Phyre^2

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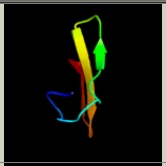
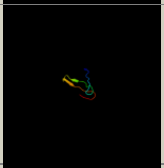
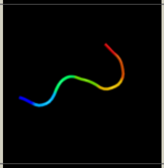
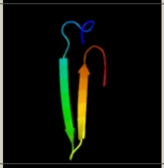
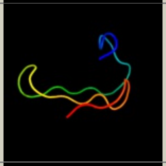
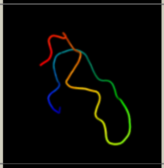
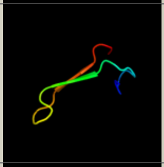
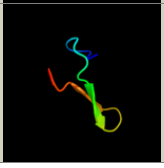
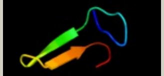
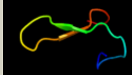
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nuiA_	Alignment		68.9	32	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna primase/helicase; **PDBTitle:** crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
2	d1wiia_	Alignment		54.8	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
3	c2dcuB_	Alignment		46.2	31	**PDB header:**translation **Chain:** B: **PDB Molecule:**translation initiation factor 2 beta subunit; **PDBTitle:** crystal structure of translation initiation factor aif2betagamma2 heterodimer with gdp
4	d2drpa2	Alignment		45.7	86	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
5	d1k81a_	Alignment		45.2	25	**Fold:**Zinc-binding domain of translation initiation factor 2 beta **Superfamily:**Zinc-binding domain of translation initiation factor 2 beta **Family:**Zinc-binding domain of translation initiation factor 2 beta
6	c2au3A_	Alignment		44.6	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna primase; **PDBTitle:** crystal structure of the aquifex aeolicus primase (zinc binding and2 rna polymerase domains)
7	c1neeA_	Alignment		42.4	21	**PDB header:**translation **Chain:** A: **PDB Molecule:**probable translation initiation factor 2 beta **PDBTitle:** structure of archaeal translation factor aif2beta from2 methanobacterium thermoautrophicum
8	c3cw2M_	Alignment		39.9	21	**PDB header:**translation **Chain:** M: **PDB Molecule:**translation initiation factor 2 subunit beta; **PDBTitle:** crystal structure of the intact archaeal translation2 initiation factor 2 from sulfolobus solfataricus .
9	d1d0qa_	Alignment		39.6	42	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**DNA primase zinc finger
10	c4a17Y_	Alignment		36.4	35	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**rpl37a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
11	d1vqoz1	Alignment		36.2	25	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae

12	d2fiya1	Alignment		35.5	29	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
13	c1yshD_	Alignment		35.0	33	**PDB header:**structural protein/rna **Chain:** D: **PDB Molecule:**ribosomal protein l37a; **PDBTitle:** localization and dynamic behavior of ribosomal protein l30e
14	c2yrmA_	Alignment		34.5	37	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**b-cell lymphoma 6 protein; **PDBTitle:** solution structure of the 1st zf-c2h2 domain from human b-2 cell lymphoma 6 protein
15	c2zkrz_	Alignment		34.4	25	**PDB header:**ribosomal protein/rna **Chain:** Z: **PDB Molecule:**e site t-rna; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
16	d1jj2y_	Alignment		33.8	22	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
17	c2e9hA_	Alignment		33.3	25	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** solution structure of the eif-5_eif-2b domain from human2 eukaryotic translation initiation factor 5
18	c2qa4Z_	Alignment		33.1	25	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
19	c1nnjA_	Alignment		31.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure complex between the lactococcus lactis fpg and an2 abasic site containing dna
20	d1ffkw_	Alignment		31.9	29	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L37ae
21	c3cc4Z_	Alignment	not modelled	29.6	25	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**50s ribosomal protein l37ae; **PDBTitle:** co-crystal structure of anisomycin bound to the 50s ribosomal subunit
22	c1s1i9_	Alignment	not modelled	28.2	29	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
23	c3jyw9_	Alignment	not modelled	27.7	29	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**60s ribosomal protein l43; **PDBTitle:** structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
24	c3hi2C_	Alignment	not modelled	26.2	57	**PDB header:**dna binding protein/toxin **Chain:** C: **PDB Molecule:**hth-type transcriptional regulator mqsa(ygit); **PDBTitle:** structure of the n-terminal domain of the e. coli antitoxin mqsa2 (ygit/b3021) in complex with the e. coli toxin mqsr (ygiu/b3022)
25	c1x31D_	Alignment	not modelled	26.0	67	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**sarcosine oxidase delta subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
26	c3eswA_	Alignment	not modelled	25.9	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
27	d1wd2a_	Alignment	not modelled	25.2	45	**Fold:**RING/U-box **Superfamily:**RING/U-box **Family:**RING finger domain, C3HC4

28	c3k7aM_	Alignment	not modelled	24.1	19	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
29	d1g6ma_	Alignment	not modelled	23.7	100	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
30	c2kdxA_	Alignment	not modelled	22.3	21	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**hydrogenase/urease nickel incorporation protein **PDBTitle:** solution structure of hypa protein
31	d1v6pa_	Alignment	not modelled	21.7	100	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
32	d1x3za1	Alignment	not modelled	21.2	27	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
33	c1k82D_	Alignment	not modelled	21.2	33	**PDB header:**hydrolase/dna **Chain:** D: **PDB Molecule:**formamidopyrimidine-dna glycosylase; **PDBTitle:** crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
34	d1pfta_	Alignment	not modelled	20.3	22	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
35	c2gb5B_	Alignment	not modelled	18.6	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
36	c2kvgA_	Alignment	not modelled	18.5	78	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger and btb domain-containing protein 32; **PDBTitle:** structure of the three-cys2his2 domain of mouse testis zinc2 finger protein
37	d1i4pa1	Alignment	not modelled	17.7	30	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Superantigen toxins, N-terminal domain
38	c3izbP_	Alignment	not modelled	17.0	44	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**40s ribosomal protein rps11 (s17p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
39	d1dx8a_	Alignment	not modelled	17.0	32	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
40	c2xqyA_	Alignment	not modelled	16.9	26	**PDB header:**immune system/viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein h; **PDBTitle:** crystal structure of pseudorabies core fragment of2 glycoprotein h in complex with fab d6.3
41	d2ds5a1	Alignment	not modelled	16.7	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**ClpX chaperone zinc binding domain
42	c1ovxB_	Alignment	not modelled	16.3	40	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** nmr structure of the e. coli clpx chaperone zinc binding domain dimer
43	d1ubdc4	Alignment	not modelled	16.0	71	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
44	c1hk8A_	Alignment	not modelled	15.4	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anaerobic ribonucleotide-triphosphate reductase; **PDBTitle:** structural basis for allosteric substrate specificity2 regulation in class iii ribonucleotide reductases:3 nrdd in complex with dgtp
45	d1hk8a_	Alignment	not modelled	15.4	26	**Fold:**PFL-like glycyl radical enzymes **Superfamily:**PFL-like glycyl radical enzymes **Family:**Class III anaerobic ribonucleotide reductase NRDD subunit
46	c3iz6P_	Alignment	not modelled	15.1	44	**PDB header:**ribosome **Chain:** P: **PDB Molecule:**40s ribosomal protein s11 (s17p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
47	c2ds8A_	Alignment	not modelled	15.1	40	**PDB header:**metal binding protein, protein binding **Chain:** A: **PDB Molecule:**atp-dependent clp protease atp-binding subunit **PDBTitle:** structure of the zbd-xb complex
48	d1qm7a_	Alignment	not modelled	13.8	83	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
49	d2g6ta1	Alignment	not modelled	13.3	41	**Fold:**CAC2185-like **Superfamily:**CAC2185-like **Family:**CAC2185-like
50	d1igtb3	Alignment	not modelled	13.2	43	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**C1 set domains (antibody constant domain-like)
51	d2f4ma1	Alignment	not modelled	12.6	22	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
52	d1vdda_	Alignment	not modelled	12.5	23	**Fold:**Recombination protein RecR **Superfamily:**Recombination protein RecR **Family:**Recombination protein RecR
53	d1l1ta3	Alignment	not modelled	12.3	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair

						proteins
54	d1tfsa_	Alignment	not modelled	12.1	67	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
55	c1vddC_	Alignment	not modelled	12.0	23	**PDB header:**recombination **Chain:** C: **PDB Molecule:**recombination protein recr; **PDBTitle:** crystal structure of recombinational repair protein recr
56	c3ov5A_	Alignment	not modelled	10.9	44	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** atomic structure of the xanthomonas citri virb7 globular domain.
57	d1iq9a_	Alignment	not modelled	10.8	83	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
58	d1tdza3	Alignment	not modelled	10.4	24	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
59	d1ntxa_	Alignment	not modelled	10.3	83	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
60	d3ebxa_	Alignment	not modelled	10.2	83	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
61	d1lkoa2	Alignment	not modelled	9.9	22	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
62	c2ja1A_	Alignment	not modelled	9.1	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
63	c2jvnA_	Alignment	not modelled	8.9	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** domain c of human parp-1
64	c3hh7A_	Alignment	not modelled	8.9	45	**PDB header:**toxin **Chain:** A: **PDB Molecule:**muscarinic toxin-like protein 3 homolog; **PDBTitle:** structural and functional characterization of a novel2 homodimeric three-finger neurotoxin from the venom of3 ophiophagus hannah (king cobra)
65	d1k3xa3	Alignment	not modelled	8.7	29	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
66	c2riqA_	Alignment	not modelled	8.5	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 1; **PDBTitle:** crystal structure of the third zinc-binding domain of human parp-1
67	d1vb0a_	Alignment	not modelled	8.2	83	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
68	c1iclA_	Alignment	not modelled	8.2	89	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**th1ox; **PDBTitle:** solution structure of designed beta-sheet mini-protein th1ox
69	c3htkC_	Alignment	not modelled	8.1	50	**PDB header:**recombination/replication/ligase **Chain:** C: **PDB Molecule:**e3 sumo-protein ligase mms21; **PDBTitle:** crystal structure of mms21 and smc5 complex
70	c2f5qA_	Alignment	not modelled	8.1	30	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**formamidopyrimidine-dna glycosidase; **PDBTitle:** catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
71	c2elpA_	Alignment	not modelled	8.0	60	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 13th c2h2 zinc finger of human2 zinc finger protein 406
72	d1r2za3	Alignment	not modelled	7.8	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
73	c3mv2A_	Alignment	not modelled	7.7	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** crystal structure of a-cop in complex with e-cop
74	d1k82a3	Alignment	not modelled	7.6	50	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
75	d1ee8a3	Alignment	not modelled	7.3	38	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**C-terminal, Zn-finger domain of MutM-like DNA repair proteins
76	c2l4wA_	Alignment	not modelled	7.2	44	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of the xanthomonas virb7
77	c2qq0B_	Alignment	not modelled	7.0	48	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from thermotoga maritima in complex with2 thymidine + appnhp
78	c2d88A_	Alignment	not modelled	6.9	33	**PDB header:**signaling protein, protein binding **Chain:** A: **PDB Molecule:**protein mical-3; **PDBTitle:** solution structure of the ch domain from human mical-32 protein
79	c3cngC_	Alignment	not modelled	6.4	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea

80	c2opfA_	Alignment	not modelled	6.3	30	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**endonuclease viii; **PDBTitle:** crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
81	d1z84a1	Alignment	not modelled	6.2	67	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase
82	c2qgpA_	Alignment	not modelled	5.8	43	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hnh endonuclease; **PDBTitle:** x-ray structure of the nhn endonuclease from geobacter2 metallireducens. northeast structural genomics consortium3 target gmr87.
83	c2eoyA_	Alignment	not modelled	5.8	83	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 557-2 589) of human zinc finger protein 473
84	c2k5cA_	Alignment	not modelled	5.8	71	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein pf0385; **PDBTitle:** nmr structure for pf0385
85	d1yuza2	Alignment	not modelled	5.7	50	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
86	d1qxfa_	Alignment	not modelled	5.6	33	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein S27e
87	c1dvbA_	Alignment	not modelled	5.5	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
88	d2j0151	Alignment	not modelled	5.5	28	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
89	d1drsa_	Alignment	not modelled	5.3	35	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Dendroaspin
90	d1wwra1	Alignment	not modelled	5.3	40	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**Deoxycytidylate deaminase-like
91	c3a9fA_	Alignment	not modelled	5.3	43	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the c-terminal domain of cytochrome cz2 from chlorobium tepidum
92	c2hr5B_	Alignment	not modelled	5.1	63	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
93	c2xznQ_	Alignment	not modelled	5.1	42	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein s17 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2