Phyre2

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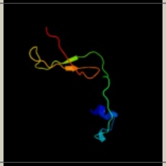
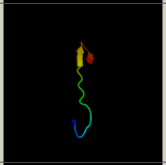
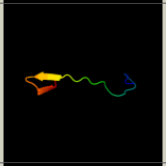
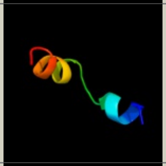
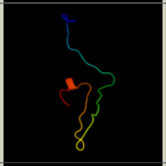
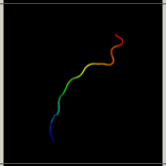
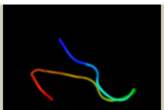
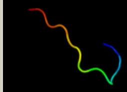
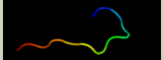
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nctC_	Alignment		100.0	96	**PDB header:**dna binding protein, chaperone **Chain:** C: **PDB Molecule:**protein psib; **PDBTitle:** x-ray crystal structure of the bacterial conjugation factor psib, a2 negative regulator of reca
2	c3d30A_	Alignment		84.1	14	**PDB header:**peptidoglycan-binding protein **Chain:** A: **PDB Molecule:**expansin like protein; **PDBTitle:** structure of an expansin like protein from bacillus subtilis at 1.9a2 resolution
3	c2w56B_	Alignment		56.9	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**vc0508; **PDBTitle:** structure of the hypothetical protein vc0508 from vibrio cholerae2 vsp-ii pathogenicity island
4	c2v1lA_	Alignment		48.6	27	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** structure of the conserved hypothetical protein vc1805 from2 pathogenicity island vpi-2 of vibrio cholerae o1 biovar3 eltor str. n16961 shares structural homology with the4 human p32 protein
5	c2noxP_	Alignment		33.7	42	**PDB header:**oxidoreductase **Chain:** P: **PDB Molecule:**tryptophan 2,3-dioxygenase; **PDBTitle:** crystal structure of tryptophan 2,3-dioxygenase from ralstonia2 metallidurans
6	d2nw8a1	Alignment		19.7	32	**Fold:**Indolic compounds 2,3-dioxygenase-like **Superfamily:**Indolic compounds 2,3-dioxygenase-like **Family:**Bacterial tryptophan 2,3-dioxygenase
7	c2nw7C_	Alignment		17.8	32	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**tryptophan 2,3-dioxygenase; **PDBTitle:** crystal structure of tryptophan 2,3-dioxygenase (tdo) from2 xanthomonas campestris in complex with ferric heme.3 northeast structural genomics target xcr13
8	c2hczX_	Alignment		16.4	14	**PDB header:**allergen **Chain:** X: **PDB Molecule:**beta-expansin 1a; **PDBTitle:** crystal structure of expb1 (zea m 1), a beta-expansin and group-12 pollen allergen from maize
9	d1dx5i3	Alignment		13.5	27	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module
10	d2i0ka1	Alignment		13.3	21	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**Cholesterol oxidase
11	d2ftxa1	Alignment		13.2	18	**Fold:**Kinetochore globular domain-like **Superfamily:**Kinetochore globular domain **Family:**Spc25-like

12	d1c3aa_	Alignment		13.0	21	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
13	c3le4A_	Alignment		12.5	50	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**microprocessor complex subunit dgcr8; **PDBTitle:** crystal structure of the dgcr8 dimerization domain
14	c3oibB_	Alignment		12.4	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acyl-coa dehydrogenase; **PDBTitle:** crystal structure of a putative acyl-coa dehydrogenase from2 mycobacterium smegmatis, iodide soak
15	c1lshB_	Alignment		11.8	23	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**lipovitellin (lv-2); **PDBTitle:** lipid-protein interactions in lipovitellin
16	d1lshb_	Alignment		11.8	23	**Fold:**Lipovitellin-phosvitin complex; beta-sheet shell regions **Superfamily:**Lipovitellin-phosvitin complex; beta-sheet shell regions **Family:**Lipovitellin-phosvitin complex; beta-sheet shell regions
