Phyre2

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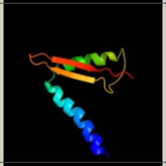
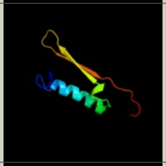
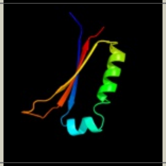
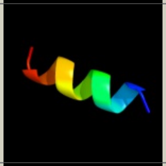
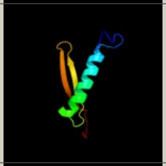
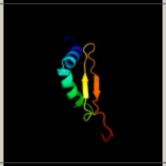
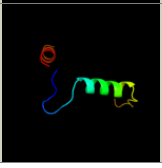
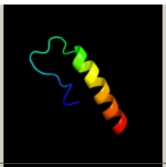
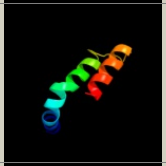
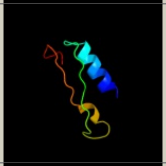
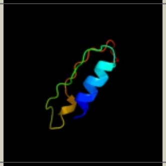
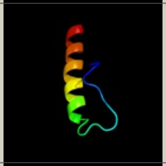
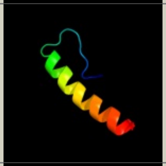
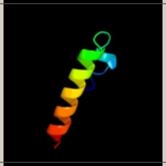
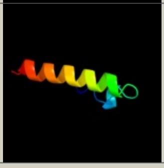
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kxoA_	Alignment		100.0	42	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
2	c3r9jD_	Alignment		99.9	99	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** D: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 4.3a resolution structure of a mind-mine(i24n) protein complex
3	d1ev0a_	Alignment		99.6	100	**Fold:**Cell division protein MinE topological specificity domain **Superfamily:**Cell division protein MinE topological specificity domain **Family:**Cell division protein MinE topological specificity domain
4	c3ku7B_	Alignment		98.8	33	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** crystal structure of helicobacter pylori mine, a cell division2 topological specificity factor
5	c3r9iG_	Alignment		88.6	100	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** G: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 2.6a resolution structure of mind complexed with mine (12-31) peptide
6	c3r9iH_	Alignment		85.9	100	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** H: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 2.6a resolution structure of mind complexed with mine (12-31) peptide
7	c3r9iE_	Alignment		85.9	100	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** E: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 2.6a resolution structure of mind complexed with mine (12-31) peptide
8	c3r9iF_	Alignment		85.9	100	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** F: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 2.6a resolution structure of mind complexed with mine (12-31) peptide
9	c2kwpA_	Alignment		75.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation protein nusa; **PDBTitle:** solution structure of the aminoterminal domain of e. coli nusa
10	d1hh2p4	Alignment		74.7	21	**Fold:**Transcription factor NusA, N-terminal domain **Superfamily:**Transcription factor NusA, N-terminal domain **Family:**Transcription factor NusA, N-terminal domain
11	c3epsB_	Alignment		55.7	22	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**isocitrate dehydrogenase kinase/phosphatase; **PDBTitle:** the crystal structure of isocitrate dehydrogenase kinase/phosphatase2 from e. coli

12	d2r40d1	Alignment		36.5	16	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
13	d1vmaa1	Alignment		33.7	16	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
14	c1rwuA_	Alignment		31.6	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0250 protein ybed; **PDBTitle:** solution structure of conserved protein ybed from e. coli
15	d1rwua_	Alignment		31.6	20	**Fold:**Ferredoxin-like **Superfamily:**YbeD/HP0495-like **Family:**YbeD-like
16	d2qw4a1	Alignment		31.4	19	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
17	c2nxxG_	Alignment		30.9	22	**PDB header:**hormone/growth factor **Chain:** G: **PDB Molecule:**ecdysone receptor (ecr, nrh1); **PDBTitle:** crystal structure of the ligand-binding domains of the2 t.castaneum (coleoptera) heterodimer ecrusp bound to3 ponasterone a
18	c3ctbA_	Alignment		28.7	16	**PDB header:**transcription, transferase **Chain:** A: **PDB Molecule:**pregnane x receptor, linker, steroid receptor **PDBTitle:** tethered pxr-lbd/src-1p apoprotein
19	d1ovle_	Alignment		22.5	19	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
20	c1nrlA_	Alignment		21.9	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**orphan nuclear receptor pxr; **PDBTitle:** crystal structure of the human pxr-lbd in complex with an2 src-1 coactivator peptide and sr12813
21	d1nrla_	Alignment	not modelled	21.9	16	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
22	d1nq7a_	Alignment	not modelled	21.6	19	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
23	c3hm5A_	Alignment	not modelled	21.4	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna methyltransferase 1-associated protein 1; **PDBTitle:** sant domain of human dna methyltransferase 1 associated2 protein 1
24	d1d0qa_	Alignment	not modelled	20.2	32	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
25	c1z5xE_	Alignment	not modelled	20.1	22	**PDB header:**hormone/growth factor receptor **Chain:** E: **PDB Molecule:**ecdysone receptor ligand binding domain; **PDBTitle:** hemipteran ecdysone receptor ligand-binding domain2 complexed with ponasterone a
26	c3pvpA_	Alignment	not modelled	20.0	17	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
27	d1j1va_	Alignment	not modelled	19.5	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
28	d1go3f_	Alignment	not modelled	19.3	33	**Fold:**SAM domain-like **Superfamily:**HRDC-like

						Family:RNA polymerase II subunit RBP4 (RpoF)
29	c2dnwA_	Alignment	not modelled	18.4	32	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
30	d1ovla_	Alignment	not modelled	17.8	19	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
31	d1pdua_	Alignment	not modelled	17.6	22	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
32	d1n83a_	Alignment	not modelled	17.4	16	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
33	c2qw4D_	Alignment	not modelled	17.3	19	**PDB header:**hormone receptor **Chain:** D: **PDB Molecule:**orphan nuclear receptor nr4a1; **PDBTitle:** human nr4a1 ligand-binding domain
34	c1xdkF_	Alignment	not modelled	16.1	22	**PDB header:**hormone/growth factor receptor **Chain:** F: **PDB Molecule:**retinoic acid receptor, beta; **PDBTitle:** crystal structure of the rarbeta/rxralpha ligand binding2 domain heterodimer in complex with 9-cis retinoic acid and3 a fragment of the trap220 coactivator
35	d1pq9a_	Alignment	not modelled	15.8	22	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
36	d1osva_	Alignment	not modelled	15.1	19	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
37	d1nava_	Alignment	not modelled	13.6	13	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
38	d1l8qa1	Alignment	not modelled	13.6	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
39	c3up0A_	Alignment	not modelled	13.1	6	**PDB header:**steroid binding protein/transcription **Chain:** A: **PDB Molecule:**acedaf-12; **PDBTitle:** nuclear receptor daf-12 from hookworm ancylostoma ceylanicum in2 complex with (25s)-delta7-dafachronic acid
40	c3pt8B_	Alignment	not modelled	13.1	7	**PDB header:**oxygen transport **Chain:** B: **PDB Molecule:**hemoglobin iii; **PDBTitle:** structure of hbii-iii-cn from lucina pectinata at ph 5.0
41	c2c0kB_	Alignment	not modelled	13.0	19	**PDB header:**oxygen transport **Chain:** B: **PDB Molecule:**hemoglobin; **PDBTitle:** the structure of hemoglobin from the botfly gasterophilus2 intestinalis
42	c3l0jA_	Alignment	not modelled	12.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear receptor ror-gamma; **PDBTitle:** crystal structure of orphan nuclear receptor rorgamma in complex with2 natural ligand
43	c2rhfA_	Alignment	not modelled	12.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna helicase recq; **PDBTitle:** d. radiodurans recq hrdc domain 3
44	d1ie9a_	Alignment	not modelled	12.4	13	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
45	c2hc4A_	Alignment	not modelled	12.1	13	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**vitamin d receptor; **PDBTitle:** crystal structure of the lbd of vdr of danio rerio in2 complex with calcitriol
46	d1ghha_	Alignment	not modelled	11.6	18	**Fold:**DNA damage-inducible protein DinI **Superfamily:**DNA damage-inducible protein DinI **Family:**DNA damage-inducible protein DinI
47	d1sqna_	Alignment	not modelled	11.2	6	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
48	c2oaxC_	Alignment	not modelled	10.7	10	**PDB header:**transcription **Chain:** C: **PDB Molecule:**mineralocorticoid receptor; **PDBTitle:** crystal structure of the s810l mutant mineralocorticoid2 receptor associated with sc9420
49	c3lbdA_	Alignment	not modelled	10.6	22	**PDB header:**nuclear receptor **Chain:** A: **PDB Molecule:**retinoic acid receptor gamma; **PDBTitle:** ligand-binding domain of the human retinoic acid receptor2 gamma bound to 9-cis retinoic acid
50	d1x9fb_	Alignment	not modelled	10.5	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
51	c3vhuA_	Alignment	not modelled	10.4	10	**PDB header:**transcription/inhibitor **Chain:** A: **PDB Molecule:**mineralocorticoid receptor; **PDBTitle:** mineralocorticoid receptor ligand-binding domain with spironolactone
52	c1p93A_	Alignment	not modelled	10.4	6	**PDB header:**hormone receptor **Chain:** A: **PDB Molecule:**glucocorticoid receptor; **PDBTitle:** crystal structure of the agonist form of glucocorticoid2 receptor
53	c2o4rA_	Alignment	not modelled	10.0	13	**PDB header:**hormone/growth factor receptor **Chain:** A: **PDB Molecule:**vitamin d3 receptor; **PDBTitle:** crystal structure of rat vitamin d receptor ligand binding2 domain complexed with vitiii 17-20e and the nr2 box of3 drip 205
54	c3gdzA_	Alignment	not modelled	9.5	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of arginyl-trna synthetase from klebsiella2 pneumoniae subsp. pneumoniae

55	d1xapa_	Alignment	not modelled	8.9	22	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
56	d1xvpb_	Alignment	not modelled	8.8	13	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
57	d3proc1	Alignment	not modelled	8.6	18	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
58	d1itha_	Alignment	not modelled	8.5	23	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
59	c2olpB_	Alignment	not modelled	8.5	5	**PDB header:**oxygen storage/transport **Chain:** B: **PDB Molecule:**hemoglobin ii; **PDBTitle:** structure and ligand selection of hemoglobin ii from lucina pectinata
60	c3ifeA_	Alignment	not modelled	8.4	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidase t; **PDBTitle:** 1.55 angstrom resolution crystal structure of peptidase t (pept-1)2 from bacillus anthracis str. 'ames ancestor'.
61	c3abfB_	Alignment	not modelled	8.2	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of a 4-oxalocrotonate tautomerase homologue2 (tthb242)
62	d2zmia1	Alignment	not modelled	8.2	13	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
63	d2b50a1	Alignment	not modelled	8.2	15	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
64	c3q9qB_	Alignment	not modelled	7.8	29	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**heat shock protein beta-1; **PDBTitle:** hspb1 fragment second crystal form
65	d1mbaa_	Alignment	not modelled	7.7	9	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
66	d2ia7a1	Alignment	not modelled	7.4	11	**Fold:**gpW/gp25-like **Superfamily:**gpW/gp25-like **Family:**gpW/gp25-like
67	d2dgxa1	Alignment	not modelled	7.1	15	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
68	c2x4kB_	Alignment	not modelled	7.0	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**4-oxalocrotonate tautomerase; **PDBTitle:** crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
69	c1usdA_	Alignment	not modelled	6.9	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** human vasp tetramerisation domain l352m
70	c2rqlA_	Alignment	not modelled	6.7	8	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable sigma-54 modulation protein; **PDBTitle:** solution structure of the e. coli ribosome hibernation2 promoting factor hpf
71	c3mb2G_	Alignment	not modelled	6.7	6	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**4-oxalocrotonate tautomerase family enzyme - alpha subunit; **PDBTitle:** kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
72	d1bjpa_	Alignment	not modelled	6.4	15	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
73	d1wuda1	Alignment	not modelled	6.3	21	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
74	d1lhta_	Alignment	not modelled	6.2	20	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
75	d1vkua_	Alignment	not modelled	6.2	22	**Fold:**Acyl carrier protein-like **Superfamily:**ACP-like **Family:**Acyl-carrier protein (ACP)
76	c3idwA_	Alignment	not modelled	6.2	15	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**actin cytoskeleton-regulatory complex protein sla1; **PDBTitle:** crystal structure of sla1 homology domain 2
77	c2zs0A_	Alignment	not modelled	6.1	11	**PDB header:**oxygen storage, oxygen transport **Chain:** A: **PDB Molecule:**extracellular giant hemoglobin major globin subunit a1; **PDBTitle:** structural basis for the heterotropic and homotropic interactions of2 invertebrate giant hemoglobin
78	c2iz2A_	Alignment	not modelled	6.1	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**nuclear hormone receptor ftz-f1; **PDBTitle:** crystal structure of the ligand binding domain of fushi2 tarazu factor 1 from drosophila melanogaster
79	d2fvja1	Alignment	not modelled	6.0	11	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
80	d1oj6a_	Alignment	not modelled	5.9	9	**Fold:**Globin-like **Superfamily:**Globin-like

						Family: Globins
81	c2yruA_	Alignment	not modelled	5.8	7	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**steroid receptor rna activator 1; **PDBTitle:** solution structure of mouse steroid receptor rna activator2 1 (sra1) protein
82	d1d02a_	Alignment	not modelled	5.8	28	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease MunI
83	d2qssa1	Alignment	not modelled	5.8	11	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
84	c3tqmD_	Alignment	not modelled	5.7	19	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**ribosome-associated factor y; **PDBTitle:** structure of an ribosomal subunit interface protein from coxiella2 burnetii
85	c2ehtA_	Alignment	not modelled	5.5	24	**PDB header:**lipid transport **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** crystal structure of acyl carrier protein from aquifex aeolicus (form2 2)
86	d1sctb_	Alignment	not modelled	5.5	10	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
87	d1l4sa_	Alignment	not modelled	5.5	10	**Fold:**Ribosome binding protein Y (YfiA homologue) **Superfamily:**Ribosome binding protein Y (YfiA homologue) **Family:**Ribosome binding protein Y (YfiA homologue)
88	c2op8A_	Alignment	not modelled	5.4	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable tautomerase ywhb; **PDBTitle:** crystal structure of ywhb- homologue of 4-oxalocrotonate tautomerase
89	d1t7ra_	Alignment	not modelled	5.4	6	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
90	c2qnwA_	Alignment	not modelled	5.3	13	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**acyl carrier protein; **PDBTitle:** toxoplasma gondii apicoplast-targeted acyl carrier protein
91	d2qssb1	Alignment	not modelled	5.3	6	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
92	c3gyuA_	Alignment	not modelled	5.2	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear hormone receptor of the steroid/thyroid **PDBTitle:** nuclear receptor daf-12 from parasitic nematode2 strongyloides stercoralis in complex with its physiological3 ligand dafachronic acid delta 7
93	d1v4wb_	Alignment	not modelled	5.1	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
94	d2htja1	Alignment	not modelled	5.1	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FaeA-like
95	d1fsla_	Alignment	not modelled	5.1	10	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
96	c2zufA_	Alignment	not modelled	5.0	12	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)