Phyre^2

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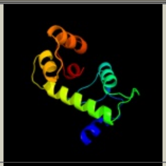
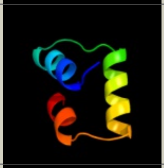
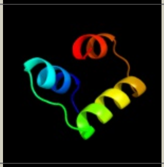
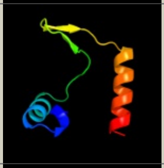
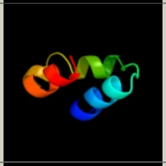
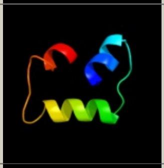
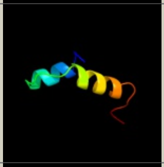
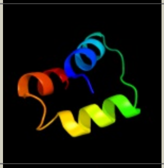
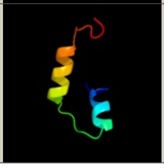
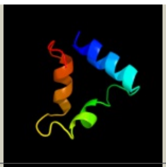
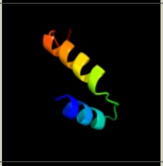
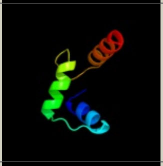
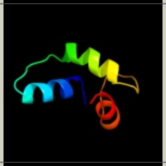
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3sibA_	Alignment		86.6	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ure3-bp sequence specific dna binding protein; **PDBTitle:** crystal structure of ure3-binding protein, wild-type
2	d1brwa1	Alignment		56.9	12	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
3	d2tpta1	Alignment		48.9	17	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
4	c3gh1A_	Alignment		48.4	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted nucleotide-binding protein; **PDBTitle:** crystal structure of predicted nucleotide-binding protein from vibrio2 cholerae
5	c3bq9A_	Alignment		48.4	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
6	d1ldda_	Alignment		44.4	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**SCF ubiquitin ligase complex WHB domain
7	c2dsjA_	Alignment		40.1	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside (thymidine) phosphorylase; **PDBTitle:** crystal structure of project id tt0128 from thermus thermophilus hb8
8	d1uoua1	Alignment		38.9	21	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
9	c3iz5w_	Alignment		37.3	17	**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
10	d1o17a1	Alignment		37.2	20	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
11	c3izcw_	Alignment		35.7	20	**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

12	c2fjrB_	Alignment		28.6	7	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci; **PDBTitle:** crystal structure of bacteriophage 186
13	c2w1oA_	Alignment		27.8	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**60s acidic ribosomal protein p2; **PDBTitle:** nmr structure of dimerization domain of human ribosomal2 protein p2
14	c3h5qA_	Alignment		26.6	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyrimidine-nucleoside phosphorylase; **PDBTitle:** crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
15	d2f76x1	Alignment		24.1	9	**Fold:**Retroviral matrix proteins **Superfamily:**Retroviral matrix proteins **Family:**Mason-Pfizer monkey virus matrix protein
16	d1n0ya_	Alignment		23.8	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
17	c2k7bA_	Alignment		23.6	8	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcium-binding protein 1; **PDBTitle:** nmr structure of mg2+-bound cabp1 n-domain
18	d1sw8a_	Alignment		23.0	9	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
19	d1khda1	Alignment		21.2	18	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
20	d2elca1	Alignment		19.4	11	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
21	c3ctnA_	Alignment	not modelled	19.2	16	**PDB header:**calcium-binding protein **Chain:** A: **PDB Molecule:**troponin c; **PDBTitle:** structure of calcium-saturated cardiac troponin c, nmr, 302 structures
22	c1wlzD_	Alignment	not modelled	18.5	13	**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
23	d1wlza1	Alignment	not modelled	18.5	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
24	c1o17A_	Alignment	not modelled	18.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**anthranilate phosphoribosyltransferase; **PDBTitle:** anthranilate phosphoribosyl-transferase (trpd)
25	c2amiA_	Alignment	not modelled	17.5	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**caltractin; **PDBTitle:** solution structure of the calcium-loaded n-terminal sensor2 domain of centrin
26	c3evrA_	Alignment	not modelled	17.0	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**myosin light chain kinase, green fluorescent **PDBTitle:** crystal structure of calcium bound monomeric gcamp2
27	d1sl7a_	Alignment	not modelled	16.2	14	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
28	c2kdhA_	Alignment	not modelled	15.5	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** the solution structure of human cardiac troponin c in2