17	c3kbhE_	Alignment		11.6	31	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**spike glycoprotein; **PDBTitle:** crystal structure of nl63 respiratory coronavirus receptor-binding2 domain complexed with its human receptor
18	d1d5va_	Alignment		11.2	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
19	d1x6va1	Alignment		10.6	9	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**ATP sulfurylase N-terminal domain
20	d1whoa_	Alignment		10.6	27	**Fold:**C2 domain-like **Superfamily:**PHL pollen allergen **Family:**PHL pollen allergen
21	d1v7wa2	Alignment	not modelled	10.6	19	**Fold:**Supersandwich **Superfamily:**Galactose mutarotase-like **Family:**Glycosyltransferase family 36 N-terminal domain
22	c2w0tA_	Alignment	not modelled	10.4	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**lethal(3)malignant brain tumor-like 2 protein; **PDBTitle:** solution structure of the fcs zinc finger domain of human2 lmbl2
23	d1qo3c_	Alignment	not modelled	10.3	24	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
24	c2y7eA_	Alignment	not modelled	10.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme; **PDBTitle:** crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
25	c2c5sA_	Alignment	not modelled	9.9	23	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**probable thiamine biosynthesis protein thii; **PDBTitle:** crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
26	c1j1eC_	Alignment	not modelled	9.8	27	**PDB header:**contractile protein **Chain:** C: **PDB Molecule:**troponin i; **PDBTitle:** crystal structure of the 52kda domain of human cardiac2 troponin in the ca2+ saturated form
27	c2qjfB_	Alignment	not modelled	9.6	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'- **PDBTitle:** crystal structure of atp-sulfurylase domain of human paps2 synthetase 1

28	c2wmhA_	Alignment	not modelled	9.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fucolectin-related protein; **PDBTitle:** crystal structure of the catalytic module of a family 982 glycoside hydrolase from streptococcus pneumoniae tigr4 in3 complex with the h-disaccharide blood group antigen.
29	c2j83B_	Alignment	not modelled	9.1	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ulilysin; **PDBTitle:** ulilysin metalloprotease in complex with batimastat.
30	d1j6ra_	Alignment	not modelled	8.7	14	**Fold:**Methionine synthase activation domain-like **Superfamily:**Methionine synthase activation domain-like **Family:**Hypothetical protein TM0269
31	d1s48a_	Alignment	not modelled	8.5	20	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**RNA-dependent RNA-polymerase
32	c1v47B_	Alignment	not modelled	8.3	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp sulfurylase; **PDBTitle:** crystal structure of atp sulfurylase from thermus2 thermophillus hb8 in complex with aps
33	d2a07f1	Alignment	not modelled	8.1	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Forkhead DNA-binding domain
34	c2zibA_	Alignment	not modelled	7.8	36	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**type ii antifreeze protein; **PDBTitle:** crystal structure analysis of calcium-independent type ii2 antifreeze protein
35	c3e4wB_	Alignment	not modelled	7.7	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a 33kda catalase-related protein from2 mycobacterium avium subsp. paratuberculosis. p2(1)2(1)2(1) crystal3 form.
