.7	20	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
47	c3dzoA_	Alignment	not modelled	6.7	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhoptry kinase domain; **PDBTitle:** crystal structure of a rhoptry kinase from toxoplasma gondii
48	c3fozB_	Alignment	not modelled	6.5	6	**PDB header:**transferase/rna **Chain:** B: **PDB Molecule:**trna delta(2)-isopentenylpyrophosphate transferase; **PDBTitle:** structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
49	c2pr1B_	Alignment	not modelled	6.5	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized n-acetyltransferase ylbp; **PDBTitle:** crystal structure of the bacillus subtilis n-acetyltransferase ylbp2 protein in complex with coenzyme-a
50	c3e46A_	Alignment	not modelled	6.1	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin-conjugating enzyme e2-25 kda; **PDBTitle:** crystal structure of ubiquitin-conjugating enzyme e2-25kda2 (huntington interacting protein 2) m172a mutant
51	d1g57a_	Alignment	not modelled	6.0	18	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
52	d1uj4a2	Alignment	not modelled	5.9	71	**Fold:**Ferredoxin-like **Superfamily:**D-ribose-5-phosphate isomerase (RpiA), lid domain **Family:**D-ribose-5-phosphate isomerase (RpiA), lid domain
						Fold: YoaC-like

53	d2es9a1	Alignment	not modelled	5.9	15	**Superfamily:**YoaC-like **Family:**YoaC-like
54	d2ozla1	Alignment	not modelled	5.9	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Branched-chain alpha-keto acid dehydrogenase PP module
55	c3lwbA_	Alignment	not modelled	5.7	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
56	c1zdbA_	Alignment	not modelled	5.7	50	**PDB header:**igg binding domain **Chain:** A: **PDB Molecule:**mini protein a domain, z38; **PDBTitle:** phage-selected mini protein a domain, z38, nmr, minimized2 mean structure
57	c3byvA_	Alignment	not modelled	5.5	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhoptry kinase; **PDBTitle:** crystal structure of toxoplasma gondii specific rhoptry2 antigen kinase domain
58	d2cyya1	Alignment	not modelled	5.4	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
59	d1q46a1	Alignment	not modelled	5.4	18	**Fold:**SAM domain-like **Superfamily:**eIF2alpha middle domain-like **Family:**eIF2alpha middle domain-like