Phyre^2

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Description	P0A7N1
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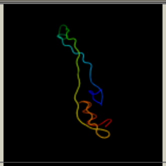
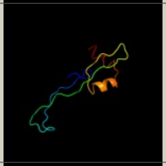
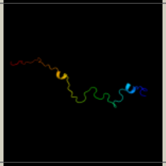
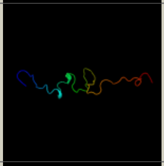
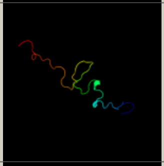
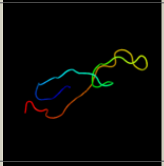
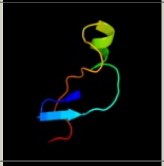
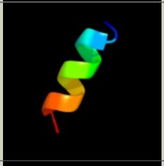
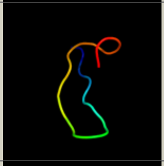
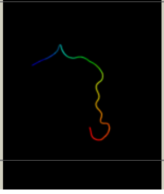
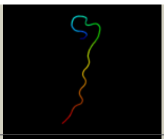
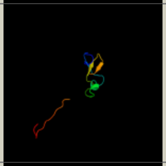
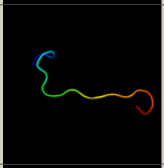
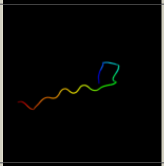
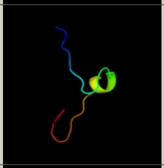
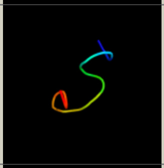
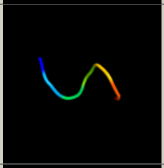
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2b664_	Alignment		100.0	32	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**50s ribosomal protein l31; **PDBTitle:** 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400
2	d1vs6z1	Alignment		100.0	46	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L31p
3	c3bbo1_	Alignment		100.0	28	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**ribosomal protein l31; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
4	d2j0141	Alignment		99.9	39	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L31p
5	c2j034_	Alignment		99.9	39	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**50s ribosomal protein l31; **PDBTitle:** structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii.
6	c3f1f4_	Alignment		97.1	27	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**50s ribosomal protein l31; **PDBTitle:** crystal structure of a translation termination complex2 formed with release factor rf2. this file contains the 50s3 subunit of one 70s ribosome. the entire crystal structure4 contains two 70s ribosomes as described in remark 400.
7	c2wh44_	Alignment		97.1	27	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**50s ribosomal protein l31; **PDBTitle:** insights into translational termination from the structure2 of rf2 bound to the ribosome
8	c2ketA_	Alignment		29.0	31	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**cathelicidin-6; **PDBTitle:** solution structure of bmap-27
9	d1x6ha1	Alignment		27.6	16	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
10	c3cucB_	Alignment		21.9	54	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**protein of unknown function with a fic domain; **PDBTitle:** crystal structure of a fic domain containing signaling protein2 (bt_2513) from bacteroides thetaiotaomicron vpi-5482 at 2.71 a3 resolution
11	d1tqza1	Alignment		20.7	25	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Necap1 N-terminal domain-like

12	c3g66A_	Alignment		17.8	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sortase c; **PDBTitle:** the crystal structure of streptococcus pneumoniae sortase c2 provides novel insights into catalysis as well as pilin3 substrate specificity
13	c3cngC_	Alignment		16.6	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
14	d1eb7a2	Alignment		16.5	25	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
15	d2fiya1	Alignment		16.5	0	**Fold:**FdhE-like **Superfamily:**FdhE-like **Family:**FdhE-like
16	c3o0pA_	Alignment		15.3	11	**PDB header:**transferase , hydrolase **Chain:** A: **PDB Molecule:**sortase family protein; **PDBTitle:** pilus-related sortase c of group b streptococcus
17	c4a1eT_	Alignment		15.2	26	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**rpl24; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
18	d1nmla2	Alignment		15.0	17	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
19	c2yiuE_	Alignment		14.7	43	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution
20	c3cwbQ_	Alignment		13.6	43	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**mitochondrial cytochrome c1, heme protein; **PDBTitle:** chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
21	c2w1jB_	Alignment	not modelled	13.5	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative sortase; **PDBTitle:** crystal structure of sortase c-1 (srtc-1) from2 streptococcus pneumoniae
22	c3n3vA_	Alignment	not modelled	12.7	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine monophosphate-protein transferase ibpa; **PDBTitle:** crystal structure of ibpafic2-h3717a in complex with adenylylated2 cdc42
23	c2fynH_	Alignment	not modelled	12.5	29	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**cytochrome c1; **PDBTitle:** crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
24	c1nmlA_	Alignment	not modelled	12.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**di-haem cytochrome c peroxidase; **PDBTitle:** di-haemic cytochrome c peroxidase from pseudomonas nautica 617, form2 in (ph 4.0)
25	d3cx5d1	Alignment	not modelled	12.5	29	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
26	c2kw8A_	Alignment	not modelled	11.8	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**lpxtg-site transpeptidase family protein; **PDBTitle:** solution structure of bacillus anthracis sortase a (srta)2 transpeptidase
27	c1p84D_	Alignment	not modelled	11.6	29	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**cytochrome c1, heme protein; **PDBTitle:** hdbt inhibited yeast cytochrome bc1 complex
28	d1ppjd1	Alignment	not modelled	11.5	43	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Cytochrome bc1 domain
						PDB header:oxidoreductase/metal transport

29	c1zrtD_	Alignment	not modelled	11.2	43	**Chain:** D: **PDB Molecule:**cytochrome c1; **PDBTitle:** rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
30	c3hq7A_	Alignment	not modelled	10.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c551 peroxidase; **PDBTitle:** ccpa from g. sulfurreducens, g94k/k97q/r100i variant
31	c1dvbA_	Alignment	not modelled	10.7	4	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
32	c3izcZ_	Alignment	not modelled	10.7	19	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**60s ribosomal protein rpl24 (l24e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
33	c2b9vB_	Alignment	not modelled	10.6	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** acetobacter turbidans alpha-amino acid ester hydrolase
34	d1oa8a_	Alignment	not modelled	10.1	20	**Fold:**AXH domain **Superfamily:**AXH domain **Family:**AXH domain
35	d1e7la1	Alignment	not modelled	10.1	60	**Fold:**LEM/SAP HeH motif **Superfamily:**Recombination endonuclease VII, C-terminal and dimerization domains **Family:**Recombination endonuclease VII, C-terminal and dimerization domains
36	c2keqA_	Alignment	not modelled	9.7	36	**PDB header:**splicing **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit, nucleic acid **PDBTitle:** solution structure of dnae intein from nostoc punctiforme
37	c3iz5Z_	Alignment	not modelled	9.4	22	**PDB header:**ribosome **Chain:** Z: **PDB Molecule:**60s ribosomal protein l24 (l24e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
38	d1mi8a_	Alignment	not modelled	9.3	25	**Fold:**Hedgehog/intein (Hint) domain **Superfamily:**Hedgehog/intein (Hint) domain **Family:**Intein (protein splicing domain)
39	c1zd7B_	Alignment	not modelled	8.7	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** 1.7 angstrom crystal structure of post-splicing form of a dnae intein2 from synechocystis sp. pcc 6803
40	c3mdnD_	Alignment	not modelled	8.6	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glutamine aminotransferase class-ii domain protein; **PDBTitle:** structure of glutamine aminotransferase class-ii domain protein2 (spo2029) from silicibacter pomeroyi
41	c3rbjB_	Alignment	not modelled	8.5	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sortase family protein; **PDBTitle:** crystal structure of the lid-mutant of streptococcus agalactiae2 sortase c1
42	d1iufa2	Alignment	not modelled	8.3	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
43	c3eqxB_	Alignment	not modelled	8.3	46	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**fic domain containing transcriptional regulator; **PDBTitle:** crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
44	c1xezA_	Alignment	not modelled	7.8	32	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of the vibrio cholerae cytolysin (hlya)2 pro-toxin with octylglucoside bound
45	c2w1kB_	Alignment	not modelled	7.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**putative sortase; **PDBTitle:** crystal structure of sortase c-3 (srtc-3) from2 streptococcus pneumoniae
46	d1wada_	Alignment	not modelled	7.7	50	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
47	d1at0a_	Alignment	not modelled	7.7	21	**Fold:**Hedgehog/intein (Hint) domain **Superfamily:**Hedgehog/intein (Hint) domain **Family:**Hedgehog C-terminal (Hog) autoprocessing domain
48	c1iqcB_	Alignment	not modelled	7.3	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**di-heme peroxidase; **PDBTitle:** crystal structure of di-heme peroxidase from nitrosomonas europaea