36	c1vq0A_	Alignment	not modelled	7.7	30	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**33 kda chaperonin; **PDBTitle:** crystal structure of 33 kda chaperonin (heat shock protein 33 homolog)2 (hsp33) (tm1394) from thermotoga maritima at 2.20 a resolution
37	c2p04B_	Alignment	not modelled	7.6	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**signal transduction histidine kinase; **PDBTitle:** 2.1 ang structure of the dimerized pas domain of signal transduction2 histidine kinase from nostoc punctiforme pcc 73102 with homology to3 the h-noxa/h-noba domain of the soluble guanylyl cyclase
38	c1xwjB_	Alignment	not modelled	7.5	78	**PDB header:**cell adhesion/protein binding **Chain:** B: **PDB Molecule:**talin; **PDBTitle:** vinculin head (1-258) in complex with the talin vinculin2 binding site 3 (1945-1969)
39	d3bdwa1	Alignment	not modelled	7.5	9	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
40	c2dlwA_	Alignment	not modelled	6.9	37	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**docking protein 2, isoform a; **PDBTitle:** solution structure of the irs domain of human docking2 protein 2, isoform a
41	c2r5kE_	Alignment	not modelled	6.6	31	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**major capsid protein l1; **PDBTitle:** pentamer structure of major capsid protein l1 of human2 papilloma virus type 11
42	d1deca_	Alignment	not modelled	6.6	33	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Hirudin-like
43	c2yruA_	Alignment	not modelled	6.6	17	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**steroid receptor rna activator 1; **PDBTitle:** solution structure of mouse steroid receptor rna activator2 1 (sra1) protein
44	c1rkcB_	Alignment	not modelled	6.4	78	**PDB header:**cell adhesion, structural protein **Chain:** B: **PDB Molecule:**talin; **PDBTitle:** human vinculin head (1-258) in complex with talin's2 vinculin binding site 3 (residues 1944-1969)
45	d1atxa_	Alignment	not modelled	6.4	25	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Defensin
46	c2lc0A_	Alignment	not modelled	6.3	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**putative uncharacterized protein tb39.8; **PDBTitle:** rv0020c_nter structure
47	d1gyxa_	Alignment	not modelled	6.3	15	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
48	c3tixB_	Alignment	not modelled	6.3	21	**PDB header:**gene regulation/protein binding **Chain:** B: **PDB Molecule:**chromo domain-containing protein 1; **PDBTitle:** crystal structure of the chp1-tas3 complex core
49	c1fm5A_	Alignment	not modelled	6.3	8	**PDB header:**immune system **Chain:** A: **PDB Molecule:**early activation antigen cd69; **PDBTitle:** crystal structure of human cd69
50	c2ox8A_	Alignment	not modelled	6.2	17	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**scavenger receptor with c-type lectin type i; **PDBTitle:** human scavenger receptor c-type lectin carbohydrate-2 recognition domain.
51	c3m9zA_	Alignment	not modelled	6.2	23	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**killer cell lectin-like receptor subfamily b member 1a; **PDBTitle:** crystal structure of extracellular domain of mouse nkr-p1a
52	d1t3ta1	Alignment	not modelled	6.0	10	**Fold:**RuvA C-terminal domain-like **Superfamily:**FGAM synthase PurL, linker domain **Family:**FGAM synthase PurL, linker domain

53	d1skza1	Alignment	not modelled	5.9	67	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Huristasin-like
54	c3hj7A_	Alignment	not modelled	5.8	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils c-terminal domain
55	d1i8gb_	Alignment	not modelled	5.7	22	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
56	d1ib8a2	Alignment	not modelled	5.6	38	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**YhbC-like, N-terminal domain **Family:**YhbC-like, N-terminal domain
57	d1umra_	Alignment	not modelled	5.6	38	**Fold:**C-type lectin-like **Superfamily:**C-type lectin-like **Family:**C-type lectin domain
58	d1gpja3	Alignment	not modelled	5.6	29	**Fold:**Ferredoxin-like **Superfamily:**Glutamyl tRNA-reductase catalytic, N-terminal domain **Family:**Glutamyl tRNA-reductase catalytic, N-terminal domain
59	c1n10A_	Alignment	not modelled	5.5	13	**PDB header:**allergen **Chain:** A: **PDB Molecule:**pollen allergen phl p 1; **PDBTitle:** crystal structure of phl p 1, a major timothy grass pollen allergen
60	c3gprC_	Alignment	not modelled	5.5	13	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**rhodocetin subunit gamma; **PDBTitle:** crystal structure of rhodocetin
61	d1psea_	Alignment	not modelled	5.3	71	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)
62	d1jb0e_	Alignment	not modelled	5.3	71	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)
63	d1dxga_	Alignment	not modelled	5.2	33	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Desulforedoxin
64	d1qp3a_	Alignment	not modelled	5.0	71	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Photosystem I accessory protein E (PsaE)