Phyre^2

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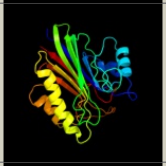
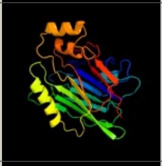
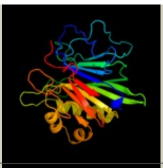
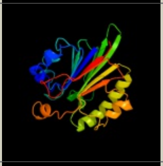
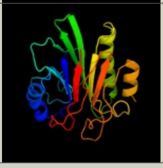
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j63B_	Alignment		100.0	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**ap-endonuclease; **PDBTitle:** crystal structure of ap endonuclease lmap from leishmania2 major
2	c3mprB_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative endonuclease/exonuclease/phosphatase family **PDBTitle:** crystal structure of endonuclease/exonuclease/phosphatase family2 protein from bacteroides thetaiotaomicron, northeast structural3 genomics consortium target btr318a
3	c1e9nB_	Alignment		100.0	13	**PDB header:**dna repair **Chain:** B: **PDB Molecule:**dna-(apurinic or apyrimidinic site) lyase; **PDBTitle:** a second divalent metal ion in the active site of a new2 crystal form of human apurinic/apyrimidinic endonuclease,3 ape1, and its implications for the catalytic mechanism
4	c3tebA_	Alignment		100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease/exonuclease/phosphatase; **PDBTitle:** endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
5	c3ngoA_	Alignment		100.0	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**ccr4-not transcription complex subunit 6-like; **PDBTitle:** crystal structure of the human cnot6l nuclease domain in complex with2 poly(a) dna
6	c3mtcA_	Alignment		100.0	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**type ii inositol-1,4,5-trisphosphate 5-phosphatase; **PDBTitle:** crystal structure of inpp5b in complex with phosphatidylinositol 4-2 phosphate
7	c3g6sA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative endonuclease/exonuclease/phosphatase **PDBTitle:** crystal structure of the2 endonuclease/exonuclease/phosphatase (bvu_0621) from3 bacteroides vulgatus. northeast structural genomics4 consortium target bvr56d
8	c3l1wE_	Alignment		100.0	17	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown conserved2 protein from enterococcus faecalis v583
9	d2imqx1	Alignment		100.0	15	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Inositol polyphosphate 5-phosphatase (IPP5)
10	c3g0rA_	Alignment		100.0	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** complex of mth0212 and an 8bp dsdna with distorted ends
11	d1vyba_	Alignment		100.0	17	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like

12	d2f1na1	Alignment		99.9	16	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
13	c2jc5A_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease; **PDBTitle:** apurinic apyrimidinic (ap) endonuclease (nape) from2 neisseria meningitidis
14	d1wdua_	Alignment		99.9	14	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
15	d1akoa_	Alignment		99.9	12	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
16	d2ddra1	Alignment		99.9	19	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Sphingomyelin phosphodiesterase-like
17	d1zwxa1	Alignment		99.9	17	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Sphingomyelin phosphodiesterase-like
18	c3nr8A_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2; **PDBTitle:** crystal structure of human ship2
19	d1sr4b_	Alignment		99.9	14	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
20	c2ei9A_	Alignment		99.9	18	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**non-ltr retrotransposon r1bmks orf2 protein; **PDBTitle:** crystal structure of r1bm endonuclease domain
21	d2a40b1	Alignment	not modelled	99.9	15	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
22	c2voaB_	Alignment	not modelled	99.9	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**exodeoxyribonuclease iii; **PDBTitle:** structure of an ap endonuclease from archaeoglobus fulgidus
23	d1hd7a_	Alignment	not modelled	99.9	16	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
24	c3i46B_	Alignment	not modelled	99.9	15	**PDB header:**toxin **Chain:** B: **PDB Molecule:**beta-hemolysin; **PDBTitle:** crystal structure of beta toxin from staphylococcus aureus f277a,2 p278a mutant with bound calcium ions
25	c2jc4A_	Alignment	not modelled	99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease iii; **PDBTitle:** 3'-5' exonuclease (nexo) from neisseria meningitidis
26	c2xswB_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**72 kda inositol polyphosphate 5-phosphatase; **PDBTitle:** crystal structure of human inpp5e
27	d1i9za_	Alignment	not modelled	99.8	16	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**Inositol polyphosphate 5-phosphatase (IPP5)
28	d2qlvb1	Alignment	not modelled	41.4	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
29	c2qlvB_	Alignment	not modelled	36.1	20	**PDB header:**transferase/protein binding **Chain:** B: **PDB Molecule:**protein sip2;

29	c2qlvB_	Alignment	not modelled	30.1	20	**PDBTitle:** crystal structure of the heterotrimer core of the s.2 cerevisiae ampk homolog snf1
30	d1z0na1	Alignment	not modelled	27.7	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
31	d2f15a1	Alignment	not modelled	26.6	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
32	d1q6za1	Alignment	not modelled	23.3	23	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
33	c3nmeA_	Alignment	not modelled	23.1	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sex4 glucan phosphatase; **PDBTitle:** structure of a plant phosphatase
34	d1z0mb1	Alignment	not modelled	20.4	35	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**AMPK-beta glycogen binding domain-like
35	d2ez9a1	Alignment	not modelled	19.3	14	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
36	d1uf3a_	Alignment	not modelled	19.1	12	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
37	d1emsa2	Alignment	not modelled	19.1	14	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase
38	c2w1vA_	Alignment	not modelled	18.1	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nitrilase homolog 2; **PDBTitle:** crystal structure of mouse nitrilase-2 at 1.4a resolution
39	d2ji7a1	Alignment	not modelled	18.0	32	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
40	d1ybha1	Alignment	not modelled	17.3	26	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
41	d2djia1	Alignment	not modelled	15.9	23	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
42	c2jzfA_	Alignment	not modelled	15.4	33	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**replicase polyprotein 1ab; **PDBTitle:** nmr conformer closest to the mean coordinates of the domain 513-651 of2 the sars-cov nonstructural protein nsp3
43	d2ihta1	Alignment	not modelled	15.2	22	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
44	d3d03a1	Alignment	not modelled	15.0	16	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**GpdQ-like
45	d1ovma1	Alignment	not modelled	14.6	9	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
46	d1ozha1	Alignment	not modelled	13.1	19	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
47	d1xm7a_	Alignment	not modelled	13.0	11	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**Hypothetical protein aq 1666
48	d2yvta1	Alignment	not modelled	12.7	19	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**TT1561-like
49	d1j31a_	Alignment	not modelled	11.3	23	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Carbamilase
50	d1f89a_	Alignment	not modelled	10.4	19	**Fold:**Carbon-nitrogen hydrolase **Superfamily:**Carbon-nitrogen hydrolase **Family:**Nitrilase
51	d1pvda1	Alignment	not modelled	10.4	11	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
52	c2e11B_	Alignment	not modelled	8.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hydrolase; **PDBTitle:** the crystal structure of xc1258 from xanthomonas campestris: a cn-2 hydrolase superfamily protein with an arsenic adduct in the active3 site
53	c3ilvA_	Alignment	not modelled	8.3	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
54	d1edqa1	Alignment	not modelled	8.0	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**E-set domains of sugar-utilizing enzymes
55	c3av0A_	Alignment	not modelled	7.9	16	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11-rad50 bound to atp s
56	d2vzsa2	Alignment	not modelled	7.8	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**beta-Galactosidase/glucuronidase domain

						Family:beta-Galactosidase/glucuronidase domain
57	c3rl4A_	Alignment	not modelled	6.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metallophosphoesterase mpped2; **PDBTitle:** rat metallophosphodiesterase mpped2 g252h mutant
58	d1zpda1	Alignment	not modelled	6.0	10	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
59	d1o51a_	Alignment	not modelled	5.9	10	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**DUF190/COG1993
60	c3jvvA_	Alignment	not modelled	5.6	8	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
61	c3n05B_	Alignment	not modelled	5.6	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
62	d2fvta1	Alignment	not modelled	5.4	13	**Fold:**MTH938-like **Superfamily:**MTH938-like **Family:**MTH938-like
63	c3auzA_	Alignment	not modelled	5.4	18	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna double-strand break repair protein mre11; **PDBTitle:** crystal structure of mre11 with manganese
64	c3dnfB_	Alignment	not modelled	5.2	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway