Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A6G3
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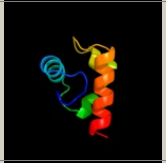
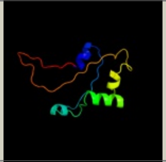
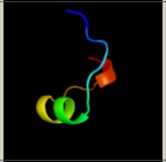
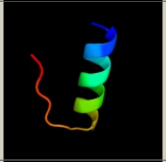
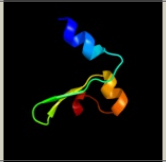
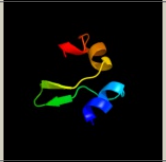
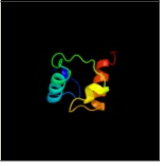
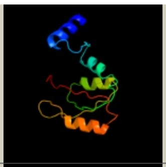
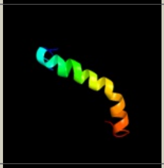
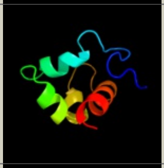
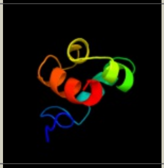
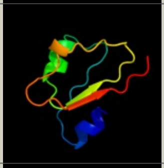
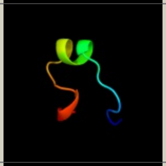
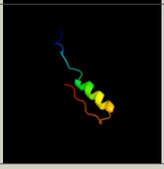
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2a9sa1	Alignment		100.0	43	**Fold:**Anticodon-binding domain-like **Superfamily:**CinA-like **Family:**CinA-like
2	d1pzna1	Alignment		51.6	18	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
3	d2i1qa1	Alignment		42.3	18	**Fold:**SAM domain-like **Superfamily:**Rad51 N-terminal domain-like **Family:**DNA repair protein Rad51, N-terminal domain
4	c3b33A_	Alignment		38.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the pas domain of nitrogen regulation protein2 nr(ii) from vibrio parahaemolyticus
5	c3a9lB_	Alignment		36.5	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly-gamma-glutamate hydrolase; **PDBTitle:** structure of bacteriophage poly-gamma-glutamate hydrolase
6	d1mzua_	Alignment		18.1	19	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
7	d1xjca_	Alignment		17.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
8	d1v9ya_	Alignment		17.0	18	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**Heme-binding PAS domain
9	c1v9yA_	Alignment		17.0	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**heme pas sensor protein; **PDBTitle:** crystal structure of the heme pas sensor domain of ec dos (ferric2 form)
10	c3mfxA_	Alignment		15.9	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sensory box/ggdef family protein; **PDBTitle:** crystal structure of the sensory box domain of the sensory-2 box/ggdef protein so_1695 from shewanella oneidensis,3 northeast structural genomics consortium target sor288b
11	d2bgwa1	Alignment		13.6	5	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like

12	c3ju7B_	Alignment		13.1	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative plp-dependent aminotransferase; **PDBTitle:** crystal structure of putative plp-dependent aminotransferase2 (np_978343.1) from bacillus cereus atcc 10987 at 2.19 a resolution
13	d3proc1	Alignment		11.8	18	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
14	c1zpdA_	Alignment		11.0	17	**PDB header:**alcohol fermentation **Chain:** A: **PDB Molecule:**pyruvate decarboxylase; **PDBTitle:** pyruvate decarboxylase from zymomonas mobilis
15	d1nwza_	Alignment		10.7	19	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
16	c1kftA_	Alignment		10.6	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**excinuclease abc subunit c; **PDBTitle:** solution structure of the c-terminal domain of uvrc from e-2 coli
17	d1kfta_	Alignment		10.6	11	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Excinuclease UvrC C-terminal domain
18	d1a4ia1	Alignment		10.3	36	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
19	c3a0vA_	Alignment		10.2	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** pas domain of histidine kinase thka (tm1359) (semet,2 f486m/f489m)
20	c2w1tB_	Alignment		9.7	23	**PDB header:**transcription **Chain:** B: **PDB Molecule:**stage v sporulation protein t; **PDBTitle:** crystal structure of b. subtilis spovt
21	d1j3ma_	Alignment	not modelled	9.6	9	**Fold:**TBP-like **Superfamily:**TT1751-like **Family:**TT1751-like
22	c3mqoB_	Alignment	not modelled	9.6	8	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** the crystal structure of the pas domain in complex with isopropanol of2 a transcriptional regulator in the luxr family from burkholderia3 thailandensis to 1.7a
23	c3fg8B_	Alignment	not modelled	9.5	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rha05790; **PDBTitle:** crystal structure of pas domain of rha05790
24	c2v3wC_	Alignment	not modelled	8.6	22	**PDB header:**lyase **Chain:** C: **PDB Molecule:**benzoylformate decarboxylase; **PDBTitle:** crystal structure of the benzoylformate decarboxylase2 variant l461a from pseudomonas putida
25	c2v1bA_	Alignment	not modelled	8.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nph1-1; **PDBTitle:** n- and c-terminal helices of oat lov2 (404-546) are2 involved in light-induced signal transduction (room3 temperature (293k) light structure of lov2 (404-546))
26	c3p7nB_	Alignment	not modelled	8.0	26	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
27	d1otda_	Alignment	not modelled	7.2	17	**Fold:**Profilin-like **Superfamily:**PYP-like sensor domain (PAS domain) **Family:**PYP-like
28	c2xc7A_	Alignment	not modelled	7.2	10	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**phosphorylated adapter rna export protein;

						PDBTitle: solution structure of phax-rbd in complex with ssrna
29	d1s2da_	Alignment	not modelled	6.5	14	**Fold:**Flavodoxin-like **Superfamily:**N-(deoxy)ribosyltransferase-like **Family:**N-deoxyribosyltransferase
30	d2a1jb1	Alignment	not modelled	6.3	13	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
31	d1rqpa2	Alignment	not modelled	6.2	31	**Fold:**Bacterial fluorinating enzyme, N-terminal domain **Superfamily:**Bacterial fluorinating enzyme, N-terminal domain **Family:**Bacterial fluorinating enzyme, N-terminal domain
32	c1wu8B_	Alignment	not modelled	6.1	31	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ph0463; **PDBTitle:** crystal structure of project ph0463 from pyrococcus horikoshii ot3
33	c3rtyA_	Alignment	not modelled	6.0	19	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**period circadian protein; **PDBTitle:** structure of an enclosed dimer formed by the drosophila period protein
34	d2ge7a1	Alignment	not modelled	6.0	23	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Coronavirus nucleocapsid protein
35	d2ca1a1	Alignment	not modelled	5.9	23	**Fold:**Nucleocapsid protein dimerization domain **Superfamily:**Nucleocapsid protein dimerization domain **Family:**Coronavirus nucleocapsid protein
36	c2npbA_	Alignment	not modelled	5.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**selenoprotein w; **PDBTitle:** nmr solution structure of mouse selw
37	d1ciia1	Alignment	not modelled	5.8	30	**Fold:**Toxins' membrane translocation domains **Superfamily:**Colicin **Family:**Colicin
38	c2zbvC_	Alignment	not modelled	5.8	23	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** crystal structure of uncharacterized conserved protein from thermotoga2 maritima
39	c2e62A_	Alignment	not modelled	5.8	25	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein at5g25060; **PDBTitle:** solution structure of the cwf21 domain in protein aak25922
40	c2guzO_	Alignment	not modelled	5.7	16	**PDB header:**chaperone, protein transport **Chain:** O: **PDB Molecule:**mitochondrial import inner membrane translocase **PDBTitle:** structure of the tim14-tim16 complex of the mitochondrial2 protein import motor
41	c3gdwA_	Alignment	not modelled	5.6	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sigma-54 interaction domain protein; **PDBTitle:** crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
42	d1e5qa2	Alignment	not modelled	5.2	23	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Homoserine dehydrogenase-like
43	c1hvwA_	Alignment	not modelled	5.2	100	**PDB header:**toxin **Chain:** A: **PDB Molecule:**omega-atracotoxin-hv1a; **PDBTitle:** hairpinless mutant of omega-atracotoxin-hv1a
44	d1hvwa_	Alignment	not modelled	5.2	100	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins