Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AFU6
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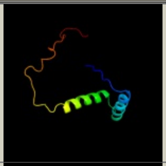
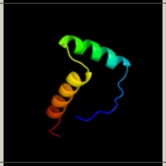
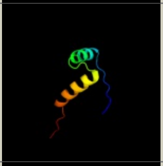
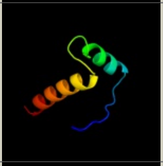
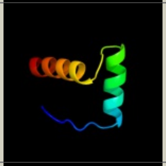
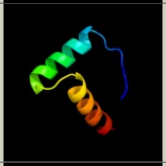
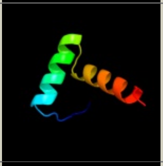
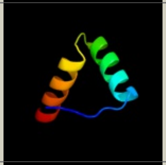
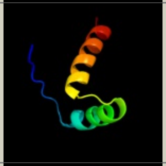
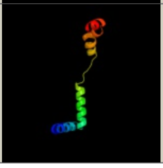
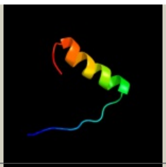
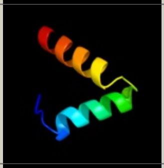
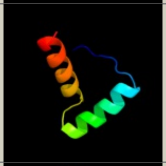
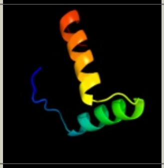
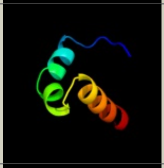
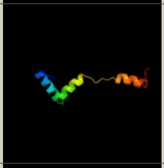
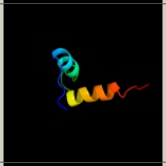
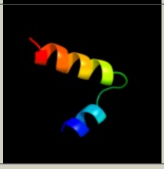
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2k5jB_	Alignment		100.0	100	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
2	c2bj3D_	Alignment		98.1	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** nikr-apo
3	d2bj7a1	Alignment		98.1	12	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
4	c1q5vB_	Alignment		98.0	21	**PDB header:**transcription **Chain:** B: **PDB Molecule:**nickel responsive regulator; **PDBTitle:** apo-nikr
5	c2ca9B_	Alignment		98.0	18	**PDB header:**transcriptional regulation **Chain:** B: **PDB Molecule:**putative nickel-responsive regulator; **PDBTitle:** apo-nikr from helicobacter pylori in closed trans-2 conformation
6	d2hzaa1	Alignment		97.3	23	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
7	d2hzab1	Alignment		97.1	23	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
8	d2cpga_	Alignment		95.0	23	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
9	c2rbfB_	Alignment		94.4	13	**PDB header:**oxidoreductase/dna **Chain:** B: **PDB Molecule:**bifunctional protein puta; **PDBTitle:** structure of the ribbon-helix-helix domain of escherichia coli puta2 (puta52) complexed with operator dna (o2)
10	c2k9iB_	Alignment		93.5	24	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**plasmid prn1, complete sequence; **PDBTitle:** nmr structure of plasmid copy control protein orf56 from2 sulfolobus islandicus
11	c3h87D_	Alignment		91.5	20	**PDB header:**toxin/antitoxin **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis

12	c2an7A_	Alignment		88.7	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein pard; **PDBTitle:** solution structure of the bacterial antidote pard
13	c2kelB_	Alignment		86.3	19	**PDB header:**transcription repressor **Chain:** B: **PDB Molecule:**uncharacterized protein 56b; **PDBTitle:** structure of the transcription regulator svtr from the2 hyperthermophilic archaeal virus sirv1
14	d2ay0a1	Alignment		79.0	13	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**PutA pre-N-terminal region-like
15	d1p94a_	Alignment		78.0	15	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
16	c2k29A_	Alignment		76.5	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
17	c3kxeD_	Alignment		66.5	11	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**antitoxin protein pard-1; **PDBTitle:** a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
18	d2bsqe1	Alignment		64.5	14	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Trafficking protein A-like
19	d1mnta_	Alignment		48.7	17	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
20	c2q2kA_	Alignment		32.9	26	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of nucleic-acid binding protein
21	c1kcfB_	Alignment	not modelled	28.1	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hypothetical 30.2 kd protein c25g10.02 in **PDBTitle:** crystal structure of the yeast mitochondrial holliday2 junction resolvase, ydc2
22	d1y9ba1	Alignment	not modelled	24.8	12	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**VCA0319-like
23	c3c5yD_	Alignment	not modelled	21.3	9	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
24	c2qhoF_	Alignment	not modelled	19.9	28	**PDB header:**protein binding/ligase **Chain:** F: **PDB Molecule:**e3 ubiquitin-protein ligase edd1; **PDBTitle:** crystal structure of the uba domain from edd ubiquitin2 ligase in complex with ubiquitin
25	c2hwyB_	Alignment	not modelled	18.6	27	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein smg5; **PDBTitle:** structure of pin domain of human smg5.
26	c2kkeA_	Alignment	not modelled	18.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of a dimeric protein of unknown2 function from methanobacterium thermoautotrophicum,3 northeast structural genomics consortium target tr5
27	c2ppwA_	Alignment	not modelled	15.6	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of uncharacterized ribose 5-phosphate isomerase2 rpib from streptococcus pneumoniae
28	c1ny9A	Alignment	not modelled	14.8	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional activator tipa-s;

28	c1ny9A_	Alignment	not modelled	14.8	13	**PDBTitle:** antibiotic binding domain of a tipa-class multidrug2 resistance transcriptional regulator
29	d1ny9a_	Alignment	not modelled	14.8	13	**Fold:**Antibiotic binding domain of TipA-like multidrug resistance regulators **Superfamily:**Antibiotic binding domain of TipA-like multidrug resistance regulators **Family:**Antibiotic binding domain of TipA-like multidrug resistance regulators
30	c1yxeA_	Alignment	not modelled	14.2	10	**PDB header:**immune system **Chain:** A: **PDB Molecule:**apical membrane antigen 1; **PDBTitle:** structure and inter-domain interactions of domain ii from the blood2 stage malarial protein, apical membrane antigen 1
31	c1u9pA_	Alignment	not modelled	12.8	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
32	c2xv9A_	Alignment	not modelled	11.3	17	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**aba-1a1 repeat unit; **PDBTitle:** the solution structure of aba-1a saturated with oleic acid
33	d2proc1	Alignment	not modelled	10.7	42	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
34	c3iwfA_	Alignment	not modelled	10.7	12	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcription regulator rpir family; **PDBTitle:** the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
35	c3onoA_	Alignment	not modelled	10.3	5	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose/galactose isomerase; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase lacab_rpib from2 vibrio parahaemolyticus
36	d2o3fa1	Alignment	not modelled	9.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**RpiR-like
37	c2o3fC_	Alignment	not modelled	9.9	18	**PDB header:**transcription **Chain:** C: **PDB Molecule:**putative hth-type transcriptional regulator ybbh; **PDBTitle:** structural genomics, the crystal structure of the n-2 terminal domain of the putative transcriptional regulator3 ybbh from bacillus subtilis subsp. subtilis str. 168.
38	c3oeoD_	Alignment	not modelled	9.8	12	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**spheroplast protein y; **PDBTitle:** the crystal structure e. coli spy
39	c3kk4B_	Alignment	not modelled	9.5	10	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bp1543; **PDBTitle:** uncharacterized protein bp1543 from bordetella pertussis tohama i
40	d2je6b2	Alignment	not modelled	9.1	25	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
41	c3o39A_	Alignment	not modelled	9.0	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**periplasmic protein related to spheroblast formation; **PDBTitle:** crystal structure of spy
42	d1uxca_	Alignment	not modelled	8.9	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
43	d2phcb1	Alignment	not modelled	8.8	12	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
44	d2qklb1	Alignment	not modelled	8.5	28	**Fold:**Dcp2 domain-like **Superfamily:**Dcp2 domain-like **Family:**Dcp2 box A domain
45	d1znda1	Alignment	not modelled	8.4	23	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
46	d1to0a_	Alignment	not modelled	8.3	10	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
47	d1gm6a_	Alignment	not modelled	8.0	13	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Retinol binding protein-like
48	d1l5aa2	Alignment	not modelled	7.5	13	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
49	c2l8nA_	Alignment	not modelled	7.5	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional repressor cytr; **PDBTitle:** nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
50	d2c2vv1	Alignment	not modelled	7.3	17	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
51	d1q9ja2	Alignment	not modelled	7.2	16	**Fold:**CoA-dependent acyltransferases **Superfamily:**CoA-dependent acyltransferases **Family:**NRPS condensation domain (amide synthase)
52	c2lcvA_	Alignment	not modelled	7.0	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**hth-type transcriptional repressor cytr; **PDBTitle:** structure of the cytidine repressor dna-binding domain; an alternate2 calculation
53	c2zp2B_	Alignment	not modelled	6.9	12	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
54	c2e4jA	Alignment	not modelled	6.9	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**prostaglandin-h2 d-isomerase;

54	c2e4jA_	Alignment	not modelled	6.9	16	**PDBTitle:** solution structure of mouse lipocalin-type prostaglandin d2 synthase
55	c3epvB_	Alignment	not modelled	6.9	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**nickel and cobalt resistance protein cnrr; **PDBTitle:** x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
56	d1cjya2	Alignment	not modelled	6.9	23	**Fold:**FabD/lysophospholipase-like **Superfamily:**FabD/lysophospholipase-like **Family:**Lysophospholipase
57	c2wteB_	Alignment	not modelled	6.8	26	**PDB header:**antiviral protein **Chain:** B: **PDB Molecule:**csa3; **PDBTitle:** the structure of the crispr-associated protein, csa3, from2 sulfolobus solfataricus at 1.8 angstrom resolution.
58	c3qzcA_	Alignment	not modelled	6.8	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic protein cpxp; **PDBTitle:** structure of the periplasmic stress response protein cpxp
59	c4a1qB_	Alignment	not modelled	6.4	26	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**orf e73; **PDBTitle:** solution structure of e73 protein from sulfolobus spindle-2 shaped virus ragged hills, a hyperthermophilic3 crenarchaeal virus from yellowstone national park
60	c2qkmF_	Alignment	not modelled	6.4	23	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**spac19a8.12 protein; **PDBTitle:** the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
61	d2obpa1	Alignment	not modelled	5.9	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ReutB4095-like
62	d1y0ya2	Alignment	not modelled	5.9	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Zn-dependent exopeptidases **Family:**Bacterial dinuclear zinc exopeptidases
63	c2kp6A_	Alignment	not modelled	5.8	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein cv0237 from2 chromobacterium violaceum. northeast structural genomics3 consortium (nesg) target cvt1
64	d1ns5a_	Alignment	not modelled	5.8	17	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
65	d1lcda_	Alignment	not modelled	5.8	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
66	d1uxda_	Alignment	not modelled	5.7	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
67	d2hsga1	Alignment	not modelled	5.7	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
68	d1qpza1	Alignment	not modelled	5.7	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
69	d2nn6d2	Alignment	not modelled	5.5	13	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
70	c2xstA_	Alignment	not modelled	5.5	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**lipocalin 15; **PDBTitle:** crystal structure of the human lipocalin 15
71	c3by0B_	Alignment	not modelled	5.4	16	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**neutrophil gelatinase-associated lipocalin; **PDBTitle:** crystal structure of siderocalin (ngal, lipocalin 2) w79a-r81a2 complexed with ferric enterobactin
72	c3p3vB_	Alignment	not modelled	5.2	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts system, n-acetylgalactosamine-specific iib component; **PDBTitle:** crystal structure of a pts dependent n-acetyl-galactosamine-iib2 component (agav, spy_0631) from streptococcus pyogenes at 1.65 a3 resolution
73	d1t1ha_	Alignment	not modelled	5.2	8	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**U-box
74	c3i8oA_	Alignment	not modelled	5.1	10	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**kh domain-containing protein mj1533; **PDBTitle:** a domain of a functionally unknown protein from2 methanocaldococcus jannaschii dsm 2661.
75	d1cuka1	Alignment	not modelled	5.1	18	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain