Phyre^{2}

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Description	P45581
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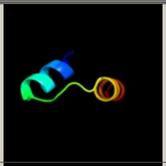
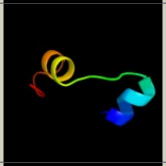
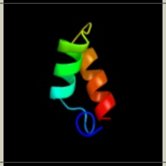
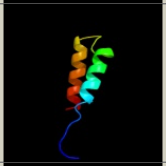
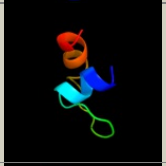
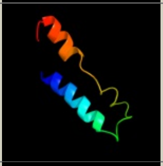
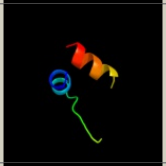
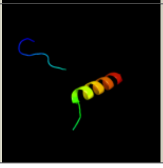
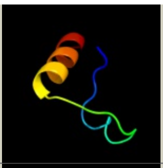
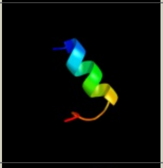
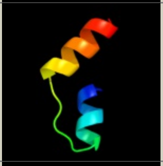
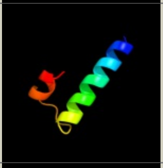
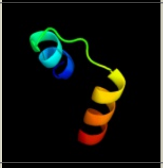
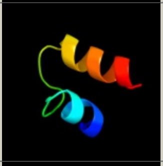
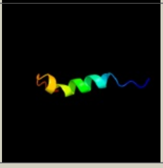
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a1yF_	Alignment		50.6	37	**PDB header:**ribosomal protein **Chain:** F: **PDB Molecule:**50s ribosomal protein p1 (l12p); **PDBTitle:** the structure of protein complex
2	c3trkA_	Alignment		46.5	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nonstructural polyprotein; **PDBTitle:** structure of the chikungunya virus nsp2 protease
3	d1m6ya1	Alignment		41.3	18	**Fold:**SAM domain-like **Superfamily:**Putative methyltransferase TM0872, insert domain **Family:**Putative methyltransferase TM0872, insert domain
4	d1sgla_	Alignment		40.3	11	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
5	d1iooa_	Alignment		39.4	7	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
6	d1or4a_	Alignment		36.5	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
7	d1bola_	Alignment		33.6	7	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
8	c2jeuA_	Alignment		27.4	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulatory protein e2; **PDBTitle:** transcription activator structure reveals redox control of2 a replication initiation reaction
9	d1wg8a1	Alignment		26.7	18	**Fold:**SAM domain-like **Superfamily:**Putative methyltransferase TM0872, insert domain **Family:**Putative methyltransferase TM0872, insert domain
10	c3d3zA_	Alignment		25.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**actibind; **PDBTitle:** crystal structure of actibind a t2 rnase
11	d1k32a4	Alignment		24.5	38	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Tail specific protease, catalytic domain

12	c2w1oA_	Alignment		21.4	11	**PDB header:**translation **Chain:** A: **PDB Molecule:**60s acidic ribosomal protein p2; **PDBTitle:** nmr structure of dimerization domain of human ribosomal2 protein p2
13	d1ev0a_	Alignment		20.6	19	**Fold:**Cell division protein MinE topological specificity domain **Superfamily:**Cell division protein MinE topological specificity domain **Family:**Cell division protein MinE topological specificity domain
14	c2q0oC_	Alignment		20.4	38	**PDB header:**transcription **Chain:** C: **PDB Molecule:**probable transcriptional repressor tram; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
15	c3iz5w_	Alignment		19.9	22	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein l22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
16	c2rchA_	Alignment		19.0	26	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cytochrome p450 74a; **PDBTitle:** crystal structure of arabidopsis thaliana allene oxide synthase (aos,2 cytochrome p450 74a, cyp74a) complexed with 13(s)-hod at 1.85 a3 resolution
17	c3izcw_	Alignment		17.8	22	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein rpl22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
18	d1r6na_	Alignment		17.5	18	**Fold:**E2 regulatory, transactivation domain **Superfamily:**E2 regulatory, transactivation domain **Family:**E2 regulatory, transactivation domain
19	d1dixa_	Alignment		17.4	11	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
20	c2kxoA_	Alignment		17.1	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** solution nmr structure of the cell division regulator mine protein2 from neisseria gonorrhoeae
21	c2w31A_	Alignment	not modelled	16.7	15	**PDB header:**oxygen transport **Chain:** A: **PDB Molecule:**globin; **PDBTitle:** globin domain of geobacter sulfurreducens globin-coupled2 sensor
22	d1jy5a_	Alignment	not modelled	16.2	14	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
23	c1n6dE_	Alignment	not modelled	15.5	38	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
24	c1k32E_	Alignment	not modelled	15.5	38	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** crystal structure of the tricorn protease
25	c1tueG_	Alignment	not modelled	15.4	15	**PDB header:**replication **Chain:** G: **PDB Molecule:**regulatory protein e2; **PDBTitle:** the x-ray structure of the papillomavirus helicase in2 complex with its molecular matchmaker e2
26	d1tueb_	Alignment	not modelled	15.3	15	**Fold:**E2 regulatory, transactivation domain **Superfamily:**E2 regulatory, transactivation domain **Family:**E2 regulatory, transactivation domain
27	d2nnua1	Alignment	not modelled	15.0	15	**Fold:**E2 regulatory, transactivation domain **Superfamily:**E2 regulatory, transactivation domain **Family:**E2 regulatory, transactivation domain
28	d1iyba_	Alignment	not modelled	14.4	14	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
						PDB header:hydrolase

