Phyre^2

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Description	P33219
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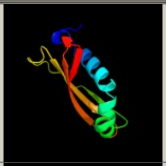
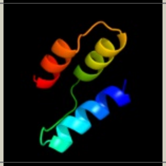
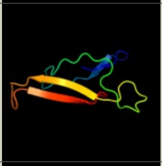
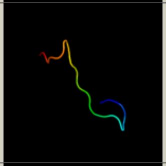
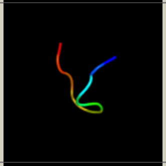
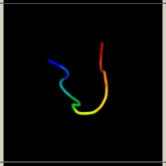
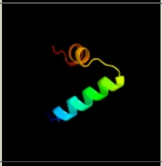
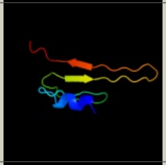
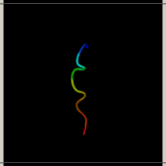
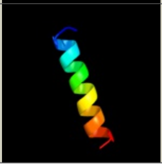
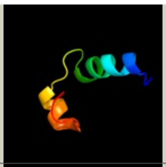
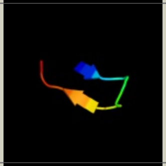
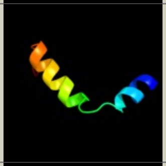
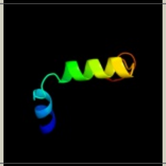
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xglB_	Alignment		100.0	26	**PDB header:**antibiotic **Chain:** B: **PDB Molecule:**colicin-m immunity protein; **PDBTitle:** the x-ray structure of the escherichia coli colicin m immunity2 protein demonstrates the presence of a disulphide bridge, which is3 functionally essential
2	c3dd7A_	Alignment		47.1	13	**PDB header:**ribosome inhibitor **Chain:** A: **PDB Molecule:**death on curing protein; **PDBTitle:** structure of doch66y in complex with the c-terminal domain of phd
3	d2nxyb2	Alignment		38.8	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C2 set domains
4	c3fsnA_	Alignment		25.1	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**retinal pigment epithelium-specific 65 kda protein; **PDBTitle:** crystal structure of rpe65 at 2.14 angstrom resolution
5	c2k87A_	Alignment		21.2	24	**PDB header:**viral protein, rna binding protein **Chain:** A: **PDB Molecule:**non-structural protein 3 of replicase polyprotein 1a; **PDBTitle:** nmr structure of a putative rna binding protein (sars1) from sars2 coronavirus
6	c2qh7A_	Alignment		19.3	40	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**zinc finger cdgsh-type domain 1; **PDBTitle:** mitoneet is a uniquely folded 2fe-2s outer mitochondrial membrane2 protein stabilized by pioglitazone
7	c3fnvB_	Alignment		18.8	50	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**cdgsh iron sulfur domain-containing protein 2; **PDBTitle:** crystal structure of miner1: the redox-active 2fe-2s protein causative2 in wolfram syndrome 2
8	d1wh6a_	Alignment		16.2	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
9	c2l25A_	Alignment		15.5	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** np_888769.1
10	c3iynR_	Alignment		14.4	40	**PDB header:**virus **Chain:** R: **PDB Molecule:**hexon-associated protein; **PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5
11	c3arcl_	Alignment		14.3	33	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution

12	d1s7ea2	Alignment		13.6	6	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
13	c3kfoA_	Alignment		13.1	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**nucleoporin nup133; **PDBTitle:** crystal structure of the c-terminal domain from the nuclear pore2 complex component nup133 from saccharomyces cerevisiae
14	d2csfa1	Alignment		13.0	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
15	d1o6ea_	Alignment		12.8	21	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
16	d1r17a1	Alignment		12.1	12	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**Bacterial adhesins **Family:**Fibrinogen-binding domain
17	d1fyhb2	Alignment		11.3	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
18	c2l9wA_	Alignment		10.4	12	**PDB header:**splicing, rna binding protein **Chain:** A: **PDB Molecule:**u4/u6 snrna-associated-splicing factor prp24; **PDBTitle:** solution structure of the c-terminal domain of prp24
19	d1iega_	Alignment		10.4	23	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
20	c3nqyA_	Alignment		9.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**secreted metalloprotease mcp02; **PDBTitle:** crystal structure of the autoprocessed complex of vibriolysin mcp-022 with a single point mutation e346a
21	d2pbka1	Alignment	not modelled	9.7	13	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
22	c2j0kB_	Alignment	not modelled	9.3	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**focal adhesion kinase 1; **PDBTitle:** crystal structure of a fragment of focal adhesion kinase2 containing the ferm and kinase domains.
23	d1at3a_	Alignment	not modelled	9.2	16	**Fold:**Herpes virus serine proteinase, assemblin **Superfamily:**Herpes virus serine proteinase, assemblin **Family:**Herpes virus serine proteinase, assemblin
24	c2eo1A_	Alignment	not modelled	9.0	22	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**cdna flj14124 fis, clone mamma1002498; **PDBTitle:** solution structure of the ig domain of human obscn protein
25	d1wh8a_	Alignment	not modelled	8.5	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
26	d1x2la1	Alignment	not modelled	8.1	26	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
27	c2druA_	Alignment	not modelled	7.9	8	**PDB header:**immune system **Chain:** A: **PDB Molecule:**chimera of cd48 antigen and t-cell surface antigen cd2; **PDBTitle:** crystal structure and binding properties of the cd2 and cd244 (2b4)2 binding protein, cd48
28	c3p02A_	Alignment	not modelled	7.8	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein of unknown function (bacova 00267) from2 bacteroides ovatus at 1.55 a resolution

