Phyre^2

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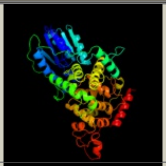
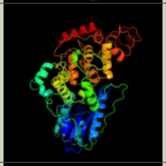
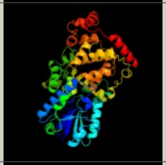
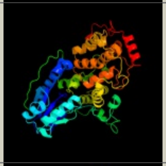
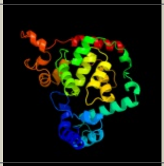
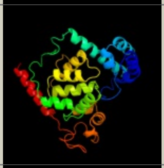
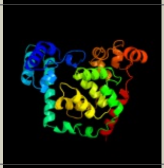
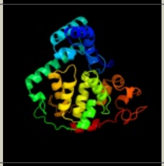
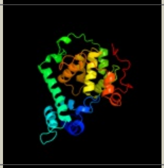
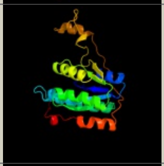
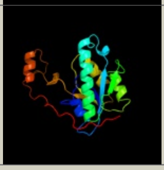
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1dnpA_	Alignment		100.0	100	**PDB header:**lyase (carbon-carbon) **Chain:** A: **PDB Molecule:**dna photolyase; **PDBTitle:** structure of deoxyribodipyrimidine photolyase
2	c3fy4C_	Alignment		100.0	27	**PDB header:**lyase **Chain:** C: **PDB Molecule:**6-4 photolyase; **PDBTitle:** (6-4) photolyase crystal structure
3	c1u3cA_	Alignment		100.0	29	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cryptochrome 1 apoprotein; **PDBTitle:** crystal structure of the phr domain of cryptochrome 1 from2 arabidopsis thaliana
4	c3cvyA_	Alignment		100.0	28	**PDB header:**lyase/dna **Chain:** A: **PDB Molecule:**re11660p; **PDBTitle:** drosophila melanogaster (6-4) photolyase bound to repaired2 ds dna
5	c1tezB_	Alignment		100.0	37	**PDB header:**lyase/dna **Chain:** B: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** complex between dna and the dna photolyase from anacystis nidulans
6	c1np7A_	Alignment		100.0	30	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dna photolyase; **PDBTitle:** crystal structure analysis of synechocystis sp. pcc6803 cryptochrome
7	c3tvsA_	Alignment		100.0	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cryptochrome-1; **PDBTitle:** structure of full-length drosophila cryptochrome
8	c2j4dA_	Alignment		100.0	26	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**cryptochrome dash; **PDBTitle:** cryptochrome 3 from arabidopsis thaliana
9	c2e0iD_	Alignment		100.0	34	**PDB header:**lyase **Chain:** D: **PDB Molecule:**432aa long hypothetical deoxyribodipyrimidine photolyase; **PDBTitle:** crystal structure of archaeal photolyase from sulfolobus tokodaii with2 two fad molecules: implication of a novel light-harvesting cofactor
10	c1iqrA_	Alignment		100.0	36	**PDB header:**lyase **Chain:** A: **PDB Molecule:**photolyase; **PDBTitle:** crystal structure of dna photolyase from thermus2 thermophilus
11	c2xrzA_	Alignment		100.0	22	**PDB header:**lyase/dna **Chain:** A: **PDB Molecule:**deoxyribodipyrimidine photolyase; **PDBTitle:** x-ray structure of archaeal class ii cpd photolyase from2 methanosarcina mazei in complex with intact cpd-lesion

12	c3umvB_	Alignment		100.0	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**deoxyribodipyrimidine photo-lyase; **PDBTitle:** eukaryotic class ii cpd photolyase structure reveals a basis for2 improved uv-tolerance in plants
13	d1dnpa1	Alignment		100.0	100	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
14	d1u3da1	Alignment		100.0	33	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
15	d1owla1	Alignment		100.0	48	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
16	d1np7a1	Alignment		100.0	34	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
17	d2j07a1	Alignment		100.0	45	**Fold:**Cryptochrome/photolyase FAD-binding domain **Superfamily:**Cryptochrome/photolyase FAD-binding domain **Family:**Cryptochrome/photolyase FAD-binding domain
18	d1dnpa2	Alignment		100.0	100	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
19	d1owla2	Alignment		100.0	23	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
20	d1u3da2	Alignment		100.0	24	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
21	d1np7a2	Alignment	not modelled	100.0	23	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
22	d2j07a2	Alignment	not modelled	100.0	26	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
23	c2gvsA_	Alignment	not modelled	75.2	15	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**chemosensory protein csp-sg4; **PDBTitle:** nmr solution structure of cspsg4
24	d1n8va_	Alignment	not modelled	72.0	17	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
25	d1kx9b_	Alignment	not modelled	68.0	17	**Fold:**alpha-alpha superhelix **Superfamily:**Chemosensory protein Csp2 **Family:**Chemosensory protein Csp2
26	c1ul1Y_	Alignment	not modelled	67.8	10	**PDB header:**hydrolase/dna binding protein **Chain:** Y: **PDB Molecule:**flap endonuclease-1; **PDBTitle:** crystal structure of the human fen1-pcna complex
