Phyre^{2}

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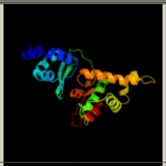
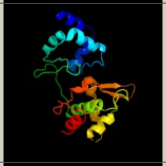
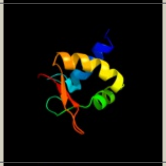
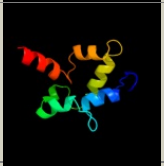
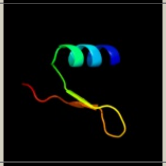
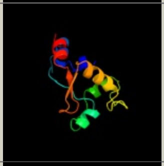
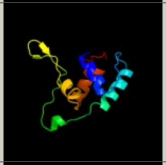
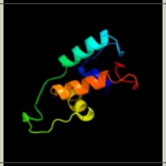
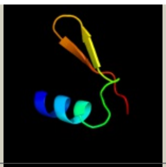
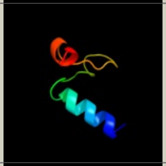
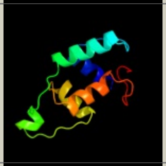
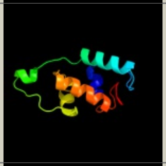
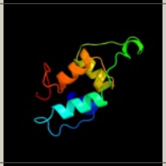
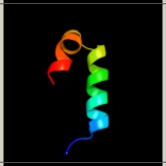
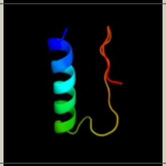
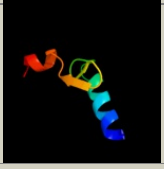
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3euhF_	Alignment		100.0	100	**PDB header:**cell cycle **Chain:** F: **PDB Molecule:**muke; **PDBTitle:** crystal structure of the muke-mukf complex
2	c3eukL_	Alignment		100.0	69	**PDB header:**cell cycle **Chain:** L: **PDB Molecule:**chromosome partition protein muke; **PDBTitle:** crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, asymmetric dimer
3	c2y75F_	Alignment		68.1	17	**PDB header:**transcription **Chain:** F: **PDB Molecule:**hth-type transcriptional regulator cymr; **PDBTitle:** the structure of cymr (yrzc) the global cysteine regulator2 of b. subtilis
4	c3lwfD_	Alignment		45.7	18	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator (np_470886.1)2 from listeria innocua at 2.06 a resolution
5	c1eg4A_	Alignment		35.4	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**dystrophin; **PDBTitle:** structure of a dystrophin ww domain fragment in complex2 with a beta-dystroglycan peptide
6	d1u5ta1	Alignment		28.3	25	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
7	c3k69A_	Alignment		27.7	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcription regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator (lp_0360)2 from lactobacillus plantarum at 1.95 a resolution
8	c3l09B_	Alignment		25.0	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator2 (jann_22dec04_contig27_revised_gene3569) from jannaschia sp. ccs1 at3 2.81 a resolution
9	d1e2ta_	Alignment		24.0	21	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
10	c3d9wA_	Alignment		23.2	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure analysis of nocardia farcinica arylamine2 n-acetyltransferase
11	d2g9wa1	Alignment		23.0	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor

12	d1p6ra_	Alignment		21.6	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
13	c2fnaA_	Alignment		20.1	12	**PDB header:**atp-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of an archaeal aaa+ atpase (sso1545) from sulfolobus2 solfataricus p2 at 2.00 a resolution
14	d1w4ta1	Alignment		18.5	16	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
15	c3kfwX_	Alignment		17.7	23	**PDB header:**structural genomics, unknown function **Chain:** X: **PDB Molecule:**uncharacterized protein; **PDBTitle:** uncharacterized protein rv0674 from mycobacterium tuberculosis
16	c2vfbA_	Alignment		17.5	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arylamine n-acetyltransferase; **PDBTitle:** the structure of mycobacterium marinum arylamine n-2 acetyltransferase
17	c2pfrB_	Alignment		17.4	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arylamine n-acetyltransferase 2; **PDBTitle:** human n-acetyltransferase 2
18	c2i2oB_	Alignment		17.3	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**eif4g-like protein; **PDBTitle:** crystal structure of an eif4g-like protein from danio rerio
19	c2z7bA_	Alignment		16.1	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**mlr6791 protein; **PDBTitle:** crystal structure of mesorhizobium loti 3-hydroxy-2-methylpyridine-4,2 5-dicarboxylate decarboxylase
20	c3lmmA_	Alignment		15.8	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of the dip2311 protein from2 corynebacterium diphtheriae, northeast structural genomics3 consortium target cdr35
21	c2k4bA_	Alignment	not modelled	15.3	24	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**transcriptional regulator; **PDBTitle:** copr repressor structure
22	d2p6ra1	Alignment	not modelled	15.3	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**RecQ helicase DNA-binding domain-like
23	c2qenA_	Alignment	not modelled	15.1	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**walker-type atpase; **PDBTitle:** the walker-type atpase paby2304 of pyrococcus abyssi
24	c3cuqA_	Alignment	not modelled	15.0	27	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
25	c2rnoA_	Alignment	not modelled	14.8	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** solution structure of the n-terminal sap domain of sumo e3 ligases2 from oryza sativa
26	d2bsza1	Alignment	not modelled	14.0	19	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
27	d2hs5a1	Alignment	not modelled	13.5	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**GntR-like transcriptional regulators
28	c3b73A_	Alignment	not modelled	13.3	17	**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
						PDB header:hormone