29	d1vcaa2	Alignment	not modelled	7.6	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
30	d1biha3	Alignment	not modelled	7.5	5	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
31	c2yqeA_	Alignment	not modelled	6.8	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**jumonji/arid domain-containing protein 1d; **PDBTitle:** solution structure of the arid domain of jarid1d protein
32	c2axtl_	Alignment	not modelled	6.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
33	c3a0bL_	Alignment	not modelled	6.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
34	c3arcL_	Alignment	not modelled	6.5	33	**PDB header:**electron transport, photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
35	c3a0bl_	Alignment	not modelled	6.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
36	c3bz1L_	Alignment	not modelled	6.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
37	c2axtL_	Alignment	not modelled	6.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** crystal structure of photosystem ii from thermosynechococcus elongatus
38	c3prrL_	Alignment	not modelled	6.5	33	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 2 of 2). this file contains second monomer of psii3 dimer
39	c3bz2L_	Alignment	not modelled	6.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 22 of 2). this file contains second monomer of psii dimer
40	c1s5lL_	Alignment	not modelled	6.5	33	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
41	c3prqL_	Alignment	not modelled	6.5	33	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of cyanobacterial photosystem ii in complex with2 terbutryn (part 1 of 2). this file contains first monomer of psii3 dimer
42	c3kziL_	Alignment	not modelled	6.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of monomeric form of cyanobacterial photosystem ii
43	c3a0hl_	Alignment	not modelled	6.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
44	d2axtl1	Alignment	not modelled	6.5	33	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction center protein L, PsbL **Family:**PsbL-like
45	c1s5ll_	Alignment	not modelled	6.5	33	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem ii reaction center l protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
46	c3a0hL_	Alignment	not modelled	6.5	33	**PDB header:**electron transport **Chain:** L: **PDB Molecule:**photosystem ii reaction center protein l; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
47	c3h6sE_	Alignment	not modelled	6.5	18	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** E: **PDB Molecule:**clitocypin analog; **PDBTitle:** strucure of clitocypin - cathepsin v complex
48	c2dkuA_	Alignment	not modelled	6.3	15	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**kiaa1556 protein; **PDBTitle:** solution structure of the third ig-like domain of human2 kiaa1556 protein
49	c3nqkA_	Alignment	not modelled	6.3	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a structural genomics, unknown function2 (bacova_03322) from bacteroides ovatus at 2.61 a resolution
50	c3ts7B_	Alignment	not modelled	6.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**geranyltranstransferase; **PDBTitle:** crystal structure of farnesyl diphosphate synthase (target efi-501951)2 from methylococcus capsulatus
51	c3epzA_	Alignment	not modelled	5.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna (cytosine-5)-methyltransferase 1; **PDBTitle:** structure of the replication foci-targeting sequence of human dna2 cytosine methyltransferase dnmt1
52	d1tdpa_	Alignment	not modelled	5.7	14	**Fold:**Bromodomain-like **Superfamily:**Bacteriocin immunity protein-like **Family:**Carnobacteriocin B2 immunity protein
53	d2cs7a1	Alignment	not modelled	5.6	38	**Fold:**IL8-like **Superfamily:**PhtA domain-like **Family:**PhtA domain-like
54	c2q97T_	Alignment	not modelled	5.4	24	**PDB header:**structural protein/cell invasion **Chain:** T: **PDB Molecule:**toxofilin; **PDBTitle:** complex of mammalian actin with toxofilin from

						toxoplasma gondii
55	c3rjoA_	Alignment	not modelled	5.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endoplasmic reticulum aminopeptidase 1; **PDBTitle:** crystal structure of erap1 peptide binding domain
56	d1gpja3	Alignment	not modelled	5.2	25	**Fold:**Ferredoxin-like **Superfamily:**Glutamyl tRNA-reductase catalytic, N-terminal domain **Family:**Glutamyl tRNA-reductase catalytic, N-terminal domain
57	d1ni5a3	Alignment	not modelled	5.2	17	**Fold:**PheT/TilS domain **Superfamily:**PheT/TilS domain **Family:**tRNA-Ile-lysidine synthetase, TilS, C-terminal domain
58	c2cpcA_	Alignment	not modelled	5.2	11	**PDB header:**immune system **Chain:** A: **PDB Molecule:**kiaa0657 protein; **PDBTitle:** solution structure of rsgi ruh-030, an ig like domain from2 human cdna