Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P77179
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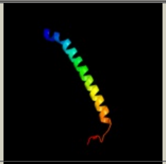
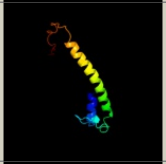
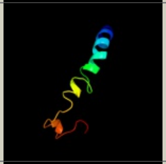
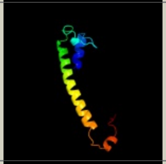
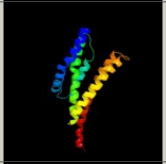
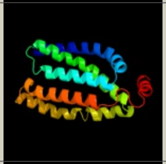
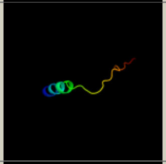
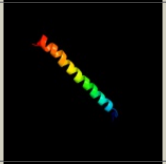
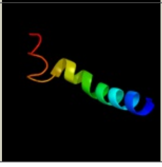
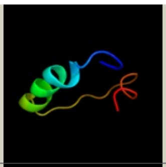
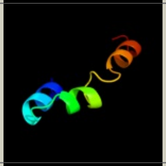
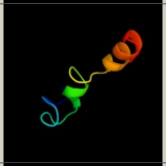
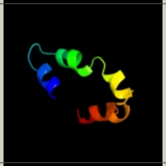
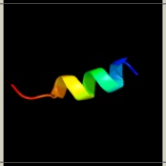
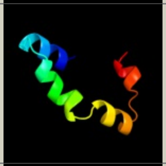
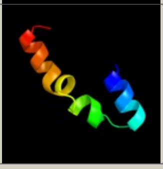
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mk7K_	Alignment		37.9	20	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit n; **PDBTitle:** the structure of cbb3 cytochrome oxidase
2	c3eh4A_	Alignment		33.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c oxidase subunit 1; **PDBTitle:** structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus
3	c2k21A_	Alignment		28.4	20	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
4	d1xmea1	Alignment		27.6	17	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
5	d1pw4a_	Alignment		26.2	16	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
6	d1pv7a_	Alignment		25.9	12	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
7	d2ecba1	Alignment		25.6	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
8	c2zmeA_	Alignment		22.8	27	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
9	c3dinD_	Alignment		21.1	7	**PDB header:**membrane protein, protein transport **Chain:** D: **PDB Molecule:**preprotein translocase subunit sece; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
10	c3pmiC_	Alignment		19.3	18	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**pwwp domain-containing protein mum1; **PDBTitle:** pwwp domain of human mutated melanoma-associated antigen 1
11	c2jp3A_	Alignment		13.4	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fxyd domain-containing ion transport regulator 4; **PDBTitle:** solution structure of the human fxyd4 (chif) protein in sds2 micelles

12	c1u5tA_	Alignment		12.9	3	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**appears to be functionally related to snf7; **PDBTitle:** structure of the escrt-ii endosomal trafficking complex
13	d1ha7b_	Alignment		12.3	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
14	d1b8da_	Alignment		12.0	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
15	c2ntxB_	Alignment		10.9	36	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**emb cab41934.1;
16	d1u5ta1	Alignment		8.4	5	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
17	d1cpca_	Alignment		8.1	5	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
18	c3mlqD_	Alignment		8.0	29	**PDB header:**transferase/transcription **Chain:** D: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
19	d1phnb_	Alignment		8.0	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
20	d1eyxb_	Alignment		7.9	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
21	c3mlqB_	Alignment	not modelled	7.8	29	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
22	c2jo1A_	Alignment	not modelled	7.6	9	**PDB header:**hydrolase regulator **Chain:** A: **PDB Molecule:**phospholemman; **PDBTitle:** structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
23	d1a6qa1	Alignment	not modelled	7.6	80	**Fold:**Another 3-helical bundle **Superfamily:**Protein serine/threonine phosphatase 2C, C-terminal domain **Family:**Protein serine/threonine phosphatase 2C, C-terminal domain
24	d1v54a_	Alignment	not modelled	7.4	9	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
25	c1qfqB_	Alignment	not modelled	7.3	43	**PDB header:**transcription/rna **Chain:** B: **PDB Molecule:**36-mer n-terminal peptide of the n protein; **PDBTitle:** bacteriophage lambda n-protein-nutboxb-rna complex
26	c2c7jB_	Alignment	not modelled	7.2	18	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**phycoerythrocyanin beta chain; **PDBTitle:** phycoerythrocyanin from mastigocladus laminosus, 295 k,2 3.0 a
27	d1ffta_	Alignment	not modelled	7.0	9	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
						PDB header:oxidoreductase

