Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P76235
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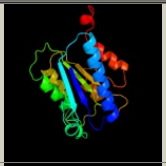
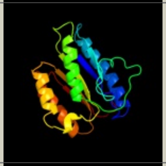
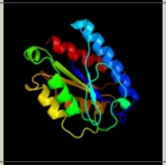
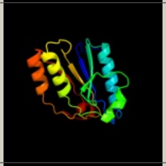
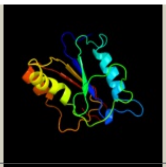
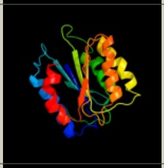
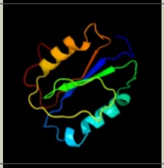
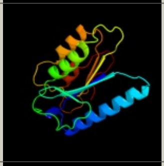
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1rs0A_	Alignment		99.6	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**complement factor b; **PDBTitle:** crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)
2	c2ok5A_	Alignment		99.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**complement factor b; **PDBTitle:** human complement factor b
3	d2ok5a1	Alignment		99.5	15	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
4	c2i6sA_	Alignment		99.4	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**complement c2a fragment; **PDBTitle:** complement component c2a
5	c2x5nA_	Alignment		99.4	11	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**26s proteasome regulatory subunit rpn10; **PDBTitle:** crystal structure of the sprpn10 vwa domain
6	c2iueA_	Alignment		99.4	13	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**pactolus i-domain; **PDBTitle:** pactolus i-domain: functional switching of the rossmann2 fold
7	d1jeyb2	Alignment		99.3	13	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Ku80 subunit N-terminal domain
8	d1ijba_	Alignment		99.2	11	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
9	c3ibsA_	Alignment		99.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein batb; **PDBTitle:** crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron
10	c2nvoA_	Alignment		99.1	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**ro sixty-related protein, rsr; **PDBTitle:** crystal structure of deinococcus radiodurans ro (rsr) protein
11	d1jeya2	Alignment		99.1	12	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Ku70 subunit N-terminal domain

12	d1yvra2	Alignment		99.1	14	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**RoRNP C-terminal domain-like
13	d1u0oc1	Alignment		99.1	11	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
14	c2x31F_	Alignment		99.1	21	**PDB header:**ligase **Chain:** F: **PDB Molecule:**magnesium-chelatase 60 kda subunit; **PDBTitle:** modelling of the complex between subunits bchi and bchd of magnesium2 chelatase based on single-particle cryo-em reconstruction at 7.5 ang
15	d1shux_	Alignment		99.0	14	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
16	d1q0pa_	Alignment		99.0	16	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
17	c2xggB_	Alignment		99.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**microneme protein 2; **PDBTitle:** structure of toxoplasma gondii micronemal protein 2 a_i2 domain
18	c3n2nC_	Alignment		98.9	14	**PDB header:**toxin receptor **Chain:** C: **PDB Molecule:**anthrax toxin receptor 1; **PDBTitle:** the crystal structure of tumor endothelial marker 8 (tem8)2 extracellular domain
19	c1jeyB_	Alignment		98.9	13	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**ku80; **PDBTitle:** crystal structure of the ku heterodimer bound to dna
20	c2b2xB_	Alignment		98.9	12	**PDB header:**immune system **Chain:** B: **PDB Molecule:**integrin alpha-1; **PDBTitle:** vla1 rdeltah i-domain complexed with a quadruple mutant of the aqc22 fab
21	d1v7pc_	Alignment	not modelled	98.9	11	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
22	d1atza_	Alignment	not modelled	98.8	13	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
23	d1n3ya_	Alignment	not modelled	98.8	15	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
24	c3gxbB_	Alignment	not modelled	98.8	10	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**von willebrand factor; **PDBTitle:** crystal structure of vwf a2 domain
25	d1pt6a_	Alignment	not modelled	98.8	11	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
26	d1mjna_	Alignment	not modelled	98.8	15	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
27	d1ck4a_	Alignment	not modelled	98.7	11	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
28	d1mf7a_	Alignment	not modelled	98.7	12	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
29	d1pd0a3	Alignment	not modelled	98.6	13	**Fold:**vWA-like **Superfamily:**vWA-like

						Family: Trunk domain of Sec23/24
30	c3ragA_	Alignment	not modelled	98.4	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
31	d1tyeb2	Alignment	not modelled	98.3	16	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Integrin A (or I) domain
32	c1yvrA_	Alignment		98.2	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**60-kda ss-a/ro ribonucleoprotein; **PDBTitle:** ro autoantigen
33	c3v4pB_	Alignment	not modelled	98.0	15	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-7; **PDBTitle:** crystal structure of a4b7 headpiece complexed with fab act-1