						complex with the green tea polyphenol; (-)-3 epigallocatechin-3-gallate
29	c2l98A_	Alignment	not modelled	15.5	16	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** structure of trans-resveratrol in complex with the cardiac regulatory2 protein troponin c
30	c3bjaA_	Alignment	not modelled	15.2	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family, putative; **PDBTitle:** crystal structure of putative marr-like transcription regulator2 (np_978771.1) from bacillus cereus atcc 10987 at 2.38 a resolution
31	c2igpA_	Alignment	not modelled	14.9	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**retinoblastoma-associated protein hec; **PDBTitle:** crystal structure of hec1 ch domain
32	d2pq3a1	Alignment	not modelled	14.7	9	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
33	d1j55a_	Alignment	not modelled	14.2	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
34	c2vqcA_	Alignment	not modelled	13.9	42	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**hypothetical 13.2 kda protein; **PDBTitle:** structure of a dna binding winged-helix protein, f-112,2 from sulfolobus spindle-shaped virus 1.
35	d2vqca1	Alignment	not modelled	13.9	42	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**F112-like
36	d1dtla_	Alignment	not modelled	13.5	14	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
37	d1xk4c1	Alignment	not modelled	13.1	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
38	d1djxb1	Alignment	not modelled	12.5	18	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
39	d2fcea1	Alignment	not modelled	12.4	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
40	c2j0fC_	Alignment	not modelled	11.9	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
41	c2g2bA_	Alignment	not modelled	11.6	15	**PDB header:**immune system **Chain:** A: **PDB Molecule:**allograft inflammatory factor 1; **PDBTitle:** nmr structure of the human allograft inflammatory factor 1
42	d1wrka1	Alignment	not modelled	11.5	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
43	d1fw4a_	Alignment	not modelled	11.2	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
44	d1m39a_	Alignment	not modelled	11.1	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
45	d1jc2a_	Alignment	not modelled	11.1	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
46	c1jc2A_	Alignment	not modelled	11.1	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, skeletal muscle; **PDBTitle:** complex of the c-domain of troponin c with residues 1-40 of2 troponin i
47	d1v8ga1	Alignment	not modelled	10.7	16	**Fold:**Methionine synthase domain-like **Superfamily:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain **Family:**Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
48	c3cecA_	Alignment	not modelled	10.6	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative antidote protein of plasmid maintenance system; **PDBTitle:** crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
49	c3oiqB_	Alignment	not modelled	10.3	27	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**dna polymerase alpha catalytic subunit a; **PDBTitle:** crystal structure of yeast telomere protein cdc13 ob1 and the2 catalytic subunit of dna polymerase alpha pol1
50	d1r2ua_	Alignment	not modelled	10.1	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
51	d1vi0a2	Alignment	not modelled	9.6	14	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
52	d1n0yb_	Alignment	not modelled	9.3	11	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
53	c3pivA_	Alignment	not modelled	9.2	17	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**interferon;

						PDBTitle: zebrafish interferon 1
54	d1eysh2	Alignment	not modelled	9.2	47	**Fold:**Single transmembrane helix **Superfamily:**Photosystem II reaction centre subunit H, transmembrane region **Family:**Photosystem II reaction centre subunit H, transmembrane region
55	c2fcdA_	Alignment	not modelled	9.0	7	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**myosin light chain 1; **PDBTitle:** solution structure of n-lobe myosin light chain from2 saccharomices cerevisiae
56	d1mzba_	Alignment	not modelled	8.9	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FUR-like
57	c2o8kA_	Alignment	not modelled	8.8	12	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpon; **PDBTitle:** nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
58	c1otpA_	Alignment	not modelled	8.8	17	**PDB header:**phosphorylase **Chain:** A: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
59	c1irjG_	Alignment	not modelled	8.5	12	**PDB header:**metal binding protein **Chain:** G: **PDB Molecule:**migration inhibitory factor-related protein 14; **PDBTitle:** crystal structure of the mrp14 complexed with chaps
60	c2b1uA_	Alignment	not modelled	8.5	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calmodulin-like protein 5; **PDBTitle:** solution structure of calmodulin-like skin protein c2 terminal domain
61	c2k6oA_	Alignment	not modelled	7.9	29	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**cathelicidin antimicrobial peptide; **PDBTitle:** human ll-37 structure
62	c1brwB_	Alignment	not modelled	7.9	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyrimidine nucleoside phosphorylase); **PDBTitle:** the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
63	d1f54a_	Alignment	not modelled	7.9	7	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
64	d1avsa_	Alignment	not modelled	7.8	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
65	c2d58A_	Alignment	not modelled	7.8	13	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**allograft inflammatory factor 1; **PDBTitle:** human microglia-specific protein iba1
66	c2jojA_	Alignment	not modelled	7.8	11	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**centrin protein; **PDBTitle:** nmr solution structure of n-terminal domain of euplotes2 octocarinatus centrin
67	c3jrtA_	Alignment	not modelled	7.5	39	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**integron cassette protein vpc_cass2; **PDBTitle:** structure from the mobile metagenome of v. paracholerae:2 integron cassette protein vpc_cass2
68	c1ih0A_	Alignment	not modelled	7.4	16	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** structure of the c-domain of human cardiac troponin c in2 complex with ca2+ sensitizer emd 57033
69	d1ih0a_	Alignment	not modelled	7.4	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
70	d2csfa1	Alignment	not modelled	7.1	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**CUT domain
71	d1q5za_	Alignment	not modelled	6.7	62	**Fold:**Invasion protein A (SipA) , C-terminal actin binding domain **Superfamily:**Invasion protein A (SipA) , C-terminal actin binding domain **Family:**Invasion protein A (SipA) , C-terminal actin binding domain
72	c1q5zA_	Alignment	not modelled	6.7	62	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**sipa; **PDBTitle:** crystal structure of the c-terminal actin binding domain of2 salmonella invasion protein a (sipa)
73	d1cmga_	Alignment	not modelled	6.7	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
74	c2aaoA_	Alignment	not modelled	6.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calcium-dependent protein kinase, isoform ak1; **PDBTitle:** regulatory apparatus of calcium dependent protein kinase from2 arabidopsis thaliana
75	c1sbjA_	Alignment	not modelled	6.7	16	**PDB header:**contractile protein, structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** nmr structure of the mg2+-loaded c terminal domain of2 cardiac troponin c bound to the n terminal domain of3 cardiac troponin i
76	c1scvA_	Alignment	not modelled	6.7	16	**PDB header:**contractile protein, structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** nmr structure of the c terminal domain of cardiac troponin2 c bound to the n terminal domain of cardiac troponin i
77	c1fi5A_	Alignment	not modelled	6.7	16	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**protein (troponin c); **PDBTitle:** nmr structure of the c terminal domain of cardiac troponin2 c bound to the n terminal domain of cardiac troponin i.

