Phyre^2

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Description	A5A605
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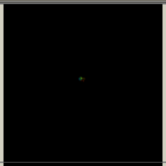
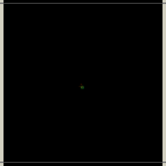
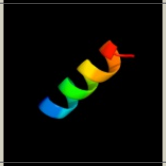
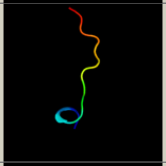
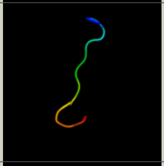
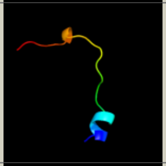
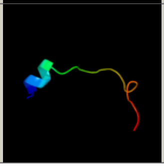
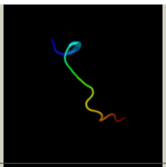
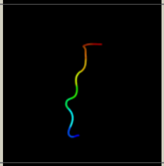
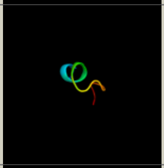
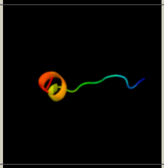
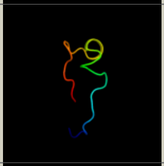
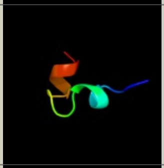
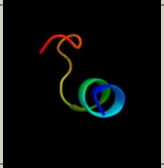
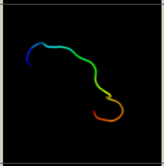
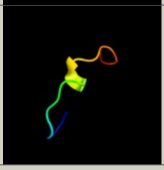
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3izci_	Alignment		46.1	35	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein rpl10 (l10e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
2	c3iz5i_	Alignment		36.8	37	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l10 (l10e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
3	c4a19L_	Alignment		32.2	40	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**rpl34; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
4	c2xcqA_	Alignment		28.0	38	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.98a crystal structure of the catalytic core (b'a'2 region) of staphylococcus aureus dna gyrase
5	c2xcsD_	Alignment		26.7	38	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna gyrase subunit b, dna gyrase subunit a; **PDBTitle:** the 2.1a crystal structure of s. aureus gyrase complex with gsk2994232 and dna
6	d1zpsa1	Alignment		23.6	23	**Fold:**HisI-like **Superfamily:**HisI-like **Family:**HisI-like
7	d1gpea2	Alignment		22.1	21	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GMC oxidoreductases
8	c2wl2B_	Alignment		22.1	44	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** crystal structure of n-terminal domain of gyra with the2 antibiotic simocyclinone d8
9	c1mv3A_	Alignment		21.6	21	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**myc box dependent interacting protein 1; **PDBTitle:** nmr structure of the tumor suppressor bin1: alternative2 splicing in melanoma and interaction with c-myc
10	d1qhma_	Alignment		20.0	27	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like
11	d1h16a_	Alignment		19.3	27	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**PFL-like

