Phyre^2

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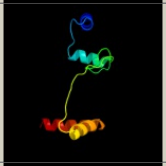
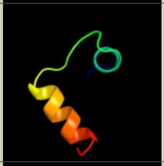
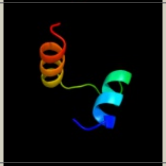
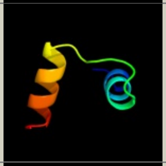
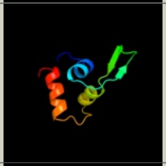
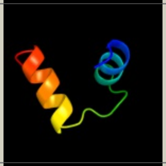
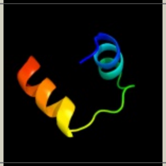
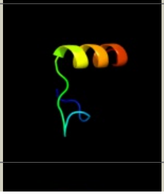
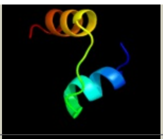
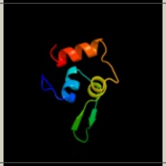
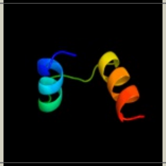
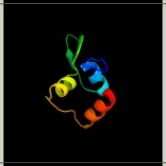
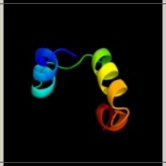
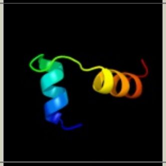
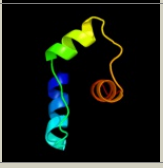
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kpjA_	Alignment		94.8	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sos-response transcriptional repressor, lexa; **PDBTitle:** solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
2	c3op9A_	Alignment		92.8	14	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**pli0006 protein; **PDBTitle:** crystal structure of transcriptional regulator from listeria innocua
3	d1llib_	Alignment		92.3	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
4	c3bs3A_	Alignment		91.9	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
5	c3omtA_	Alignment		91.5	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
6	d1y7ya1	Alignment		91.2	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
7	d1utxa_	Alignment		91.2	3	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
8	d2b5aa1	Alignment		90.1	25	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
9	c3f52A_	Alignment		90.0	30	**PDB header:**transcription activator **Chain:** A: **PDB Molecule:**clp gene regulator (clgr); **PDBTitle:** crystal structure of the clp gene regulator clgr from c. glutamicum
10	d1x57a1	Alignment		89.9	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**EDF1-like
11	c3lisB_	Alignment		89.4	16	**PDB header:**transcription **Chain:** B: **PDB Molecule:**csp231i c protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)

12	c3ivpD_	Alignment		89.1	17	**PDB header:**dna binding protein **Chain:** D: **PDB Molecule:**putative transposon-related dna-binding protein; **PDBTitle:** the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
13	d1y9qa1	Alignment		88.9	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Probable transcriptional regulator VC1968, N-terminal domain
14	d1adra_	Alignment		88.9	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
15	c3clcC_	Alignment		88.2	13	**PDB header:**transcription regulator/dna **Chain:** C: **PDB Molecule:**regulatory protein; **PDBTitle:** crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
16	c3trbA_	Alignment		88.1	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**virulence-associated protein i; **PDBTitle:** structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
17	d2r1jl1	Alignment		88.1	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
18	c2xcjB_	Alignment		87.9	26	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**c protein; **PDBTitle:** crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
19	c2ebyA_	Alignment		87.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative hth-type transcriptional regulator ybaq; **PDBTitle:** crystal structure of a hypothetical protein from e. coli
20	c3r1fO_	Alignment		87.8	26	**PDB header:**transcription **Chain:** O: **PDB Molecule:**esx-1 secretion-associated regulator espr; **PDBTitle:** crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
21	d1lmb3_	Alignment	not modelled	87.4	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
22	d1rioa_	Alignment	not modelled	86.7	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
23	c2jvlA_	Alignment	not modelled	86.6	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
24	c3cecA_	Alignment	not modelled	86.3	17	**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
25	c3mlfC_	Alignment	not modelled	86.0	10	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
26	c3dnvB_	Alignment	not modelled	85.9	10	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator hipb; **PDBTitle:** mdt protein
27	c2ewtA_	Alignment	not modelled	85.4	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of the dna-binding domain of bldd
28	d1b0na2	Alignment	not modelled	84.0	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
						PDB header:transcription/dna