34	c3fcuB_	Alignment	not modelled	98.0	16	**PDB header:**cell adhesion/blood clotting **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** structure of headpiece of integrin aiibb3 in open conformation
35	c1jeqA_	Alignment	not modelled	97.5	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ku70; **PDBTitle:** crystal structure of the ku heterodimer
36	c1u8cB_	Alignment	not modelled	97.2	15	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-3; **PDBTitle:** a novel adaptation of the integrin psi domain revealed from its2 crystal structure
37	c3k6sB_	Alignment	not modelled	96.1	14	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**integrin beta-2; **PDBTitle:** structure of integrin alphaxbeta2 ectodomain
38	c1pd0A_	Alignment	not modelled	96.0	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
39	c1m2vB_	Alignment	not modelled	95.2	14	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24; **PDBTitle:** crystal structure of the yeast sec23/24 heterodimer
40	c3eg9B_	Alignment	not modelled	89.8	14	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**sec24 related gene family, member d; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
41	c3egxB_	Alignment	not modelled	89.1	13	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23a/24a complexed with the snare protein sec22b and3 bound to the transport signal sequence of the snare protein4 bet1
42	c3eg9A_	Alignment	not modelled	84.2	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec23a; **PDBTitle:** crystal structure of the mammalian copii-coat protein2 sec23/24 bound to the transport signal sequence of membrin
43	d2qtva3	Alignment	not modelled	82.5	15	**Fold:**vWA-like **Superfamily:**vWA-like **Family:**Trunk domain of Sec23/24
44	c3eh2B_	Alignment	not modelled	78.2	13	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein transport protein sec24c; **PDBTitle:** crystal structure of the human copii-coat protein sec24c
45	c1m2oA_	Alignment	not modelled	54.8	17	**PDB header:**protein transport/signaling protein **Chain:** A: **PDB Molecule:**protein transport protein sec23; **PDBTitle:** crystal structure of the sec23-sar1 complex
46	d1h7na_	Alignment	not modelled	37.0	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
47	c3atyA_	Alignment	not modelled	33.5	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**prostaglandin f2a synthase; **PDBTitle:** crystal structure of tcoye
48	c2ftpA_	Alignment	not modelled	31.8	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
49	d1vjia_	Alignment	not modelled	26.4	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
50	d2c1ha1	Alignment	not modelled	25.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
51	d1ja1a2	Alignment	not modelled	25.2	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
52	d1boba_	Alignment	not modelled	23.0	8	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
53	c3sggA_	Alignment	not modelled	21.8	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical hydrolase; **PDBTitle:** crystal structure of a hypothetical hydrolase (bt_2193) from2 bacteroides thetaiotaomicron vpi-5482 at 1.25 a resolution
54	d1icpa_	Alignment	not modelled	20.7	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases

						Family:FMN-linked oxidoreductases
55	d1gwja_	Alignment	not modelled	20.4	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
56	c3czpA_	Alignment	not modelled	20.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative polyphosphate kinase 2; **PDBTitle:** crystal structure of putative polyphosphate kinase 2 from pseudomonas2 aeruginosa pa01
57	c1ydnA_	Alignment	not modelled	18.3	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hydroxymethylglutaryl-coa lyase; **PDBTitle:** crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
58	d1irud_	Alignment	not modelled	17.5	21	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits
59	c1ydoC_	Alignment	not modelled	15.4	16	**PDB header:**lyase **Chain:** C: **PDB Molecule:**hmg-coa lyase; **PDBTitle:** crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
60	c3komB_	Alignment	not modelled	14.5	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**transketolase; **PDBTitle:** crystal structure of apo transketolase from francisella tularensis
61	d1l6sa_	Alignment	not modelled	13.4	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
62	c3l5aA_	Alignment	not modelled	13.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh/flavin oxidoreductase/nadh oxidase; **PDBTitle:** crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
63	d1uiza_	Alignment	not modelled	12.0	11	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
64	d1w5fa2	Alignment	not modelled	11.9	11	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
65	c3mwbA_	Alignment	not modelled	11.7	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**prephenate dehydratase; **PDBTitle:** the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
66	c3fwtA_	Alignment	not modelled	11.5	11	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
67	d1gzga_	Alignment	not modelled	10.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