28	c1fftF_	Alignment	not modelled	7.0	9	**Chain:** F: **PDB Molecule:**ubiquinol oxidase; **PDBTitle:** the structure of ubiquinol oxidase from escherichia coli
29	c2e19A_	Alignment	not modelled	6.8	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor 8; **PDBTitle:** solution structure of the homeobox domain from human nil-2-2 a zinc finger protein, transcription factor 8
30	d1cpcb_	Alignment	not modelled	6.8	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
31	c3mp7A_	Alignment	not modelled	6.7	50	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
32	c2kncA_	Alignment	not modelled	6.7	8	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin alpha-iib; **PDBTitle:** platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
33	d1hynp_	Alignment	not modelled	6.6	26	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**Anion transport protein, cytoplasmic domain
34	c2rddB_	Alignment	not modelled	6.6	14	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
35	d1liab_	Alignment	not modelled	6.5	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
36	c1hynQ_	Alignment	not modelled	6.5	16	**PDB header:**membrane protein **Chain:** Q: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein
37	d1kn1a_	Alignment	not modelled	6.4	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
38	d1ar1a_	Alignment	not modelled	6.4	2	**Fold:**Cytochrome c oxidase subunit I-like **Superfamily:**Cytochrome c oxidase subunit I-like **Family:**Cytochrome c oxidase subunit I-like
39	d1xmec1	Alignment	not modelled	6.3	53	**Fold:**Single transmembrane helix **Superfamily:**Bacterial ba3 type cytochrome c oxidase subunit IIa **Family:**Bacterial ba3 type cytochrome c oxidase subunit IIa
40	d1f99b_	Alignment	not modelled	6.2	20	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
41	c2bbjB_	Alignment	not modelled	6.1	17	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
42	c3smaD_	Alignment	not modelled	6.0	41	**PDB header:**transferase **Chain:** D: **PDB Molecule:**frbf; **PDBTitle:** a new n-acetyltransferase fold in the structure and mechanism of the2 phosphonate biosynthetic enzyme frbf
43	d1vp8a_	Alignment	not modelled	5.9	25	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
44	c2vmlD_	Alignment	not modelled	5.8	13	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**phycocyanin beta chain; **PDBTitle:** the monoclinic structure of phycocyanin from gloeobacter2 violaceus
45	c3hwpA_	Alignment	not modelled	5.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phlg; **PDBTitle:** crystal structure and computational analyses provide insights into the2 catalytic mechanism of 2, 4-diacetylphloroglucinol hydrolase phlg3 from pseudomonas fluorescens
46	c2da7A_	Alignment	not modelled	5.8	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**zinc finger homeobox protein 1b; **PDBTitle:** solution structure of the homeobox domain of zinc finger2 homeobox protein 1b (smad interacting protein 1)
47	c3e4fB_	Alignment	not modelled	5.8	41	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aminoglycoside n3-acetyltransferase; **PDBTitle:** crystal structure of ba2930- a putative aminoglycoside n3-2 acetyltransferase from bacillus anthracis
48	c1cw5A_	Alignment	not modelled	5.7	29	**PDB header:**toxin **Chain:** A: **PDB Molecule:**type iia bacteriocin carnobacteriocin b2; **PDBTitle:** solution structure of carnobacteriocin b2
49	d2h8pc1	Alignment	not modelled	5.7	11	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels
50	d1mtyg_	Alignment	not modelled	5.7	15	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Methane monooxygenase hydrolase, gamma subunit **Family:**Methane monooxygenase hydrolase, gamma subunit
51	c1jb0K_	Alignment	not modelled	5.7	11	**PDB header:**photosynthesis **Chain:** K: **PDB Molecule:**photosystem 1 reaction centre subunit x; **PDBTitle:** crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
52	d1jb0k_	Alignment	not modelled	5.7	11	**Fold:**Photosystem I reaction center subunit X, PsaK **Superfamily:**Photosystem I reaction center subunit X, PsaK **Family:**Photosystem I reaction center subunit X, PsaK
53	c3gitA_	Alignment	not modelled	5.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbon monoxide dehydrogenase/acetyl-coa synthase subunit **PDBTitle:** crystal structure of a truncated acetyl-coa synthase
54	d1unld_	Alignment	not modelled	5.6	29	**Fold:**Cyclin-like **Superfamily:**Cyclin-like

						Family: Cyclin
55	c1q90L_	Alignment	not modelled	5.6	38	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**cytochrome b6f complex subunit petl; **PDBTitle:** structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
56	d1q90l_	Alignment	not modelled	5.6	38	**Fold:**Single transmembrane helix **Superfamily:**PetL subunit of the cytochrome b6f complex **Family:**PetL subunit of the cytochrome b6f complex
57	d1mhyg_	Alignment	not modelled	5.6	10	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Methane monooxygenase hydrolase, gamma subunit **Family:**Methane monooxygenase hydrolase, gamma subunit
58	c2ka2A_	Alignment	not modelled	5.4	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
59	c2ka1B_	Alignment	not modelled	5.4	33	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
60	c2ka1A_	Alignment	not modelled	5.4	33	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles
61	c2ka2B_	Alignment	not modelled	5.4	33	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**bcl2/adenovirus e1b 19 kda protein-interacting **PDBTitle:** solution nmr structure of bnip3 transmembrane peptide dimer2 in detergent micelles with his173-ser172 intermonomer3 hydrogen bond restraints
62	d1ha7a_	Alignment	not modelled	5.4	14	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
63	d1jboa_	Alignment	not modelled	5.4	10	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
64	c1m56G_	Alignment	not modelled	5.3	5	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**cytochrome c oxidase; **PDBTitle:** structure of cytochrome c oxidase from rhodobactor2 sphaeroides (wild type)
65	c1peiA_	Alignment	not modelled	5.3	50	**PDB header:**nucleotidyltransferase **Chain:** A: **PDB Molecule:**pepc22; **PDBTitle:** nmr structure of the membrane-binding domain of ctp2 phosphocholine cytidylyltransferase, 10 structures
66	d1xg0c_	Alignment	not modelled	5.2	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
67	c2kluA_	Alignment	not modelled	5.1	23	**PDB header:**immune system, membrane protein **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd4; **PDBTitle:** nmr structure of the transmembrane and cytoplasmic domains2 of human cd4
68	c2diiA_	Alignment	not modelled	5.1	23	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex p62 **PDBTitle:** solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
69	c1ifpA_	Alignment	not modelled	5.1	32	**PDB header:**virus **Chain:** A: **PDB Molecule:**major coat protein assembly; **PDBTitle:** inovirus (filamentous bacteriophage) strain pf3 major coat2 protein assembly
70	d1sana_	Alignment	not modelled	5.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
71	d1f99a_	Alignment	not modelled	5.1	7	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins