Phyre^2

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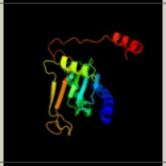
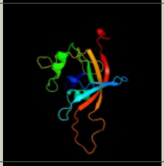
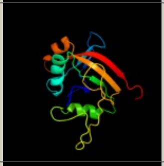
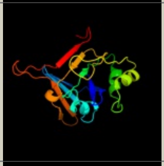
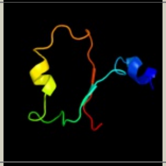
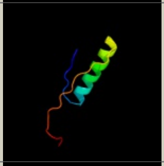
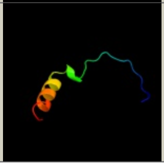
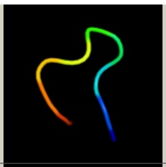
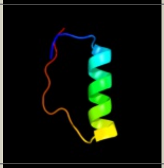
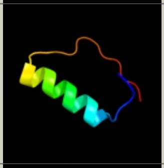
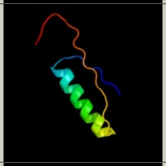
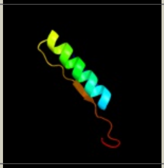
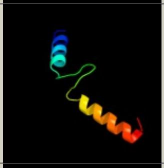
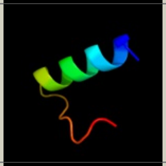
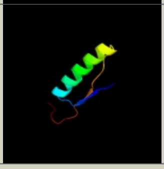
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2idbB_	Alignment		100.0	98	**PDB header:**lyase **Chain:** B: **PDB Molecule:**3-octaprenyl-4-hydroxybenzoate carboxy-lyase; **PDBTitle:** crystal structure of 3-octaprenyl-4-hydroxybenzoate decarboxylase2 (ubid) from escherichia coli, northeast structural genomics target3 er459.
2	d2idba1	Alignment		100.0	98	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**UbiD middle domain-like
3	d2idba2	Alignment		100.0	97	**Fold:**UbiD C-terminal domain-like **Superfamily:**UbiD C-terminal domain-like **Family:**UbiD C-terminal domain-like
4	c3bpkB_	Alignment		68.5	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase component b; **PDBTitle:** crystal structure of nitrilotriacetate monooxygenase2 component b from bacillus cereus
5	c3e4vA_	Alignment		59.7	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**nadh:fmn oxidoreductase like protein; **PDBTitle:** crystal structure of nadh:fmn oxidoreductase like protein in complex2 with fmn (yp_544701.1) from methylobacillus flagellatus kt at 1.40 a3 resolution
6	d1ejea_	Alignment		57.5	14	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**NADH:FMN oxidoreductase-like
7	c3ibpA_	Alignment		35.8	22	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**chromosome partition protein mukb; **PDBTitle:** the crystal structure of the dimerization domain of escherichia coli2 structural maintenance of chromosomes protein mukb
8	c3fgeA_	Alignment		17.1	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative flavin reductase with split barrel domain; **PDBTitle:** crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution
9	c2k29A_	Alignment		16.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
10	c2iu6B_	Alignment		16.6	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dihydroxyacetone kinase; **PDBTitle:** regulation of the dha operon of lactococcus lactis
11	c2i46A_	Alignment		16.5	23	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**adrenocortical dysplasia protein homolog; **PDBTitle:** crystal structure of human tpp1

12	d1j98a_	Alignment		16.4	67	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
13	c1uv7A_	Alignment		15.8	10	**PDB header:**transport **Chain:** A: **PDB Molecule:**general secretion pathway protein m; **PDBTitle:** periplasmic domain of epsm from vibrio cholerae
14	d1uv7a_	Alignment		15.8	10	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**General secretion pathway protein M, EpsM **Family:**General secretion pathway protein M, EpsM
15	d1oi2a_	Alignment		15.7	26	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DAK1
16	c3ct4B_	Alignment		15.1	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pts-dependent dihydroxyacetone kinase, **PDBTitle:** structure of dha-kinase subunit dhak from l. lactis
17	d1vjea_	Alignment		15.1	56	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
18	c2pjpA_	Alignment		14.5	21	**PDB header:**translation/rna **Chain:** A: **PDB Molecule:**selenocysteine-specific elongation factor; **PDBTitle:** structure of the mrna-binding domain of elongation factor2 selb from e.coli in complex with secis rna
19	d1lvaa3	Alignment		14.5	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
20	d1un8a4	Alignment		14.2	19	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DAK1
21	d1h32a1	Alignment	not modelled	13.1	18	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c SoxA
22	d2bj7a1	Alignment	not modelled	12.5	19	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
23	d2ezwa1	Alignment	not modelled	12.4	28	**Fold:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Superfamily:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit **Family:**Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
24	c1iweB_	Alignment	not modelled	12.1	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** imp complex of the recombinant mouse-muscle2 adenylosuccinate synthetase
25	d1cf1a1	Alignment	not modelled	10.7	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Arrestin/Vps26-like
26	c2ixaA_	Alignment	not modelled	10.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
27	d1iwea_	Alignment	not modelled	9.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
28	c2b7fD_	Alignment	not modelled	9.4	23	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**htlv protease; **PDBTitle:** crystal structure of human t-cell leukemia virus protease, a novel2 target for anti-cancer design