29	c3bdnB_	Alignment	not modelled	82.2	23	**Chain:** B: **PDB Molecule:**lambda repressor; **PDBTitle:** crystal structure of the lambda repressor
30	c3eusB_	Alignment	not modelled	80.6	10	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna-binding protein; **PDBTitle:** the crystal structure of the dna binding protein from silicibacter2 pomeroyi
31	d2icta1	Alignment	not modelled	80.3	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
32	c1b0nA_	Alignment	not modelled	79.9	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**protein (sinr protein); **PDBTitle:** sinr protein/sini protein complex
33	d2croa_	Alignment	not modelled	79.4	10	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
34	d1sq8a_	Alignment	not modelled	79.1	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
35	c3f6wE_	Alignment	not modelled	78.0	17	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
36	c2ef8A_	Alignment	not modelled	75.9	19	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
37	d1r69a_	Alignment	not modelled	75.1	24	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
38	c3t76A_	Alignment	not modelled	73.2	10	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator vanug; **PDBTitle:** crystal structure of transcriptional regulator vanug, form ii
39	c3b7hA_	Alignment	not modelled	70.3	27	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**prophage lp1 protein 11; **PDBTitle:** crystal structure of the prophage lp1 protein 11
40	c3kxaD_	Alignment	not modelled	70.0	17	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
41	d2a6ca1	Alignment	not modelled	68.3	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
42	d2ofya1	Alignment	not modelled	65.2	23	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
43	c2o38A_	Alignment	not modelled	64.9	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
44	d2o38a1	Alignment	not modelled	64.9	17	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
45	c1y9qA_	Alignment	not modelled	62.9	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, hth_3 family; **PDBTitle:** crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
46	d1r8ja1	Alignment	not modelled	42.1	47	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
47	d1sv1a_	Alignment	not modelled	38.9	53	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
48	d1v2za_	Alignment	not modelled	38.3	53	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
49	c2bnoA_	Alignment	not modelled	36.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of the hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
50	d1r89a3	Alignment	not modelled	33.3	78	**Fold:**Ferredoxin-like **Superfamily:**PAP/Archaeal CCA-adding enzyme, C-terminal domain **Family:**Archaeal tRNA CCA-adding enzyme
51	c2qfcB_	Alignment	not modelled	28.2	18	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**plcr protein; **PDBTitle:** crystal structure of bacillus thuringiensis plcr complexed with papr
52	c1r8jB_	Alignment	not modelled	26.6	47	**PDB header:**circadian clock protein **Chain:** B: **PDB Molecule:**kaia; **PDBTitle:** crystal structure of circadian clock protein kaia from2 synechococcus elongatus
53	c2axzC_	Alignment	not modelled	25.4	15	**PDB header:**transcription **Chain:** C: **PDB Molecule:**prgx; **PDBTitle:** crystal structure of prgx/ccf10 complex
54	d1e9ma_	Alignment	not modelled	22.7	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
55	c3ci9B_	Alignment	not modelled	22.1	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**heat shock factor-binding protein 1; **PDBTitle:** crystal structure of the human hsbp1
56	c2fjrB_	Alignment	not modelled	17.5	17	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**repressor protein ci;