29	c2rn5B_	Alignment	not modelled	12.7	50	**Chain:** B: **PDB Molecule:**insulin; **PDBTitle:** humal insulin mutant b31lys-b32arg
30	d1e4cp_	Alignment	not modelled	12.6	24	**Fold:**AraD/HMP-PK domain-like **Superfamily:**AraD/HMP-PK domain-like **Family:**AraD-like aldolase/epimerase
31	d1j93a_	Alignment	not modelled	12.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
32	c2zmeA_	Alignment	not modelled	11.4	27	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar-sorting protein snf8; **PDBTitle:** integrated structural and functional model of the human escrt-ii2 complex
33	c3g12A_	Alignment	not modelled	11.2	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative lactoylglutathione lyase; **PDBTitle:** crystal structure of a putative lactoylglutathione lyase2 from bdellovibrio bacteriovorus
34	c2p1nD_	Alignment	not modelled	10.8	15	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
35	d1mzba_	Alignment	not modelled	10.8	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FUR-like
36	c2lbfA_	Alignment	not modelled	10.7	28	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**60s acidic ribosomal protein p1; **PDBTitle:** solution structure of the dimerization domain of human ribosomal2 protein p1/p2 heterodimer
37	c3iynN_	Alignment	not modelled	10.6	22	**PDB header:**virus **Chain:** N: **PDB Molecule:**peripentonal hexon-associated protein; **PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5
38	c2dvzA_	Alignment	not modelled	10.5	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** structure of a periplasmic transporter
39	c1t98B_	Alignment	not modelled	10.3	14	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**chromosome partition protein mukf; **PDBTitle:** crystal structure of mukf(1-287)
40	d1tgra_	Alignment	not modelled	10.0	14	**Fold:**Insulin-like **Superfamily:**Insulin-like **Family:**Insulin-like
41	c2fk5B_	Alignment	not modelled	10.0	28	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fuculose-1-phosphate aldolase; **PDBTitle:** crystal structure of l-fuculose-1-phosphate aldolase from thermus2 thermophilus hb8
42	c3q90A_	Alignment	not modelled	10.0	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ras gtpase-activating protein-binding protein 1; **PDBTitle:** crystal structure of the ntf2 domain of ras gtpase-activating protein-2 binding protein 1
43	c2ovqA_	Alignment	not modelled	9.8	14	**PDB header:**transcription/cell cycle **Chain:** A: **PDB Molecule:**s-phase kinase-associated protein 1a; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex
44	d1mkma1	Alignment	not modelled	9.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator IclR, N-terminal domain
45	d1l1sa_	Alignment	not modelled	9.8	22	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
46	d1jjcb2	Alignment	not modelled	9.7	23	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Domains B1 and B5 of PheRS-beta, PheT
47	c3lnbA_	Alignment	not modelled	9.4	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**n-acetyltransferase family protein; **PDBTitle:** crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
48	d2ex3b1	Alignment	not modelled	9.4	14	**Fold:**DNA terminal protein **Superfamily:**DNA terminal protein **Family:**DNA terminal protein
49	c2o4cB_	Alignment	not modelled	9.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
50	c1qoyA_	Alignment	not modelled	9.2	8	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin e; **PDBTitle:** e.coli hemolysin e (hlye, clya, shea)
51	d1ecsa_	Alignment	not modelled	9.0	17	**Fold:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Superfamily:**Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase **Family:**Antibiotic resistance proteins
52	c3edpB_	Alignment	not modelled	8.9	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lin2111 protein; **PDBTitle:** the crystal structure of the protein lin2111 (functionally unknown)2 from listeria innocua clip11262
53	d1xd7a_	Alignment	not modelled	8.6	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
54	d1ylfa1	Alignment	not modelled	8.6	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Transcriptional regulator Rrf2
55	c3iz5t_	Alignment	not modelled	8.3	31	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**60s ribosomal protein l19 (l19e); **PDBTitle:** localization of the large subunit ribosomal proteins into

						a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
56	d1stza1	Alignment	not modelled	8.0	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
57	c3oetF_	Alignment	not modelled	8.0	11	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** d-erythronate-4-phosphate dehydrogenase complexed with nad
58	c3eqxB_	Alignment	not modelled	7.8	11	**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
59	d1efea_	Alignment	not modelled	7.6	20	**Fold:**Insulin-like **Superfamily:**Insulin-like **Family:**Insulin-like
60	d2fnaa1	Alignment	not modelled	7.3	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
61	c3euhB_	Alignment	not modelled	7.3	10	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**chromosome partition protein mukf; **PDBTitle:** crystal structure of the muke-mukf complex
62	c2fe3B_	Alignment	not modelled	7.3	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**peroxide operon regulator; **PDBTitle:** the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
63	c3g2bA_	Alignment	not modelled	7.0	8	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
64	d2e45a1	Alignment	not modelled	7.0	13	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
65	c2g7uB_	Alignment	not modelled	7.0	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**transcriptional regulator; **PDBTitle:** 2.3 a structure of putative catechol degradative operon regulator from2 rhodococcus sp. rha1
66	d1zeia_	Alignment	not modelled	6.8	26	**Fold:**Insulin-like **Superfamily:**Insulin-like **Family:**Insulin-like
67	d1jhfa1	Alignment	not modelled	6.8	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
68	d1sd4a_	Alignment	not modelled	6.8	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Penicillinase repressor
69	c3mwmA_	Alignment	not modelled	6.6	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative metal uptake regulation protein; **PDBTitle:** graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
70	d2b5ga1	Alignment	not modelled	6.4	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
71	d1edla_	Alignment	not modelled	6.4	32	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
72	d1d1la_	Alignment	not modelled	6.3	38	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
73	c3m1gC_	Alignment	not modelled	6.3	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**putative glutathione s-transferase; **PDBTitle:** the structure of a putative glutathione s-transferase from2 corynebacterium glutamicum
74	d1w5ra1	Alignment	not modelled	6.3	27	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Arylamine N-acetyltransferase
75	d2al6a3	Alignment	not modelled	6.2	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**First domain of FERM
76	c3gy9A_	Alignment	not modelled	6.2	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**gcn5-related n-acetyltransferase; **PDBTitle:** crystal structure of putative acetyltransferase (yp_001815201.1) from2 exiguobacterium sp. 255-15 at 1.52 a resolution
77	d1lp1a_	Alignment	not modelled	6.1	21	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Bacterial immunoglobulin/albumin-binding domains **Family:**Immunoglobulin-binding protein A modules
78	d4croa_	Alignment	not modelled	5.8	38	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
79	c1jpkA_	Alignment	not modelled	5.8	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen decarboxylase; **PDBTitle:** gly156asp mutant of human urod, human uroporphyrinogen iii2 decarboxylase
80	c3f8mA_	Alignment	not modelled	5.8	31	**PDB header:**transcription **Chain:** A: **PDB Molecule:**gntr-family protein transcriptional regulator; **PDBTitle:** crystal structure of phnf from mycobacterium smegmatis
81	c2advB_	Alignment	not modelled	5.8	43	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutaryl 7- aminocephalosporanic acid acylase; **PDBTitle:** crystal structures of glutaryl 7-aminocephalosporanic acid acylase:2 mutational study of activation mechanism

82	d2v5pc1	Alignment	not modelled	5.7	17	**Fold:**Insulin-like **Superfamily:**Insulin-like **Family:**Insulin-like
83	c2de0X_	Alignment	not modelled	5.7	13	**PDB header:**transferase **Chain:** X: **PDB Molecule:**alpha-(1,6)-fucosyltransferase; **PDBTitle:** crystal structure of human alpha 1,6-fucosyltransferase, fut8
84	d1pmxa_	Alignment	not modelled	5.6	16	**Fold:**Insulin-like **Superfamily:**Insulin-like **Family:**Insulin-like
85	c3ic7A_	Alignment	not modelled	5.4	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator of gntr family2 from bacteroides thetaiotaomicron
86	c2du9A_	Alignment	not modelled	5.4	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulators; **PDBTitle:** crystal structure of the transcriptional factor from c.glutamicum
87	d1r3sa_	Alignment	not modelled	5.4	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**UROD/MetE-like **Family:**Uroporphyrinogen decarboxylase, UROD
88	c2jobA_	Alignment	not modelled	5.3	19	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
89	d2cyya1	Alignment	not modelled	5.3	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
90	c2qpqC_	Alignment	not modelled	5.3	3	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
91	d1nn4a_	Alignment	not modelled	5.2	11	**Fold:**Ribose/Galactose isomerase RpiB/AlsB **Superfamily:**Ribose/Galactose isomerase RpiB/AlsB **Family:**Ribose/Galactose isomerase RpiB/AlsB
92	c3izct_	Alignment	not modelled	5.2	12	**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