Phyre^2

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Description	P52129
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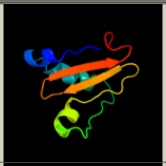
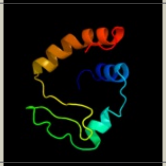
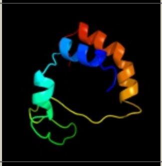
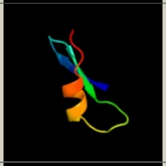
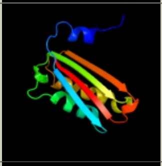
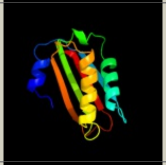
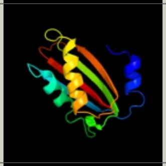
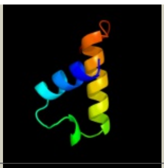
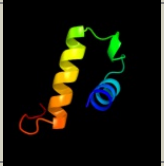
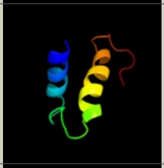
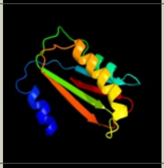
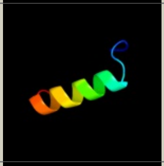
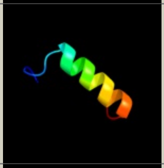
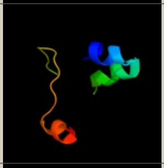
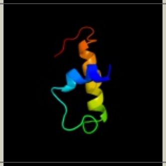
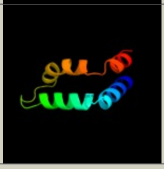
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2d0bA_	Alignment		69.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribonuclease hiii; **PDBTitle:** crystal structure of bst-rnase hiii in complex with mg2+
2	c1bo1A_	Alignment		57.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (phosphatidylinositol phosphate kinase **PDBTitle:** phosphatidylinositol phosphate kinase type ii beta
3	d1bo1a_	Alignment		57.4	17	**Fold:**SAICAR synthase-like **Superfamily:**SAICAR synthase-like **Family:**Phosphatidylinositol phosphate kinase IIbeta, PIPK IIbeta
4	c2gk9D_	Alignment		43.7	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**phosphatidylinositol-4-phosphate 5-kinase, type **PDBTitle:** human phosphatidylinositol-4-phosphate 5-kinase, type ii,2 gamma
5	d2vapa2	Alignment		35.9	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
6	c1ofuB_	Alignment		33.3	17	**PDB header:**bacterial cell division inhibitor **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of sula:ftsz from pseudomonas aeruginosa
7	d2ix0a3	Alignment		32.9	32	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
8	c2q1yB_	Alignment		30.0	17	**PDB header:**cell cycle, signaling protein **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** crystal structure of cell division protein ftsz from mycobacterium2 tuberculosis in complex with gtp-gamma-s
9	c2vawA_	Alignment		28.0	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** ftsz pseudomonas aeruginosa gdp
10	c2r6r1_	Alignment		24.9	12	**PDB header:**cell cycle **Chain:** 1: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** aquifex aeolicus ftsz
11	c2vxyA_	Alignment		22.9	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** the structure of ftsz from bacillus subtilis at 1.7a2 resolution

12	d1eyva_	Alignment		22.5	14	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**Antitermination factor NusB
13	c1eyvA_	Alignment		22.5	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n-utilizing substance protein b homolog; **PDBTitle:** the crystal structure of nusb from mycobacterium2 tuberculosis
14	c2jr0A_	Alignment		19.2	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**n utilization substance protein b homolog; **PDBTitle:** solution structure of nusb from aquifex aeolicus
15	d1w5fa2	Alignment		16.0	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**Tubulin C-terminal domain-like **Family:**Tubulin, C-terminal domain
16	d1dpua_	Alignment		15.5	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal domain of RPA32
17	c1dpuA_	Alignment		15.5	23	**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)
18	d2doaa1	Alignment		15.4	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**ELL N2 domain-like
19	d1ey1a_	Alignment		15.2	11	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**Antitermination factor NusB
20	c3fwcO_	Alignment		14.8	18	**PDB header:**cell cycle, transcription **Chain:** O: **PDB Molecule:**protein sus1; **PDBTitle:** sac3:sus1:cdc31 complex
21	c2kdxA_	Alignment	not modelled	14.3	9	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
22	d1tzva_	Alignment	not modelled	14.1	14	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**Antitermination factor NusB
23	c2rhoB_	Alignment	not modelled	13.1	16	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division protein ftsz; **PDBTitle:** synthetic gene encoded bacillus subtilis ftsz ncs dimer with2 bound gdp and gtp-gamma-s
24	c2cw1A_	Alignment	not modelled	13.0	20	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**sn4m; **PDBTitle:** solution structure of the de novo-designed lambda cro fold2 protein
25	d2yt9a2	Alignment	not modelled	12.9	40	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
26	c3f62A_	Alignment	not modelled	11.9	13	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**interleukin 18 binding protein; **PDBTitle:** crystal structure of human il-18 in complex with ectromelia virus il-2 18 binding protein
27	c3al3A_	Alignment	not modelled	11.6	7	**PDB header:**dna binding protein/protein binding **Chain:** A: **PDB Molecule:**dna topoisomerase 2-binding protein 1; **PDBTitle:** crystal structure of topbp1 brct7/8-bach1 peptide complex
28	d1vela_	Alignment	not modelled	10.6	14	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
						Fold:DNA/RNA-binding 3-helical bundle

29	d2bbya_	Alignment	not modelled	10.2	26	**Superfamily:**"Winged helix" DNA-binding domain **Family:**DNA-binding domain from rap30
30	d1vh8a_	Alignment	not modelled	9.9	15	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
31	d1vmea1	Alignment	not modelled	9.8	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
32	d2v4jb2	Alignment	not modelled	9.2	13	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**DsrA/DsrB N-terminal-domain-like
33	d1aopa2	Alignment	not modelled	8.9	13	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
34	c2wscL_	Alignment	not modelled	8.2	29	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem i reaction center subunit xi, **PDBTitle:** improved model of plant photosystem i
35	d1zq1c2	Alignment	not modelled	7.7	22	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
36	d1jb0l_	Alignment	not modelled	7.5	36	**Fold:**Photosystem I reaction center subunit XI, PsaL **Superfamily:**Photosystem I reaction center subunit XI, PsaL **Family:**Photosystem I reaction center subunit XI, PsaL
37	c1w59B_	Alignment	not modelled	7.2	18	**PDB header:**cell division **Chain:** B: **PDB Molecule:**cell division protein ftsz homolog 1; **PDBTitle:** ftsz dimer, empty (m. jannaschii)
38	d2cufa1	Alignment	not modelled	6.8	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
39	d1sqga1	Alignment	not modelled	6.7	19	**Fold:**NusB-like **Superfamily:**NusB-like **Family:**RmsB N-terminal domain-like
40	c3m05A_	Alignment	not modelled	6.7	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pepe_1480; **PDBTitle:** the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745
41	c3h0dB_	Alignment	not modelled	6.7	32	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**ctsr; **PDBTitle:** crystal structure of ctsr in complex with a 26bp dna duplex
42	c2kokA_	Alignment	not modelled	6.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** solution structure of an arsenate reductase (arsc) related protein2 from brucella melitensis. seattle structural genomics center for3 infectious disease target braba.00007.a.
43	c2v6xA_	Alignment	not modelled	6.6	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** stractural insight into the interaction between escrt-iii2 and vps4
44	c2e5nA_	Alignment	not modelled	6.6	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase ii elongation factor ell2; **PDBTitle:** solution structure of the ell_n2 domain of target of rna2 polymerase ii elongation factor ell2
45	c2da2A_	Alignment	not modelled	6.5	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**alpha-fetoprotein enhancer binding protein; **PDBTitle:** solution structure of the second homeobox domain of at-2 binding transcription factor 1 (atbf1)
46	c3sb1B_	Alignment	not modelled	6.2	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hydrogenase expression protein; **PDBTitle:** hydrogenase expression protein huph from thiobacillus denitrificans2 atcc 25259
47	d2onka1	Alignment	not modelled	6.1	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
48	d2d6fc2	Alignment	not modelled	6.0	20	**Fold:**DCoH-like **Superfamily:**GAD domain-like **Family:**GAD domain
49	d1q40b_	Alignment	not modelled	5.9	12	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**NTF2-like
50	c2o01L_	Alignment	not modelled	5.9	29	**PDB header:**photosynthesis **Chain:** L: **PDB Molecule:**photosystem i reaction center subunit xi, **PDBTitle:** the structure of a plant photosystem i supercomplex at 3.42 angstrom resolution
51	d2p02a3	Alignment	not modelled	5.5	23	**Fold:**S-adenosylmethionine synthetase **Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
52	d2c5lc1	Alignment	not modelled	5.4	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
53	c2vdwB_	Alignment	not modelled	5.3	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mrna-capping enzyme small subunit; **PDBTitle:** guanosine n7 methyl-transferase sub-complex (d1-d12) of the2 vaccinia virus mrna capping enzyme
54	c3e5aB_	Alignment	not modelled	5.3	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**targeting protein for xklp2; **PDBTitle:** crystal structure of aurora a in complex with vx-680 and tpx2
						Fold:S-adenosylmethionine synthetase

55	d1qm4a3	Alignment	not modelled	5.2	23	**Superfamily:**S-adenosylmethionine synthetase **Family:**S-adenosylmethionine synthetase
56	c2wukD_	Alignment	not modelled	5.2	16	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**septum site-determining protein diviva; **PDBTitle:** diviva n-terminal domain, f17a mutant
57	c2hsbA_	Alignment	not modelled	5.1	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0332 protein af0298; **PDBTitle:** crystal structure of a hepn domain containing protein (af_0298) from2 archaeoglobus fulgidus at 1.95 a resolution
58	d1lfba_	Alignment	not modelled	5.1	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
59	d1t01a1	Alignment	not modelled	5.0	14	**Fold:**Four-helical up-and-down bundle **Superfamily:**alpha-catenin/vinculin-like **Family:**alpha-catenin/vinculin