Phyre^2

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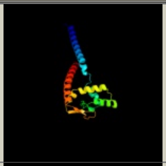
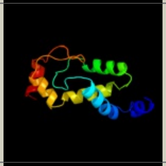
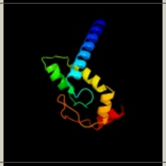
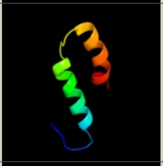
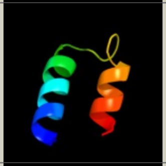
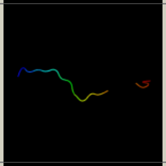
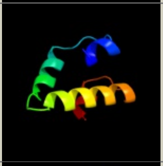
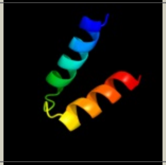
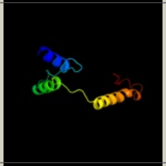
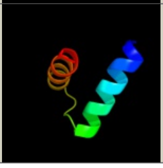
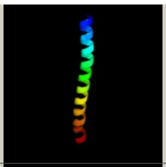
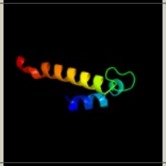
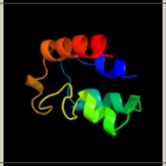
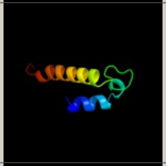
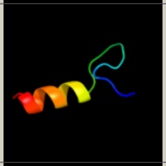
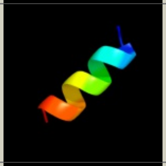
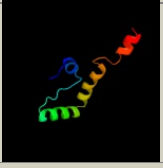
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1dvoa_	Alignment		100.0	97	**Fold:**FinO-like **Superfamily:**FinO-like **Family:**FinO-like
2	d2hxja1	Alignment		100.0	23	**Fold:**FinO-like **Superfamily:**FinO-like **Family:**FinO-like
3	c2hxjF_	Alignment		100.0	23	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a protein of unknown function nmb1681 from2 neisseria meningitidis mc58, possible nucleic acid binding protein
4	c2k19A_	Alignment		53.1	30	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**putative piscicolin 126 immunity protein; **PDBTitle:** nmr solution structure of pisi
5	c2zrrA_	Alignment		37.4	36	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**mundticin ks immunity protein; **PDBTitle:** crystal structure of an immunity protein that contributes2 to the self-protection of bacteriocin-producing3 enterococcus mundtii 15-1a
6	d2jdqd1	Alignment		26.1	37	**Fold:**PB2 C-terminal domain-like **Superfamily:**PB2 C-terminal domain-like **Family:**PB2 C-terminal domain-like
7	c2yicC_	Alignment		21.3	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of the suca domain of mycobacterium smegmatis2 alpha-ketoglutarate decarboxylase (triclinic form)
8	d2i5ua1	Alignment		14.1	15	**Fold:**DnaD domain-like **Superfamily:**DnaD domain-like **Family:**DnaD domain
9	c2w50B_	Alignment		13.4	9	**PDB header:**hormone **Chain:** B: **PDB Molecule:**armet-like protein 1; **PDBTitle:** n-terminal domain of human conserved dopamine neurotrophic2 factor (cdnf)
10	c2xt6B_	Alignment		12.4	17	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-oxoglutarate decarboxylase; **PDBTitle:** crystal structure of mycobacterium smegmatis alpha-ketoglutarate2 decarboxylase homodimer (orthorhombic form)
11	c2w51A_	Alignment		12.4	14	**PDB header:**hormone **Chain:** A: **PDB Molecule:**protein armet; **PDBTitle:** human mesencephalic astrocyte-derived neurotrophic factor (2 manf)