12	d1cf3a2	Alignment		17.9	29	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GMC oxidoreductases
13	c2kl7A_	Alignment		15.5	60	**PDB header:**signaling protein, structural protein **Chain:** A: **PDB Molecule:**fibulin-4; **PDBTitle:** solution nmr structure of the egf-like 1 domain of human2 fibulin-4. northeast structural genomics target hr6275
14	d1ab4a_	Alignment		15.3	44	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
15	c1wkwB_	Alignment		14.9	40	**PDB header:**translation/protein binding **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 4e **PDBTitle:** crystal structure of the ternary complex of eif4e-m7gpppa-2 4ebp1 peptide
16	d1p9ja_	Alignment		13.1	17	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**EGF/Laminin **Family:**EGF-type module
17	d2awia1	Alignment		11.9	42	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**PrgX N-terminal domain-like
18	c2novD_	Alignment		11.4	31	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** breakage-reunion domain of s.pneumoniae topo iv: crystal2 structure of a gram-positive quinolone target
19	c2jxbA_	Alignment		10.4	36	**PDB header:**signaling protein complex **Chain:** A: **PDB Molecule:**t-cell surface glycoprotein cd3 epsilon chain, **PDBTitle:** structure of cd3epsilon-nck2 first sh3 domain complex
20	c2dlpA_	Alignment		10.3	36	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**kiaa1783 protein; **PDBTitle:** solution structure of the sh3 domain of human kiaa17832 protein
21	d1hlya_	Alignment	not modelled	9.6	60	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
22	d1vh4a_	Alignment	not modelled	9.1	15	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Stabilizer of iron transporter SufD **Family:**Stabilizer of iron transporter SufD
23	d1awwa_	Alignment	not modelled	8.7	21	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
24	d1qlya_	Alignment	not modelled	7.7	21	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
25	d1ju2a2	Alignment	not modelled	7.6	22	**Fold:**FAD-linked reductases, C-terminal domain **Superfamily:**FAD-linked reductases, C-terminal domain **Family:**GMC oxidoreductases
26	c1jdmA_	Alignment	not modelled	7.5	41	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**sarcolipin; **PDBTitle:** nmr structure of sarcolipin
27	c3u7xC_	Alignment	not modelled	7.2	46	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic translation initiation factor 4e-binding protein **PDBTitle:** crystal structure of the human eif4e-4ebp1 peptide complex without cap
28	c3smuC_	Alignment	not modelled	7.2	46	**PDB header:**translation **Chain:** C: **PDB Molecule:**eukaryotic translation initiation factor 4e-binding protein **PDBTitle:** crystal structure of the human eif4e-4ebp1 peptide complex without cap

29	c3u7xD_	Alignment	not modelled	7.2	46	**PDB header:**translation **Chain:** D: **PDB Molecule:**eukaryotic translation initiation factor 4e-binding protein **PDBTitle:** crystal structure of the human eif4e-4ebp1 peptide complex without cap
30	c3smuD_	Alignment	not modelled	7.2	46	**PDB header:**translation **Chain:** D: **PDB Molecule:**eukaryotic translation initiation factor 4e-binding protein **PDBTitle:** crystal structure of the human eif4e-4ebp1 peptide complex without cap
31	c1x6bA_	Alignment	not modelled	7.2	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**rho guanine exchange factor (gef) 16; **PDBTitle:** solution structures of the sh3 domain of human rho guanine2 exchange factor (gef) 16
32	c2j06B_	Alignment	not modelled	6.3	6	**PDB header:**signal transduction **Chain:** B: **PDB Molecule:**ras gtpase-activating protein 1; **PDBTitle:** crystal structure of the rasgap sh3 domain at 1.8 angstrom2 resolution
33	c2a28D_	Alignment	not modelled	6.0	43	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**bzz1 protein; **PDBTitle:** atomic-resolution crystal structure of the second sh32 domain of yeast bzz1 determined from a pseudomerohedrally3 twinned crystal
34	d1wt8a1	Alignment	not modelled	6.0	63	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
35	c2oa9B_	Alignment	not modelled	6.0	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**r.mvai; **PDBTitle:** restriction endonuclease mvai in the absence of dna
36	c3n7sB_	Alignment	not modelled	5.9	56	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**calcitonin gene-related peptide type 1 receptor; **PDBTitle:** crystal structure of the ectodomain complex of the cgrp receptor, a2 class-b gpcr, reveals the site of drug antagonism
37	d2hf5a1	Alignment	not modelled	5.6	67	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
38	c2drmB_	Alignment	not modelled	5.6	29	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**acanthamoeba myosin ib; **PDBTitle:** acanthamoeba myosin i sh3 domain bound to acan125
39	c2kdcC_	Alignment	not modelled	5.6	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
40	d2dmda2	Alignment	not modelled	5.5	28	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
41	c2axkA_	Alignment	not modelled	5.4	55	**PDB header:**toxin **Chain:** A: **PDB Molecule:**discrepin; **PDBTitle:** solution structure of discrepin, a scorpion venom toxin2 blocking k+ channels.
42	c1griA_	Alignment	not modelled	5.1	43	**PDB header:**signal transduction adaptor **Chain:** A: **PDB Molecule:**growth factor bound protein 2; **PDBTitle:** grb2