Phyre^2

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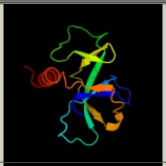
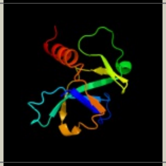
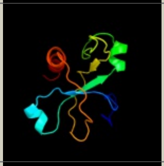
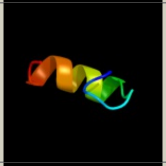
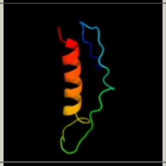
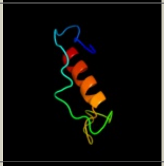
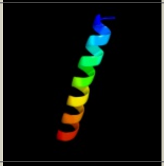
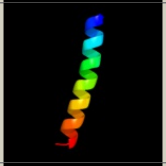
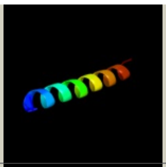
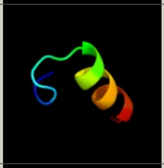
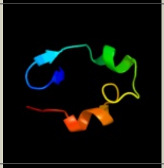
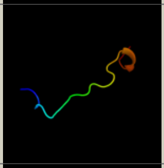
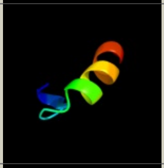
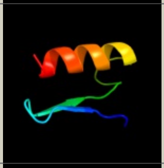
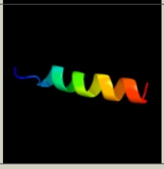
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3vuba_	Alignment		100.0	100	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**CcdB
2	c3jrzA_	Alignment		100.0	42	**PDB header:**toxin **Chain:** A: **PDB Molecule:**ccdb; **PDBTitle:** ccdbvfi-formii-ph5.6
3	d1ub4a_	Alignment		95.5	13	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
4	d1m1fa_	Alignment		90.4	8	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
5	d1ne8a_	Alignment		89.9	11	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Kid/PemK
6	d1ifya_	Alignment		29.8	26	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
7	c3l9vE_	Alignment		28.9	8	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative thiol-disulfide isomerase or thioredoxin; **PDBTitle:** crystal structure of salmonella enterica serovar typhimurium srga
8	d1fvka_	Alignment		24.4	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
9	c1mofA_	Alignment		17.8	20	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**moloney murine leukemia virus p15; **PDBTitle:** coat protein
10	c1y4mC_	Alignment		17.1	8	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**herv-frd_6p24.1 provirus ancestral env polyprotein; **PDBTitle:** crystal structure of human endogenous retrovirus herv-frd envelope2 protein (syncitin-2)
11	d2bwba1	Alignment		16.5	17	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain

12	c2eboB_	Alignment		16.0	12	**PDB header:**envelope glycoprotein **Chain:** B: **PDB Molecule:**ebola virus envelope glycoprotein; **PDBTitle:** core structure of gp2 from ebola virus
13	c1wr1B_	Alignment		15.8	17	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**ubiquitin-like protein dsk2; **PDBTitle:** the complex sturcture of dsk2p uba with ubiquitin
14	d1exbe_	Alignment		13.5	14	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
15	c2cwbA_	Alignment		11.1	39	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**chimera of immunoglobulin g binding protein g **PDBTitle:** solution structure of the ubiquitin-associated domain of2 human bmsc-ubp and its complex with ubiquitin
16	c2wtaA_	Alignment		10.2	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** acinetobacter baumanii nicotinamidase pyrazinamidease
17	c2jy5A_	Alignment		9.7	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ubiquilin-1; **PDBTitle:** nmr structure of ubiquilin 1 uba domain
18	c3h93A_	Alignment		9.2	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of pseudomonas aeruginosa dsba
19	d2v8qa1	Alignment		8.7	21	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Ssp2 C-terminal domain-like
20	d1q1va_	Alignment		8.6	25	**Fold:**Another 3-helical bundle **Superfamily:**DEK C-terminal domain **Family:**DEK C-terminal domain
21	d3kvta_	Alignment	not modelled	8.4	7	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
22	c1eboE_	Alignment	not modelled	8.3	9	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**ebola virus envelope protein chimera consisting **PDBTitle:** crystal structure of the ebola virus membrane-fusion2 subunit, gp2, from the envelope glycoprotein ectodomain
23	c3lqyA_	Alignment	not modelled	7.7	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative isochorismatase hydrolase; **PDBTitle:** crystal structure of putative isochorismatase hydrolase from2 oleispira antarctica
24	d1nf9a_	Alignment	not modelled	7.4	21	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
25	c3mcwA_	Alignment	not modelled	7.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of an a putative hydrolase of the isochorismatase2 family (cv_1320) from chromobacterium violaceum atcc 12472 at 1.06 a3 resolution
26	c2a67C_	Alignment	not modelled	7.0	29	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**isochorismatase family protein; **PDBTitle:** crystal structure of isochorismatase family protein
27	d1t1da_	Alignment	not modelled	6.7	12	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
28	d1nn7a_	Alignment	not modelled	6.7	12	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels

29	c1hynQ_	Alignment	not modelled	6.5	8	**PDB header:**membrane protein **Chain:** Q: **PDB Molecule:**band 3 anion transport protein; **PDBTitle:** crystal structure of the cytoplasmic domain of human2 erythrocyte band-3 protein
30	d1nbaa_	Alignment	not modelled	6.3	6	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
31	c3feuA_	Alignment	not modelled	6.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
32	d1dsxa_	Alignment	not modelled	6.1	19	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
33	d1hynp_	Alignment	not modelled	6.1	8	**Fold:**Phoshotransferase/anion transport protein **Superfamily:**Phoshotransferase/anion transport protein **Family:**Anion transport protein, cytoplasmic domain
34	d1b7yb4	Alignment	not modelled	6.1	10	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
35	d2qrda1	Alignment	not modelled	5.8	20	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Ssp2 C-terminal domain-like
36	c1dpuA_	Alignment	not modelled	5.7	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication protein a (rpa32) c-terminal domain; **PDBTitle:** solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
37	d1dpua_	Alignment	not modelled	5.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
38	d1s1ga_	Alignment	not modelled	5.7	15	**Fold:**POZ domain **Superfamily:**POZ domain **Family:**Tetramerization domain of potassium channels
39	c3oqpB_	Alignment	not modelled	5.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative isochorismatase; **PDBTitle:** crystal structure of a putative isochorismatase (bxe_a0706) from2 burkholderia xenovorans lb400 at 1.22 a resolution
40	c2wsfH_	Alignment	not modelled	5.4	32	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**photosystem i reaction center subunit vi, **PDBTitle:** improved model of plant photosystem i
41	c3lw5H_	Alignment	not modelled	5.4	28	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** improved model of plant photosystem i
42	d1jjcb4	Alignment	not modelled	5.4	10	**Fold:**Ferredoxin-like **Superfamily:**Anticodon-binding domain of PheRS **Family:**Anticodon-binding domain of PheRS
43	c2h0rD_	Alignment	not modelled	5.3	42	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**nicotinamidase; **PDBTitle:** structure of the yeast nicotinamidase pnc1p
44	d1ev7a_	Alignment	not modelled	5.2	13	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease NaeI