29	c1vd3A_	Alignment	not modelled	12.3	15	**Chain:** A: **PDB Molecule:**rnase ngr3; **PDBTitle:** ribonuclease nt in complex with 2'-ump
30	d1faoa_	Alignment	not modelled	11.8	15	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
31	c1faoA_	Alignment	not modelled	11.8	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dual adaptor of phosphotyrosine and 3- **PDBTitle:** structure of the pleckstrin homology domain from2 dapp1/phish in complex with inositol 1,3,4,5-3 tetrakisphosphate
32	c1m6yA_	Alignment	not modelled	11.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**s-adenosyl-methyltransferase mraw; **PDBTitle:** crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah
33	d2p5ka1	Alignment	not modelled	11.4	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
34	c3uo9B_	Alignment	not modelled	10.9	15	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**glutaminase kidney isoform, mitochondrial; **PDBTitle:** crystal structure of human gac in complex with glutamate and bptes
35	d1wsca1	Alignment	not modelled	10.6	18	**Fold:**AMMECR1-like **Superfamily:**AMMECR1-like **Family:**AMMECR1-like
36	c3ayhA_	Alignment	not modelled	10.5	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-directed rna polymerase iii subunit rpc9; **PDBTitle:** crystal structure of the c17/25 subcomplex from s. pombe rna2 polymerase iii
37	d1aoya_	Alignment	not modelled	10.3	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
38	c3b73A_	Alignment	not modelled	10.3	8	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**phih1 repressor-like protein; **PDBTitle:** crystal structure of the phih1 repressor-like protein from2 haloarcula marismortui
39	c1b4aA_	Alignment	not modelled	10.2	29	**PDB header:**repressor **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** structure of the arginine repressor from bacillus stearothermophilus
40	d1xdza_	Alignment	not modelled	10.1	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Glucose-inhibited division protein B (GidB)
41	d1f9na1	Alignment	not modelled	10.1	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
42	c2p0vA_	Alignment	not modelled	10.0	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein bt3781; **PDBTitle:** crystal structure of bt3781 protein from bacteroides2 thetaiotaomicron, northeast structural genomics target3 btr58
43	d2p0va1	Alignment	not modelled	10.0	24	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
44	d1v9va1	Alignment	not modelled	9.7	19	**Fold:**Bromodomain-like **Superfamily:**MAST3 pre-PK domain-like **Family:**MAST3 pre-PK domain-like
45	d2nvpa1	Alignment	not modelled	9.3	33	**Fold:**alpha/alpha toroid **Superfamily:**Six-hairpin glycosidases **Family:**CPF0428-like
46	d1b4aa1	Alignment	not modelled	9.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
47	c3ereD_	Alignment	not modelled	9.1	36	**PDB header:**dna binding protein/dna **Chain:** D: **PDB Molecule:**arginine repressor; **PDBTitle:** crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
48	d2nn5a1	Alignment	not modelled	8.6	24	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**AHSA1 domain
49	c2kxwB_	Alignment	not modelled	8.3	50	**PDB header:**calcium-binding protein/metal transport **Chain:** B: **PDB Molecule:**sodium channel protein type 2 subunit alpha; **PDBTitle:** structure of the c-domain fragment of apo calmodulin bound to the iq2 motif of nav1.2
50	d1eo0a_	Alignment	not modelled	7.8	21	**Fold:**N-cbl like **Superfamily:**Conserved domain common to transcription factors TFIIS, elongin A, CRSP70 **Family:**Conserved domain common to transcription factors TFIIS, elongin A, CRSP70
51	c2dymE_	Alignment	not modelled	7.8	8	**PDB header:**protein turnover/protein turnover **Chain:** E: **PDB Molecule:**autophagy protein 5; **PDBTitle:** the crystal structure of saccharomyces cerevisiae atg5-2 atg16(1-46) complex
52	c3ivuB_	Alignment	not modelled	7.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**homocitrate synthase, mitochondrial; **PDBTitle:** homocitrate synthase lys4 bound to 2-og
53	c3r9jD_	Alignment	not modelled	7.6	19	**PDB header:**cell cycle,hydrolase/cell cycle **Chain:** D: **PDB Molecule:**cell division topological specificity factor; **PDBTitle:** 4.3a resolution structure of a mind-mine(i24n) protein complex
54	d2c35a1	Alignment	not modelled	7.4	17	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**RNA polymerase II subunit RBP4 (RpoF)

55	c3ss4C_	Alignment	not modelled	7.4	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glutaminase c; **PDBTitle:** crystal structure of mouse glutaminase c, phosphate-bound form
56	c3htuE_	Alignment	not modelled	7.2	20	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**vacuolar protein-sorting-associated protein 25; **PDBTitle:** crystal structure of the human vps25-vps20 subcomplex
57	d2etha1	Alignment	not modelled	6.7	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
58	c2q9rA_	Alignment	not modelled	6.6	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein of unknown function; **PDBTitle:** crystal structure of a duf416 family protein (sbal_3149) from2 shewanella baltica os155 at 1.91 a resolution
59	c3izct_	Alignment	not modelled	6.5	25	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**60s ribosomal protein rpl19 (l19e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
60	c3lvuB_	Alignment	not modelled	6.5	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding protein; **PDBTitle:** crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
61	d1wjta_	Alignment	not modelled	6.4	23	**Fold:**N-cbl like **Superfamily:**Conserved domain common to transcription factors TFIIS, elongin A, CRSP70 **Family:**Conserved domain common to transcription factors TFIIS, elongin A, CRSP70
62	d2c0sa1	Alignment	not modelled	6.4	38	**Fold:**ROP-like **Superfamily:**BAS1536-like **Family:**BAS1536-like
63	c3v4gA_	Alignment	not modelled	6.3	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
64	c2kwuA_	Alignment	not modelled	6.3	38	**PDB header:**protein binding/signaling protein **Chain:** A: **PDB Molecule:**dna polymerase iota; **PDBTitle:** solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
65	d1zq7a1	Alignment	not modelled	6.3	19	**Fold:**AMMECR1-like **Superfamily:**AMMECR1-like **Family:**AMMECR1-like
66	d2ea9a1	Alignment	not modelled	6.3	42	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
67	d1wfya_	Alignment	not modelled	6.0	39	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
68	d2h28a1	Alignment	not modelled	6.0	39	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
69	c2wqmA_	Alignment	not modelled	5.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase nek7; **PDBTitle:** structure of apo human nek7
70	d2dy1a4	Alignment	not modelled	5.8	31	**Fold:**Ferredoxin-like **Superfamily:**EF-G C-terminal domain-like **Family:**EF-G/eEF-2 domains III and V
71	c1wlzD_	Alignment	not modelled	5.6	20	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**cap-binding protein complex interacting protein **PDBTitle:** crystal structure of djbp fragment which was obtained by2 limited proteolysis
72	d1wlza1	Alignment	not modelled	5.6	20	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
73	d1gh6a_	Alignment	not modelled	5.6	15	**Fold:**Long alpha-hairpin **Superfamily:**Chaperone J-domain **Family:**Chaperone J-domain
74	d2fcea1	Alignment	not modelled	5.6	25	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
75	d1iira_	Alignment	not modelled	5.6	26	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
76	d1mw7a_	Alignment	not modelled	5.6	23	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
77	d1ucda_	Alignment	not modelled	5.5	11	**Fold:**Ribonuclease Rh-like **Superfamily:**Ribonuclease Rh-like **Family:**Ribonuclease Rh-like
78	d2inwa1	Alignment	not modelled	5.5	44	**Fold:**Profilin-like **Superfamily:**YeeU-like **Family:**YagB/YeeU/YfjZ-like
79	c2ckzC_	Alignment	not modelled	5.3	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**dna-directed rna polymerase iii 18 kd **PDBTitle:** x-ray structure of rna polymerase iii subcomplex c17-c25.
80	c2k42A_	Alignment	not modelled	5.3	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wiskott-aldrich syndrome protein; **PDBTitle:** solution structure of the gtpase binding domain of wasp

						in2 complex with espfu, an ehec effector
81	d2nxpa1	Alignment	not modelled	5.2	10	**Fold:**Taf5 N-terminal domain-like **Superfamily:**Taf5 N-terminal domain-like **Family:**Taf5 N-terminal domain-like
82	c2p6pB_	Alignment	not modelled	5.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glycosyl transferase; **PDBTitle:** x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
83	c1wg8B_	Alignment	not modelled	5.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted s-adenosylmethionine-dependent **PDBTitle:** crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.