12	c3pp5A_	Alignment		12.3	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**brk1; **PDBTitle:** high-resolution structure of the trimeric scar/wave complex precursor2 brk1
13	d1b33a_	Alignment		12.1	17	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
14	c3mixA_	Alignment		12.1	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** crystal structure of the cytosolic domain of b. subtilis flha
15	c3a5iB_	Alignment		11.2	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** structure of the cytoplasmic domain of flha
16	c2kq6A_	Alignment		11.1	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**polycystin-2; **PDBTitle:** the structure of the ef-hand domain of polycystin-2 suggests a2 mechanism for ca2+-dependent regulation of polycystin-2 channel3 activity
17	d1alla_	Alignment		11.0	17	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
18	c1us2A_	Alignment		10.9	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-beta-1,4-xylanase; **PDBTitle:** xylanase10c (mutant e385a) from cellvibrio japonicus in2 complex with xylopentaose
19	d1qnta2	Alignment		10.7	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Methylated DNA-protein cysteine methyltransferase domain **Family:**Methylated DNA-protein cysteine methyltransferase domain
20	d1v4va_	Alignment		10.7	12	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
21	c3dv9A_	Alignment	not modelled	9.7	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**beta-phosphoglucomutase; **PDBTitle:** putative beta-phosphoglucomutase from bacteroides vulgatus.
22	d1qh8b_	Alignment	not modelled	9.6	15	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**Nitrogenase iron-molybdenum protein
23	d1kn1a_	Alignment	not modelled	9.4	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
24	d1cpcb_	Alignment	not modelled	9.1	23	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
25	c3aicC_	Alignment	not modelled	8.9	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**glucosyltransferase-si; **PDBTitle:** crystal structure of glucansucrase from streptococcus mutans
26	d1gjja2	Alignment	not modelled	8.9	29	**Fold:**LEM/SAP HeH motif **Superfamily:**LEM domain **Family:**LEM domain
27	d1xg0c_	Alignment	not modelled	8.8	21	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
28	c3mydA_	Alignment	not modelled	8.4	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**flagellar biosynthesis protein flha; **PDBTitle:** structure of the cytoplasmic domain of flha from helicobacter pylori
						Fold:DNA/RNA-binding 3-helical bundle

29	d1ka8a_	Alignment	not modelled	7.9	15	**Superfamily:**"Winged helix" DNA-binding domain **Family:**P4 origin-binding domain-like
30	c3hz3A_	Alignment	not modelled	7.6	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glucansucrase; **PDBTitle:** lactobacillus reuteri n-terminally truncated glucansucrase2 gtf180(d1025n)-sucrose complex
31	c4ktqA_	Alignment	not modelled	7.2	25	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (large fragment of dna polymerase i); **PDBTitle:** binary complex of the large fragment of dna polymerase i2 from t. aquaticus bound to a primer/template dna
32	d1s9aa_	Alignment	not modelled	6.8	3	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
33	c3hj8A_	Alignment	not modelled	6.8	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure determination of catechol 1,2-dioxygenase from2 rhodococcus opacus 1cp in complex with 4-chlorocatechol
34	c3s2xB_	Alignment	not modelled	6.7	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**acetyl-coa synthase subunit alpha; **PDBTitle:** structure of acetyl-coenzyme a synthase alpha subunit c-terminal2 domain
35	c1tmxA_	Alignment	not modelled	6.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hydroxyquinol 1,2-dioxygenase; **PDBTitle:** crystal structure of hydroxyquinol 1,2-dioxygenase from2 nocardioides simplex 3e
36	c2boyC_	Alignment	not modelled	6.4	7	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**3-chlorocatechol 1,2-dioxygenase; **PDBTitle:** crystal structure of 3-chlorocatechol 1,2-dioxygenase from2 rhodococcus opacus 1cp
37	c2c7jB_	Alignment	not modelled	6.4	21	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**phycoerythrocyanin beta chain; **PDBTitle:** phycoerythrocyanin from mastigocladus laminosus, 295 k,2 3.0 a
38	d1dmha_	Alignment	not modelled	6.4	10	**Fold:**Prealbumin-like **Superfamily:**Aromatic compound dioxygenase **Family:**Aromatic compound dioxygenase
39	c2azqA_	Alignment	not modelled	6.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catechol 1,2-dioxygenase; **PDBTitle:** crystal structure of catechol 1,2-dioxygenase from pseudomonas arvilla2 c-1
40	d2c7fa2	Alignment	not modelled	6.0	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
41	d2b1xa1	Alignment	not modelled	6.0	17	**Fold:**ISP domain **Superfamily:**ISP domain **Family:**Ring hydroxylating alpha subunit ISP domain
42	d2ijqa1	Alignment	not modelled	5.9	11	**Fold:**Hyaluronidase domain-like **Superfamily:**TTHA0068-like **Family:**TTHA0068-like
43	c2kpqA_	Alignment	not modelled	5.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of agrobacterium tumefaciens protein atu1219:2 northeast structural genomics consortium target att14
44	c2zc2A_	Alignment	not modelled	5.5	22	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnad-like replication protein; **PDBTitle:** crystal structure of dnad-like replication protein from2 streptococcus mutans ua159, gi 24377835, residues 127-199
45	c2vmlA_	Alignment	not modelled	5.5	17	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**phycocyanin alpha chain; **PDBTitle:** the monoclinic structure of phycocyanin from gloeobacter2 violaceus
46	d1ezfa_	Alignment	not modelled	5.5	26	**Fold:**Terpenoid synthases **Superfamily:**Terpenoid synthases **Family:**Squalene synthase
47	d1liab_	Alignment	not modelled	5.4	23	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins
48	d2ghra1	Alignment	not modelled	5.2	33	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
49	d1b8da_	Alignment	not modelled	5.2	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Phycocyanin-like phycobilisome proteins