Phyre^2

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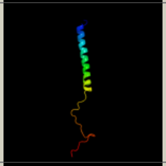
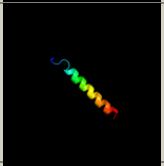
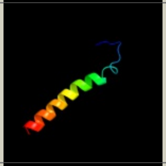
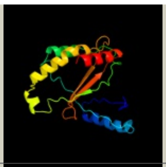
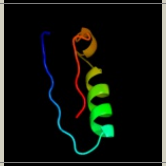
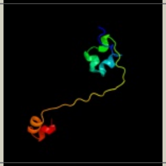
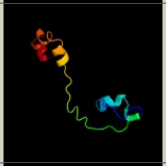
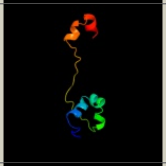
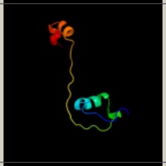
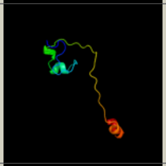
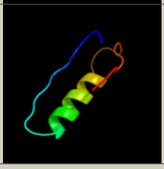
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2wx6B_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxidase ycdb; **PDBTitle:** x-ray crystallographic structure of e. coli apo-efeb
2	d2iiza1	Alignment		100.0	24	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Dyp-type peroxidase-like
3	d2gvka1	Alignment		100.0	20	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Dyp-type peroxidase-like
4	c3qnsA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dyp peroxidase; **PDBTitle:** dypb from rhodococcus jostii rha1, crystal form 2
5	d2d3qa1	Alignment		100.0	25	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Dyp-type peroxidase-like
6	c2e76D_	Alignment		89.5	11	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**cytochrome b6-f complex iron-sulfur subunit; **PDBTitle:** crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
7	c3nn4C_	Alignment		73.8	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**chlorite dismutase; **PDBTitle:** structure of chlorite dismutase from candidatus nitrospira defluvii2 r173k mutant
8	c1p84E_	Alignment		69.1	10	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
9	c2fynO_	Alignment		69.1	18	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
10	c2fyuE_	Alignment		68.7	12	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**ubiquinol-cytochrome c reductase iron-sulfur subunit, **PDBTitle:** crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
11	c2pq4B_	Alignment		53.6	21	**PDB header:**chaperone/oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic nitrate reductase precursor; **PDBTitle:** nmr solution structure of napd in complex with napa1-352 signal peptide

12	c2vxhF_	Alignment		47.4	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**chlorite dismutase; **PDBTitle:** the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
13	d1t0tv_	Alignment		36.3	21	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
14	c2hpgB_	Alignment		33.4	13	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding **PDBTitle:** the crystal structure of a thermophilic trap periplasmic2 binding protein
15	c3b0vD_	Alignment		33.3	17	**PDB header:**oxidoreductase/rna **Chain:** D: **PDB Molecule:**trna-dihydrouridine synthase; **PDBTitle:** trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
16	c2hzkB_	Alignment		25.0	14	**PDB header:**ligand binding, transport protein **Chain:** B: **PDB Molecule:**trap-t family sorbitol/mannitol transporter, periplasmic **PDBTitle:** crystal structures of a sodium-alpha-keto acid binding subunit from a2 trap transporter in its open form
17	c3b50A_	Alignment		24.3	16	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sialic acid-binding periplasmic protein siap; **PDBTitle:** structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
18	c2pfyA_	Alignment		24.1	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp7, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
19	c3gyyC_	Alignment		18.1	18	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**periplasmic substrate binding protein; **PDBTitle:** the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
20	d1vdha_	Alignment		18.0	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
21	c3fxbB_	Alignment	not modelled	17.3	16	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**trap dicarboxylate transporter, dctp subunit; **PDBTitle:** crystal structure of the ectoine-binding protein ueha
22	d1vjja1	Alignment	not modelled	15.5	35	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
23	d1g0da1	Alignment	not modelled	15.3	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
24	c3njqB_	Alignment	not modelled	14.8	25	**PDB header:**viral protein/inhibitor **Chain:** B: **PDB Molecule:**orf 17; **PDBTitle:** crystal structure of kaposi's sarcoma-associated herpesvirus protease2 in complex with dimer disruptor
25	d1kfia4	Alignment	not modelled	14.8	33	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
26	d2q3za1	Alignment	not modelled	14.6	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
27	d3pmga4	Alignment	not modelled	14.1	24	**Fold:**TBP-like **Superfamily:**Phosphoglucomutase, C-terminal domain **Family:**Phosphoglucomutase, C-terminal domain
28	c2r8kB_	Alignment	not modelled	12.9	6	**PDB header:**replication, transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase eta; **PDBTitle:** structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna
						Fold: Cytochrome c

29	d1nmla2	Alignment	not modelled	12.9	33	**Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
30	d1ex0a1	Alignment	not modelled	12.6	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Transglutaminase N-terminal domain
31	d1jiha2	Alignment	not modelled	12.1	6	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**Lesion bypass DNA polymerase (Y-family), catalytic domain
32	c2pfzA_	Alignment	not modelled	11.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of dctp6, a bordetella pertussis2 extracytoplasmic solute receptor binding pyroglutamic acid
33	d1uoua3	Alignment	not modelled	11.8	11	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
34	c1jihA_	Alignment	not modelled	11.7	6	**PDB header:**translation **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** yeast dna polymerase eta
35	d2pbka1	Alignment	not modelled	11.7	25	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
36	c3hq7A_	Alignment	not modelled	11.6	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** ccpa from g. sulfurreducens, g94k/k97q/r100i variant
37	c1yqmA_	Alignment	not modelled	11.3	17	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**n-glycosylase/dna lyase; **PDBTitle:** catalytically inactive human 8-oxoguanine glycosylase2 crosslinked to 7-deazaguanine containing dna
38	c2x29A_	Alignment	not modelled	11.0	25	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**tumor necrosis factor ligand superfamily member **PDBTitle:** crystal structure of human4-1bb ligand ectodomain
39	c2aq4A_	Alignment	not modelled	10.8	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** ternary complex of the catalytic core of rev1 with dna and dctp.
40	c2oh2B_	Alignment	not modelled	10.5	9	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase kappa; **PDBTitle:** ternary complex of human dna polymerase
41	d1tdja3	Alignment	not modelled	9.4	27	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**Allosteric threonine deaminase C-terminal domain
42	d1na6a1	Alignment	not modelled	9.4	40	**Fold:**DNA-binding pseudobarrel domain **Superfamily:**DNA-binding pseudobarrel domain **Family:**Type II restriction endonuclease effector domain
43	c3eq1A_	Alignment	not modelled	9.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**porphobilinogen deaminase; **PDBTitle:** the crystal structure of human porphobilinogen deaminase at2 2.8a resolution
44	d1at3a_	Alignment	not modelled	8.4	19	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
45	d2i09a2	Alignment	not modelled	7.9	21	**Fold:**DeoB insert domain-like **Superfamily:**DeoB insert domain-like **Family:**DeoB insert domain-like
46	c3gqcB_	Alignment	not modelled	7.8	9	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** structure of human rev1-dna-dntp ternary complex
47	c2p5xB_	Alignment	not modelled	7.8	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**n-acetylserotonin o-methyltransferase-like protein; **PDBTitle:** crystal structure of maf domain of human n-acetylserotonin o-2 methyltransferase-like protein
48	c3ps9A_	Alignment	not modelled	7.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of mnmc from e. coli
49	d1o6ea_	Alignment	not modelled	7.2	16	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
50	c3mr2A_	Alignment	not modelled	7.1	6	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase eta; **PDBTitle:** human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
51	c2vfyA_	Alignment	not modelled	6.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**akap18 delta; **PDBTitle:** akap18 delta central domain
52	c1nmlA_	Alignment	not modelled	6.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**di-haem cytochrome c peroxidase; **PDBTitle:** di-haemic cytochrome c peroxidase from pseudomonas nautica 617, form2 in (ph 4.0)
53	c2c1uB_	Alignment	not modelled	6.8	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**di-haem cytochrome c peroxidase; **PDBTitle:** crystal structure of the di-haem cytochrome c peroxidase2 from paracoccus pantotrophus - oxidised form
54	d1eb7a2	Alignment	not modelled	6.7	16	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
55	c3pt1A_	Alignment	not modelled	6.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0364 protein ymr027w; **PDBTitle:** structure of duf89 from saccharomyces cerevisiae co-crystallized with2 f6p.

56	c2e1aD_	Alignment	not modelled	6.6	11	**PDB header:**transcription **Chain:** D: **PDB Molecule:**75aa long hypothetical regulatory protein asnc; **PDBTitle:** crystal structure of ffrp-dm1
57	c1ko9A_	Alignment	not modelled	5.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**8-oxoguanine dna glycosylase; **PDBTitle:** native structure of the human 8-oxoguanine dna glycosylase2 hogg1
58	c2qdrA_	Alignment	not modelled	5.7	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative dioxygenase (npun_f5605) from nostoc2 punctiforme pcc 73102 at 2.60 a resolution
59	c3dtzB_	Alignment	not modelled	5.7	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative chlorite dismutase ta0507; **PDBTitle:** crystal structure of putative chlorite dismutase ta0507
60	c1cq0A_	Alignment	not modelled	5.6	78	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**protein (new hypothalamic neuropeptide/orexin- **PDBTitle:** solution structure of a human hypocretin-2/orexin-2 b'solution structure of a human hypocretin-2/orexin-b '
61	d1iega_	Alignment	not modelled	5.6	20	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
62	d2cg4a2	Alignment	not modelled	5.5	17	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Lrp/AsnC-like transcriptional regulator C-terminal domain
63	c1t94B_	Alignment	not modelled	5.3	9	**PDB header:**replication **Chain:** B: **PDB Molecule:**polymerase (dna directed) kappa; **PDBTitle:** crystal structure of the catalytic core of human dna2 polymerase kappa