Phyre^2

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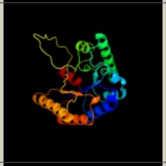
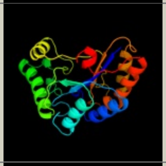
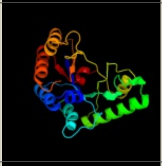
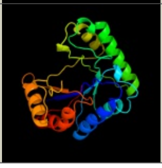
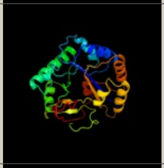
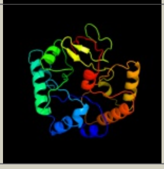
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2c1iA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan glcnac deacetylase; **PDBTitle:** structure of streptococcus pnemoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant.
2	c1w17A_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
3	d1ny1a_	Alignment		100.0	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
4	d1z7aa1	Alignment		100.0	19	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**PA1517-like
5	d2cc0a1	Alignment		100.0	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
6	c3qbuD_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of putative peptidoglyacn deactelyase (hp0310) from2 helicobacter pylori
7	d2iw0a1	Alignment		100.0	22	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
8	d2j13a1	Alignment		100.0	20	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
9	c2vyoA_	Alignment		100.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitooligosaccharide deacetylase; **PDBTitle:** chitin deacetylase family member from encephalitozoon2 cuniculi
10	c3s6oD_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**polysaccharide deacetylase family protein; **PDBTitle:** crystal structure of a polysaccharide deacetylase family protein from2 burkholderia pseudomallei
11	c2w3zA_	Alignment		100.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase

12	d2c1ia1	Alignment		100.0	22	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
13	c2iw0A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitin deacetylase; **PDBTitle:** structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
14	d2c71a1	Alignment		100.0	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
15	c3rxzA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**polysaccharide deacetylase; **PDBTitle:** crystal structure of putative polysaccharide deacetylase from2 mycobacterium smegmatis
16	d2nlya1	Alignment		100.0	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
17	d1k1xa3	Alignment		99.4	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**4-alpha-glucanotransferase, N-terminal domain
18	c1k1yA_	Alignment		99.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-alpha-glucanotransferase; **PDBTitle:** crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
19	c2b5dX_	Alignment		99.0	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
20	d2b5dx2	Alignment		98.9	13	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**AmyC N-terminal domain-like
21	c3hftA_	Alignment	not modelled	98.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**wbms, polysaccharide deacetylase involved in o-antigen **PDBTitle:** crystal structure of a putative polysaccharide deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution
22	d1ufaa2	Alignment	not modelled	98.6	24	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**AmyC N-terminal domain-like
23	c2qv5A_	Alignment	not modelled	98.5	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
24	c1ufaA_	Alignment	not modelled	98.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**tt1467 protein; **PDBTitle:** crystal structure of tt1467 from thermus thermophilus hb8
25	c3n92A_	Alignment	not modelled	98.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-amylase, gh57 family; **PDBTitle:** crystal structure of tk1436, a gh57 branching enzyme from2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose
26	c2wyhA_	Alignment	not modelled	95.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase; **PDBTitle:** structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
27	d1v6ta_	Alignment	not modelled	94.8	17	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
						Fold:7-stranded beta/alpha barrel

28	d2i5ia1	Alignment	not modelled	89.9	12	**Superfamily:**Glycoside hydrolase/deacetylase **Family:**YdjC-like
29	c1htyA_	Alignment	not modelled	88.2	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase ii; **PDBTitle:** golgi alpha-mannosidase ii
30	d3bvua3	Alignment	not modelled	79.8	11	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**alpha-mannosidase
31	c1o7dA_	Alignment	not modelled	79.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysosomal alpha-mannosidase; **PDBTitle:** the structure of the bovine lysosomal a-mannosidase2 suggests a novel mechanism for low ph activation
32	c2ow7A_	Alignment	not modelled	76.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase 2; **PDBTitle:** golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thioniabicyclo[4.3.0]nonan-7,8-diol chloride
33	c3k2gA_	Alignment	not modelled	74.4	16	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
34	d1tqha_	Alignment	not modelled	56.8	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carboxylesterase/lipase
35	d1dxqa_	Alignment	not modelled	55.0	10	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
36	d2qwxa1	Alignment	not modelled	50.3	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
37	d1xkla_	Alignment	not modelled	50.2	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
38	c2qiwA_	Alignment	not modelled	50.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pep phosphonomutase; **PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
39	c3dqzB_	Alignment	not modelled	48.3	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**alpha-hydroxynitrile lyase-like protein; **PDBTitle:** structure of the hydroxynitrile lyase from arabidopsis2 thaliana
40	d1xjca_	Alignment	not modelled	47.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
41	d1qrda_	Alignment	not modelled	42.5	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
42	c3dyvA_	Alignment	not modelled	41.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**esterase d; **PDBTitle:** snapshots of esterase d from lactobacillus rhamnosus:2 insights into a rotation driven catalytic mechanism
43	d2dfaa1	Alignment	not modelled	41.1	14	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
44	d3c70a1	Alignment	not modelled	40.0	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
45	c2x5eA_	Alignment	not modelled	35.5	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**upf0271 protein pa4511; **PDBTitle:** crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
46	d1d4aa_	Alignment	not modelled	34.4	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
47	c3gzjB_	Alignment	not modelled	32.3	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polyneuridine-aldehyde esterase; **PDBTitle:** crystal structure of polyneuridine aldehyde esterase2 complexed with 16-epi-vellosimine
48	d1e89a_	Alignment	not modelled	32.2	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
49	c2vdaA_	Alignment	not modelled	31.9	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**translocase subunit seca; **PDBTitle:** solution structure of the seca-signal peptide complex
50	c1nl3B_	Alignment	not modelled	28.8	21	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**preprotein translocase seca 1 subunit; **PDBTitle:** crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
51	d1x8da1	Alignment	not modelled	28.0	21	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YiiL-like
52	c2ipcB_	Alignment	not modelled	27.9	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
53	c3dinB_	Alignment	not modelled	25.1	18	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
54	d1pnea_	Alignment	not modelled	24.3	7	**Fold:**Profilin-like **Superfamily:**Profilin (actin-binding protein)

						Family: Profilin (actin-binding protein)
55	c3juxA_	Alignment	not modelled	24.2	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the translocation atpase seca from thermotoga2 maritima
56	d2pbdp1	Alignment	not modelled	23.3	7	**Fold:**Profilin-like **Superfamily:**Profilin (actin-binding protein) **Family:**Profilin (actin-binding protein)
57	c1u2eA_	Alignment	not modelled	22.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**2-hydroxy-6-ketonona-2,4-dienedioic acid **PDBTitle:** crystal structure of the c-c bond hydrolase mhpc
58	c2k6xA_	Alignment	not modelled	20.7	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
59	c3lvtA_	Alignment	not modelled	20.6	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase, family 38; **PDBTitle:** the crystal structure of a protein in the glycosyl hydrolase2 family 38 from enterococcus faecalis to 2.55a
60	c3fobA_	Alignment	not modelled	20.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**bromoperoxidase; **PDBTitle:** crystal structure of bromoperoxidase from bacillus anthracis
61	d1jmsa4	Alignment	not modelled	20.3	11	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**DNA polymerase beta-like
62	d1xw8a_	Alignment	not modelled	19.6	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
63	d1a8sa_	Alignment	not modelled	18.4	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
64	d1prtf_	Alignment	not modelled	18.2	21	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
65	d1r57a_	Alignment	not modelled	17.9	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
66	c2qlxA_	Alignment	not modelled	17.8	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**l-rhamnose mutarotase; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
67	c2qlwA_	Alignment	not modelled	17.8	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rhau; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
68	c3m1yA_	Alignment	not modelled	17.3	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphoserine phosphatase (serb); **PDBTitle:** crystal structure of a phosphoserine phosphatase (serb) from2 helicobacter pylori
69	d1brta_	Alignment	not modelled	17.1	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
70	d1vp8a_	Alignment	not modelled	16.8	9	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
71	d1a8qa_	Alignment	not modelled	16.7	24	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
72	d1uk8a_	Alignment	not modelled	16.3	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
73	d1va4a_	Alignment	not modelled	16.0	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
74	d1c4xa_	Alignment	not modelled	15.6	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
75	c3u1tA_	Alignment	not modelled	15.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dmma haloalkane dehalogenase; **PDBTitle:** haloalkane dehalogenase, dmma, of marine microbial origin
76	d1r3da_	Alignment	not modelled	15.3	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein VC1974
77	d1l7da2	Alignment	not modelled	14.3	7	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**L-alanine dehydrogenase-like
78	d1s2oa1	Alignment	not modelled	14.0	15	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
79	d1b6ga_	Alignment	not modelled	13.8	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloalkane dehalogenase
80	d1t57a_	Alignment	not modelled	13.8	15	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
						PDB header:oxidoreductase

81	c3dnfB_	Alignment	not modelled	13.5	21	**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
82	c3rhgA_	Alignment	not modelled	13.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative phophotriesterase; **PDBTitle:** crystal structure of amidohydrolase pmi1525 (target efi-500319) from2 proteus mirabilis hi4320
83	c2cjpA_	Alignment	not modelled	13.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** structure of potato (solanum tuberosum) epoxide hydrolase i2 (steh1)
84	d2c7fa2	Alignment	not modelled	12.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
85	d1hkha_	Alignment	not modelled	12.7	16	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Haloperoxidase
86	c2wtaA_	Alignment	not modelled	12.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** acinetobacter baumanii nicotinamidase pyrazinamidease
87	c2e3jA_	Alignment	not modelled	11.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase ephb; **PDBTitle:** the crystal structure of epoxide hydrolase b (rv1938) from2 mycobacterium tuberculosis at 2.1 angstrom
88	c3obeB_	Alignment	not modelled	11.7	9	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
89	c1vjqB_	Alignment	not modelled	11.6	23	**PDB header:**structural genomics, de novo protein **Chain:** B: **PDB Molecule:**designed protein; **PDBTitle:** designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
90	d1yqea1	Alignment	not modelled	11.6	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**AF0625-like **Family:**AF0625-like
91	d2rhwa1	Alignment	not modelled	11.6	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Carbon-carbon bond hydrolase
92	d1ufoa_	Alignment	not modelled	11.5	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hypothetical protein TT1662
93	d1pava_	Alignment	not modelled	10.8	14	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like
94	d1p6va_	Alignment	not modelled	10.7	23	**Fold:**Small protein B (SmpB) **Superfamily:**Small protein B (SmpB) **Family:**Small protein B (SmpB)
95	c3kc2A_	Alignment	not modelled	10.7	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ykr070w; **PDBTitle:** crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
96	c2xt0A_	Alignment	not modelled	10.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** dehalogenase dppa from plesiocystis pacifica sir-i
97	c2xfyA_	Alignment	not modelled	10.3	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-amylase; **PDBTitle:** crystal structure of barley beta-amylase complexed with2 alpha-cyclodextrin
98	c1cr6A_	Alignment	not modelled	10.2	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**epoxide hydrolase; **PDBTitle:** crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
99	d1zd3a2	Alignment	not modelled	10.1	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Epoxide hydrolase