78	d1fi5a_	Alignment	not modelled	6.7	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
79	d1tn4a_	Alignment	not modelled	6.6	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
80	c2k2aA_	Alignment	not modelled	6.6	15	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**troponin c; **PDBTitle:** solution structure of the apo c terminal domain of lethocerus troponin2 c isoform f1
81	d1oqpa_	Alignment	not modelled	6.5	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
82	c1ozsA_	Alignment	not modelled	6.4	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** c-domain of human cardiac troponin c in complex with the2 inhibitory region of human cardiac troponin i
83	d1xrxa1	Alignment	not modelled	6.4	67	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**SeqA N-terminal domain-like
84	c1xrxD_	Alignment	not modelled	6.4	67	**PDB header:**replication inhibitor **Chain:** D: **PDB Molecule:**seqa protein; **PDBTitle:** crystal structure of a dna-binding protein
85	d1jw2a_	Alignment	not modelled	6.3	19	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Hemolysin expression modulating protein HHA **Family:**Hemolysin expression modulating protein HHA
86	d2p5ka1	Alignment	not modelled	6.1	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
87	d1tiza_	Alignment	not modelled	6.1	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
88	c2e8mA_	Alignment	not modelled	6.0	27	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**epidermal growth factor receptor kinase **PDBTitle:** solution structure of the c-terminal sam-domain of2 epidermal growth receptor pathway substrate 8
89	d1lj9a_	Alignment	not modelled	5.9	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
90	d1a03a_	Alignment	not modelled	5.8	10	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
91	c2a4jA_	Alignment	not modelled	5.7	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**centrin 2; **PDBTitle:** solution structure of the c-terminal domain (t94-y172) of2 the human centrin 2 in complex with a 17 residues peptide3 (p1-xpc) from xeroderma pigmentosum group c protein
92	d1jjcb2	Alignment	not modelled	5.7	19	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
93	c2ktgA_	Alignment	not modelled	5.5	9	**PDB header:**ca-binding protein **Chain:** A: **PDB Molecule:**calmodulin, putative; **PDBTitle:** calmodulin like protein from entamoeba histolytica: solution structure2 and calcium binding properties of a partially folded protein
94	d1b4aa1	Alignment	not modelled	5.5	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
95	c2bcwC_	Alignment	not modelled	5.4	20	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**elongation factor g; **PDBTitle:** coordinates of the n-terminal domain of ribosomal protein2 l11,c-terminal domain of ribosomal protein l7/l12 and a3 portion of the g' domain of elongation factor g, as fitted4 into cryo-em map of an escherichia coli 70s*ef-5 g*gdp*fusidic acid complex
96	d1fi4a1	Alignment	not modelled	5.4	22	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**GHMP Kinase, N-terminal domain
97	d1f9na1	Alignment	not modelled	5.3	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Arginine repressor (ArgR), N-terminal DNA-binding domain
98	d1np8a_	Alignment	not modelled	5.3	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Penta-EF-hand proteins
99	d1ap4a_	Alignment	not modelled	5.2	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like