68	c2p0wB_	Alignment	not modelled	10.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**histone acetyltransferase type b catalytic subunit; **PDBTitle:** human histone acetyltransferase 1 (hat1)
69	d1vh4a_	Alignment	not modelled	10.6	25	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Stabilizer of iron transporter SufD **Family:**Stabilizer of iron transporter SufD
70	d2vapa2	Alignment	not modelled	9.9	4	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
71	c2l42A_	Alignment	not modelled	9.4	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna-binding protein rap1; **PDBTitle:** the solution structure of rap1 brct domain from saccharomyces2 cerevisiae
72	c3vcbB_	Alignment	not modelled	9.2	20	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**rna-directed rna polymerase; **PDBTitle:** c425s mutant of the c-terminal cytoplasmic domain of non-structural2 protein 4 from mouse hepatitis virus a59
73	d2fcja1	Alignment	not modelled	9.1	24	**Fold:**Toprim domain **Superfamily:**Toprim domain **Family:**Toprim domain
74	d1q45a_	Alignment	not modelled	8.8	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
75	d1bmlc1	Alignment	not modelled	8.6	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase
76	d1g8fa3	Alignment	not modelled	8.4	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
77	c3luyA_	Alignment	not modelled	8.2	7	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**probable chorismate mutase; **PDBTitle:** putative chorismate mutase from bifidobacterium adolescentis
78	d1xhoa_	Alignment	not modelled	8.1	45	**Fold:**Bacillus chorismate mutase-like **Superfamily:**YjgF-like **Family:**Chorismate mutase
79	c2xczA_	Alignment	not modelled	8.0	12	**PDB header:**immune system **Chain:** A: **PDB Molecule:**possible atls1-like light-inducible protein; **PDBTitle:** crystal structure of macrophage migration inhibitory factor2 homologue from prochlorococcus marinus
80	c1xhoB_	Alignment	not modelled	7.7	42	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**chorismate mutase;

80	c1xhoB_	Alignment	not modelled	7.7	42	**PDBTitle:** chorismate mutase from clostridium thermocellum cth-682
81	c3lukB_	Alignment	not modelled	7.4	9	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein argonaute-2; **PDBTitle:** crystal structure of mid domain from hago2
82	d1rhya2	Alignment	not modelled	7.4	20	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
83	d1xg8a_	Alignment	not modelled	7.4	35	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**YuzD-like
84	c3gzfD_	Alignment	not modelled	7.2	28	**PDB header:**viral protein **Chain:** D: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** structure of the c-terminal domain of nsp4 from feline coronavirus
85	c3dmaA_	Alignment	not modelled	7.1	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**exopolyphosphatase-related protein; **PDBTitle:** crystal structure of an exopolyphosphatase-related protein2 from bacteroides fragilis. northeast structural genomics3 target bfr192
86	c2k19A_	Alignment	not modelled	7.1	15	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**putative piscicolin 126 immunity protein; **PDBTitle:** nmr solution structure of pisi
87	c2qtxL_	Alignment	not modelled	7.0	86	**PDB header:**rna binding protein **Chain:** L: **PDB Molecule:**uncharacterized protein mj1435; **PDBTitle:** crystal structure of an hfq-like protein from methanococcus2 jannaschii
88	c3b64A_	Alignment	not modelled	7.0	9	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
89	d2qmwa2	Alignment	not modelled	7.0	12	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Phenylalanine metabolism regulatory domain
90	d1nxha_	Alignment	not modelled	6.8	24	**Fold:**Hypothetical protein MTH393 **Superfamily:**Hypothetical protein MTH393 **Family:**Hypothetical protein MTH393
91	d2cp8a1	Alignment	not modelled	6.6	44	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
92	c3cs5B_	Alignment	not modelled	6.5	28	**PDB header:**photosynthesis **Chain:** B: **PDB Molecule:**phycobilisome degradation protein nbla; **PDBTitle:** nbla protein from synechococcus elongatus pcc 7942
93	d2dfaa1	Alignment	not modelled	6.5	11	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
94	c2h90A_	Alignment	not modelled	6.5	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xenobiotic reductase a; **PDBTitle:** xenobiotic reductase a in complex with coumarin
95	c3eukC_	Alignment	not modelled	6.3	18	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**chromosome partition protein mukb, linker; **PDBTitle:** crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, asymmetric dimer
96	d2ae8a2	Alignment	not modelled	6.3	27	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
97	d1vyra_	Alignment	not modelled	6.3	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
98	d1pv8a_	Alignment	not modelled	6.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
99	d1l4zb_	Alignment	not modelled	6.2	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Staphylokinase/streptokinase **Family:**Staphylokinase/streptokinase