29	c2wmmA_	Alignment	not modelled	9.2	25	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**chromosome partition protein mukb; **PDBTitle:** crystal structure of the hinge domain of mukb
30	d1p9ba_	Alignment	not modelled	9.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
31	c2rjzA_	Alignment	not modelled	9.1	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pilo protein; **PDBTitle:** crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
32	c3nuhB_	Alignment	not modelled	9.1	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
33	c3ip3D_	Alignment	not modelled	8.3	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
34	c1un9B_	Alignment	not modelled	8.1	19	**PDB header:**kinase **Chain:** B: **PDB Molecule:**dihydroxyacetone kinase; **PDBTitle:** crystal structure of the dihydroxyacetone kinase from c.2 freundii in complex with amp-pnp and mg2+
35	d1ldda_	Alignment	not modelled	7.8	35	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**SCF ubiquitin ligase complex WHB domain
36	d1kwga1	Alignment	not modelled	7.8	13	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
37	c5acnA_	Alignment	not modelled	7.0	18	**PDB header:**lyase(carbon-oxygen) **Chain:** A: **PDB Molecule:**aconitase; **PDBTitle:** structure of activated aconitase. formation of the (4fe-4s)2 cluster in the crystal
38	d1acoa2	Alignment	not modelled	7.0	18	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
39	d1g8fa3	Alignment	not modelled	6.9	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
40	c1ayrA_	Alignment	not modelled	6.8	12	**PDB header:**sensory transduction **Chain:** A: **PDB Molecule:**arrestin; **PDBTitle:** arrestin from bovine rod outer segments
41	d1vjja3	Alignment	not modelled	6.8	24	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
42	d2gaxa1	Alignment	not modelled	6.5	31	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
43	c2zjtB_	Alignment	not modelled	6.4	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit b; **PDBTitle:** crystal structure of dna gyrase b' domain sheds lights on2 the mechanism for t-segment navigation
44	d1qmga1	Alignment	not modelled	6.2	43	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Acetohydroxy acid isomeroreductase (ketol-acid reductoisomerase, KARI)
45	d1na6a1	Alignment	not modelled	5.9	33	**Fold:**DNA-binding pseudobarrel domain **Superfamily:**DNA-binding pseudobarrel domain **Family:**Type II restriction endonuclease effector domain
46	d3bvua3	Alignment	not modelled	5.9	19	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**alpha-mannosidase
47	d1ex0a3	Alignment	not modelled	5.9	21	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Transglutaminase, two C-terminal domains **Family:**Transglutaminase, two C-terminal domains
48	c2ow7A_	Alignment	not modelled	5.9	21	**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
49	c3fofD_	Alignment	not modelled	5.8	11	**PDB header:**isomerase/dna **Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit b; **PDBTitle:** structural insight into the quinolone-dna cleavage complex2 of type iia topoisomerases
50	d2hzab1	Alignment	not modelled	5.7	19	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**CopG-like
51	c3bnkB_	Alignment	not modelled	5.7	14	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoredoxin; **PDBTitle:** x-ray crystal structure of flavoredoxin from methanosarcina2 acetivorans
52	c1htyA_	Alignment	not modelled	5.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase ii; **PDBTitle:** golgi alpha-mannosidase ii
53	c2zkra_	Alignment	not modelled	5.6	18	**PDB header:**ribosomal protein/rna **Chain:** A: **PDB Molecule:**rna expansion segment es3; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
54	d1rl6a1	Alignment	not modelled	5.4	30	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6

55	d1vqoe1	Alignment	not modelled	5.3	26	**Fold:**Ribosomal protein L6 **Superfamily:**Ribosomal protein L6 **Family:**Ribosomal protein L6
56	c3r7tA_	Alignment	not modelled	5.1	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**adenylosuccinate synthetase; **PDBTitle:** crystal structure of adenylosuccinate synthetase from campylobacter2 jejuni