27	c3obkH_	Alignment	not modelled	49.4	18	**PDB header:**lyase **Chain:** H: **PDB Molecule:**delta-aminolevulinic acid dehydratase; **PDBTitle:** crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
28	d1ul1x2	Alignment	not modelled	32.6	14	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
						PDB header:transferase

29	c3lgbB_	Alignment	not modelled	30.6	12	**Chain:** B: **PDB Molecule:**dna primase large subunit; **PDBTitle:** crystal structure of the fe-s domain of the yeast dna primase
30	c2l06A_	Alignment	not modelled	29.3	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phycobilisome lcm core-membrane linker polypeptide; **PDBTitle:** solution nmr structure of the pbs linker polypeptide domain (fragment2 254-400) of phycobilisome linker protein apce from synechocystis sp.3 pcc 6803. northeast structural genomics consortium target sgr209c
31	c3oryA_	Alignment	not modelled	27.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap endonuclease 1; **PDBTitle:** crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
32	c2pbyB_	Alignment	not modelled	25.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaminase; **PDBTitle:** probable glutaminase from geobacillus kaustophilus hta426
33	d1l6sa_	Alignment	not modelled	24.2	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
34	c2pfsA_	Alignment	not modelled	23.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**universal stress protein; **PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea
35	c2l3wA_	Alignment	not modelled	22.8	17	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**phycobilisome rod linker polypeptide; **PDBTitle:** solution nmr structure of the pbs linker domain of phycobilisome rod2 linker polypeptide from synechococcus elongatus, northeast structural3 genomics consortium target snr168a
36	d1u7ia_	Alignment	not modelled	22.5	13	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**3-demethylubiquinone-9 3-methyltransferase
37	c1a77A_	Alignment	not modelled	21.3	13	**PDB header:**5'-3' exo/endo nuclease **Chain:** A: **PDB Molecule:**flap endonuclease-1 protein; **PDBTitle:** flap endonuclease-1 from methanococcus jannaschii
38	d2d13a1	Alignment	not modelled	20.0	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
39	c3mwdA_	Alignment	not modelled	19.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp-citrate synthase; **PDBTitle:** truncated human atp-citrate lyase with citrate bound
40	c2ky4A_	Alignment	not modelled	19.9	13	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**phycobilisome linker polypeptide; **PDBTitle:** solution nmr structure of the pbs linker domain of phycobilisome2 linker polypeptide from anabaena sp. northeast structural genomics3 consortium target nsr123e
41	d1gzga_	Alignment	not modelled	19.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
42	c3odhB_	Alignment	not modelled	17.9	47	**PDB header:**hydrolase/dna **Chain:** B: **PDB Molecule:**okrai endonuclease; **PDBTitle:** structure of okrai/dna complex
43	d1k8kd2	Alignment	not modelled	17.8	40	**Fold:**Secretion chaperone-like **Superfamily:**Arp2/3 complex subunits **Family:**Arp2/3 complex subunits
44	c2z86D_	Alignment	not modelled	17.4	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**chondroitin synthase; **PDBTitle:** crystal structure of chondroitin polymerase from2 escherichia coli strain k4 (k4cp) complexed with udp-glcua3 and udp
45	c2izoA_	Alignment	not modelled	16.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flap structure-specific endonuclease; **PDBTitle:** structure of an archaeal pcna1-pcna2-fen1 complex
46	c2p9lD_	Alignment	not modelled	16.4	40	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**actin-related protein 2/3 complex subunit 2; **PDBTitle:** crystal structure of bovine arp2/3 complex
47	d1b43a2	Alignment	not modelled	15.1	16	**Fold:**PIN domain-like **Superfamily:**PIN domain-like **Family:**5' to 3' exonuclease catalytic domain
48	d1zela1	Alignment	not modelled	14.3	46	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Rv2827c N-terminal domain-like
49	c3dwlI_	Alignment	not modelled	14.2	40	**PDB header:**structural protein **Chain:** I: **PDB Molecule:**actin-related protein 2/3 complex subunit 2; **PDBTitle:** crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
50	d2bdua1	Alignment	not modelled	14.1	16	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Pyrimidine 5'-nucleotidase (UMPH-1)
51	d2fsqa1	Alignment	not modelled	13.2	32	**Fold:**LigT-like **Superfamily:**LigT-like **Family:**Atu0111-like
52	d2b8ea1	Alignment	not modelled	13.1	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
53	d2vkqa1	Alignment	not modelled	11.4	13	**Fold:**HAD-like **Superfamily:**HAD-like

						Family: Pyrimidine 5'-nucleotidase (UMPH-1)
54	c2qqcC_	Alignment	not modelled	11.3	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**pyruvoyl-dependent arginine decarboxylase (ec **PDBTitle:** e109q mutant of pyruvoyl-dependent arginine decarboxylase2 from methanococcus jannashii
55	c1b43A_	Alignment	not modelled	10.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (fen-1); **PDBTitle:** fen-1 from p. furiosus
56	d1nyna_	Alignment	not modelled	9.2	0	**Fold:**FYSH domain **Superfamily:**FYSH domain **Family:**Hypothetical protein Yhr087W
57	c3ew8A_	Alignment	not modelled	9.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histone deacetylase 8; **PDBTitle:** crystal structure analysis of human hdac8 d101l variant
58	d1t64a_	Alignment	not modelled	9.0	16	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Histone deacetylase, HDAC
59	d1sgma1	Alignment	not modelled	9.0	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
60	d1pv8a_	Alignment	not modelled	8.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
61	d2ipqx1	Alignment	not modelled	8.2	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**STY4665 C-terminal domain-like
62	d2vkva1	Alignment	not modelled	8.1	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
63	d1evsa_	Alignment	not modelled	8.0	17	**Fold:**4-helical cytokines **Superfamily:**4-helical cytokines **Family:**Long-chain cytokines
64	d1ru8a_	Alignment	not modelled	7.7	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
65	d1b74a2	Alignment	not modelled	7.5	25	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
66	d2dy1a3	Alignment	not modelled	7.2	27	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
67	d2bv3a3	Alignment	not modelled	7.1	50	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Translational machinery components
68	d2o7ta1	Alignment	not modelled	6.8	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
69	c3l9qB_	Alignment	not modelled	6.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna primase large subunit; **PDBTitle:** crystal structure of human polymerase alpha-primase p58 iron-sulfur2 cluster domain
70	c1p4eB_	Alignment	not modelled	6.5	30	**PDB header:**dna binding protein/recombination/dna **Chain:** B: **PDB Molecule:**recombinase flp protein; **PDBTitle:** flpe w330f mutant-dna holliday junction complex
71	c3q8lA_	Alignment	not modelled	6.2	20	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**flap endonuclease 1; **PDBTitle:** crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
72	c2lmdA_	Alignment	not modelled	6.2	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**prospero homeobox protein 1; **PDBTitle:** minimal constraints solution nmr structure of prospero homeobox2 protein 1 from homo sapiens, northeast structural genomics consortium3 target hr4660b
73	c2ld7A_	Alignment	not modelled	6.1	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone deacetylase complex subunit sap30; **PDBTitle:** solution structure of the msin3a pah3-sap30 sid complex
74	d1g8fa3	Alignment	not modelled	6.1	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
75	c1rxvA_	Alignment	not modelled	5.8	11	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**flap structure-specific endonuclease; **PDBTitle:** crystal structure of a. fulgidus fen-1 bound to dna
76	c3lklB_	Alignment	not modelled	5.5	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**antisigma-factor antagonist stas; **PDBTitle:** crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
77	d2i10a1	Alignment	not modelled	5.5	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Tetracyclin repressor-like, N-terminal domain
78	c3dloC_	Alignment	not modelled	5.2	8	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**universal stress protein; **PDBTitle:** structure of universal stress protein from archaeoglobus fulgidus
79	c3j09A_	Alignment	not modelled	5.1	13	**PDB header:**hydrolase, metal transport **Chain:** A: **PDB Molecule:**copper-exporting p-type atpase a; **PDBTitle:** high resolution helical reconstruction of the bacterial p-type atpase2 copper transporter copa