49	c1mpxB_	Alignment	not modelled	7.2	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-amino acid ester hydrolase; **PDBTitle:** alpha-amino acid ester hydrolase labeled with selenomethionine
50	d1am2a_	Alignment	not modelled	7.1	20	**Fold:**Hedgehog/intein (Hint) domain **Superfamily:**Hedgehog/intein (Hint) domain **Family:**Intein (protein splicing domain)
51	c3dd7A_	Alignment	not modelled	6.8	20	**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
52	d1j5ya2	Alignment	not modelled	6.6	19	**Fold:**HPr-like **Superfamily:**Putative transcriptional regulator TM1602, C-terminal domain **Family:**Putative transcriptional regulator TM1602, C-terminal domain
53	c1l7qA_	Alignment	not modelled	6.5	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cocaine esterase; **PDBTitle:** ser117ala mutant of bacterial cocaine esterase coce
54	c2lcjA_	Alignment	not modelled	6.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pab polc intein;

						PDBTitle: solution nmr structure of pab polii intein
55	c2xwgA_	Alignment	not modelled	6.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sortase; **PDBTitle:** crystal structure of sortase c-1 from actinomyces oris (formerly2 actinomyces naeslundii)
56	c3ougA_	Alignment	not modelled	6.4	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis
57	c1uheA_	Alignment	not modelled	6.3	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase alpha chain; **PDBTitle:** crystal structure of aspartate decarboxylase, isoaspargine complex
58	c2jspA_	Alignment	not modelled	6.2	10	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**transcriptional regulatory protein ros; **PDBTitle:** the prokaryotic cys2his2 zinc finger adopts a novel fold as2 revealed by the nmr structure of a. tumefaciens ros dna3 binding domain
59	c3re9A_	Alignment	not modelled	6.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sortase-like protein; **PDBTitle:** crystal structure of sortasec1 from streptococcus suis
60	c2imzA_	Alignment	not modelled	6.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease pi-mtui; **PDBTitle:** crystal structure of mtu reca intein splicing domain
61	c3floD_	Alignment	not modelled	5.9	15	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase alpha catalytic subunit a; **PDBTitle:** crystal structure of the carboxyl-terminal domain of yeast2 dna polymerase alpha in complex with its b subunit
62	c1iufA_	Alignment	not modelled	5.8	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**centromere abp1 protein; **PDBTitle:** low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
63	c2in0A_	Alignment	not modelled	5.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease pi-mtui; **PDBTitle:** crystal structure of mtu reca intein splicing domain
64	c2c45F_	Alignment	not modelled	5.7	13	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aspartate 1-decarboxylase precursor; **PDBTitle:** native precursor of pyruvoyl dependent aspartate2 decarboxylase
65	d1i77a_	Alignment	not modelled	5.6	67	**Fold:**Multiheme cytochromes **Superfamily:**Multiheme cytochromes **Family:**Cytochrome c3-like
66	c3hq2A_	Alignment	not modelled	5.6	42	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**bacillus subtilis m32 carboxypeptidase; **PDBTitle:** bsucp crystal structure
67	c2jmzA_	Alignment	not modelled	5.5	30	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein mj0781; **PDBTitle:** solution structure of a klba intein precursor from2 methanococcus jannaschii
68	c1v0eB_	Alignment	not modelled	5.4	41	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endo-alpha-sialidase; **PDBTitle:** endosialidase of bacteriophage k1f
69	c3gycB_	Alignment	not modelled	5.2	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative glycoside hydrolase; **PDBTitle:** crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
70	c4znfA_	Alignment	not modelled	5.2	21	**PDB header:**zinc finger dna binding domain **Chain:** A: **PDB Molecule:**zinc finger; **PDBTitle:** high-resolution three-dimensional structure of a single2 zinc finger from a human enhancer binding protein in3 solution
71	c3znfA_	Alignment	not modelled	5.2	21	**PDB header:**zinc finger dna binding domain **Chain:** A: **PDB Molecule:**zinc finger; **PDBTitle:** high-resolution three-dimensional structure of a single2 zinc finger from a human enhancer binding protein in3 solution
72	d4znfa_	Alignment	not modelled	5.2	21	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2