						PDBTitle: crystal structure of bacteriophage 186
57	d1u04a2	Alignment	not modelled	15.4	45	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**PIWI domain
58	d1fpoa2	Alignment	not modelled	15.3	31	**Fold:**Open three-helical up-and-down bundle **Superfamily:**HSC20 (HSCB), C-terminal oligomerisation domain **Family:**HSC20 (HSCB), C-terminal oligomerisation domain
59	d1r5qa_	Alignment	not modelled	14.1	50	**Fold:**KaiA/RbsU domain **Superfamily:**KaiA/RbsU domain **Family:**Circadian clock protein KaiA, C-terminal domain
60	d1xlqa1	Alignment	not modelled	12.5	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
61	d2ebfx2	Alignment	not modelled	11.0	41	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**PMT domain-like
62	c3rylB_	Alignment	not modelled	9.8	62	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**protein vpa1370; **PDBTitle:** dimerization domain of vibrio parahemolyticus vopl
63	c2wlbB_	Alignment	not modelled	9.2	13	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**electron transfer protein 1, mitochondrial; **PDBTitle:** adrenodoxin-like ferredoxin etp1fd(516-618) of2 schizosaccharomyces pombe mitochondria
64	c2is8A_	Alignment	not modelled	9.2	21	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
65	d1sv6a_	Alignment	not modelled	8.9	21	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
66	d1hywa_	Alignment	not modelled	8.7	47	**Fold:**gpW/XkdW-like **Superfamily:**Head-to-tail joining protein W, gpW **Family:**Head-to-tail joining protein W, gpW
67	d1b4ub_	Alignment	not modelled	8.6	53	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
68	c2zvnF_	Alignment	not modelled	8.5	37	**PDB header:**signaling protein/transcription **Chain:** F: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cozi domain incomplex with diubiquitin in p2121212 space group
69	d1grja1	Alignment	not modelled	8.5	47	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
70	d1ejxb_	Alignment	not modelled	7.9	38	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
71	c3swfA_	Alignment	not modelled	7.7	30	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**cgmp-gated cation channel alpha-1; **PDBTitle:** cnga1 621-690 containing clz domain
72	c2v4hA_	Alignment	not modelled	7.7	37	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nf-kappa-b essential modulator; **PDBTitle:** nemo cc2-lz domain - 1d5 darpin complex
73	c2ppxA_	Alignment	not modelled	7.4	38	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1735; **PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
74	d2ppxa1	Alignment	not modelled	7.4	38	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
75	d1ob8a_	Alignment	not modelled	7.4	24	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
76	c2re3A_	Alignment	not modelled	7.3	40	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
77	c2kddB_	Alignment	not modelled	7.2	24	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**borealin; **PDBTitle:** solution structure of the conserved c-terminal dimerization2 domain of borealin
78	d4ubpb_	Alignment	not modelled	6.9	34	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
79	c2ib1A_	Alignment	not modelled	6.8	25	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain containing membrane protein nradd; **PDBTitle:** solution structure of p45 death domain
80	d2bt6a1	Alignment	not modelled	6.7	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
81	c3fmyA_	Alignment	not modelled	6.6	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
82	c2w4sD_	Alignment	not modelled	6.5	24	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**ankyrin-repeat protein; **PDBTitle:** novel rna-binding domain in cryptosporidium parvum at 2.52 angstrom resolution

83	c2of5A_	Alignment	not modelled	6.4	21	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**death domain-containing protein cradd; **PDBTitle:** oligomeric death domain complex
84	c3r3kA_	Alignment	not modelled	6.3	54	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**cchex-phi22 helix; **PDBTitle:** crystal structure of a parallel 6-helix coiled coil
85	c3r3kB_	Alignment	not modelled	6.3	54	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**cchex-phi22 helix; **PDBTitle:** crystal structure of a parallel 6-helix coiled coil
86	c3r3kC_	Alignment	not modelled	6.3	54	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**cchex-phi22 helix; **PDBTitle:** crystal structure of a parallel 6-helix coiled coil
87	d1jwya1	Alignment	not modelled	6.3	71	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain
88	c3lxfC_	Alignment	not modelled	6.1	29	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
89	d3bz7a1	Alignment	not modelled	6.0	71	**Fold:**SH3-like barrel **Superfamily:**Myosin S1 fragment, N-terminal domain **Family:**Myosin S1 fragment, N-terminal domain
90	d1e9ya1	Alignment	not modelled	6.0	28	**Fold:**beta-clip **Superfamily:**Urease, beta-subunit **Family:**Urease, beta-subunit
91	d2f23a1	Alignment	not modelled	6.0	35	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
92	c2yqfA_	Alignment	not modelled	5.8	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ankyrin-1; **PDBTitle:** solution structure of the death domain of ankyrin-1
93	c1l8dB_	Alignment	not modelled	5.7	38	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** rad50 coiled-coil zn hook
94	c1r48A_	Alignment	not modelled	5.5	54	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**proline/betaine transporter; **PDBTitle:** solution structure of the c-terminal cytoplasmic domain2 residues 468-497 of escherichia coli protein prop
95	d2gf5a1	Alignment	not modelled	5.5	21	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
96	c3ri2B_	Alignment	not modelled	5.3	25	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, padr-like family; **PDBTitle:** crystal structure of padr family transcriptional regulator from2 eggerthella lenta dsm 2243
97	c1xmaA_	Alignment	not modelled	5.2	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**predicted transcriptional regulator; **PDBTitle:** structure of a transcriptional regulator from clostridium thermocellum2 cth-833
98	d1xmaa_	Alignment	not modelled	5.2	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**PadR-like
99	d1jnda2	Alignment	not modelled	5.1	38	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain