Phyre^2

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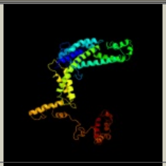
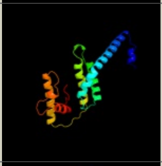
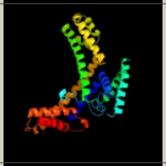
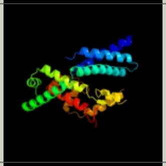
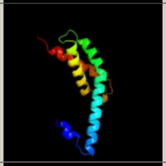
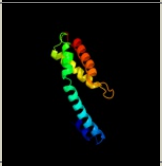
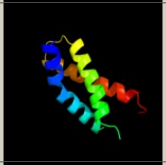
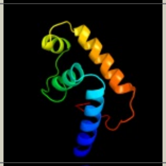
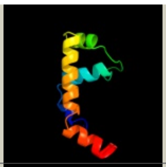
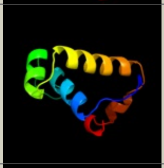
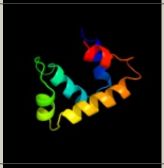
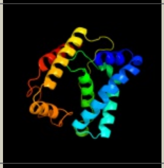
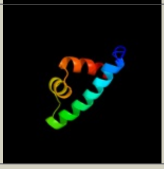
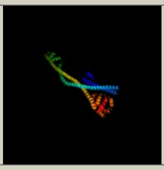
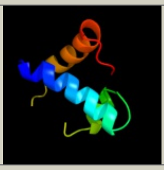
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3iydF_	Alignment		100.0	96	**PDB header:**transcription/dna **Chain:** F: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
2	c2a6eF_	Alignment		100.0	59	**PDB header:**transferase **Chain:** F: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** crystal structure of the t. thermophilus rna polymerase2 holoenzyme
3	c1l9uH_	Alignment		100.0	56	**PDB header:**transcription **Chain:** H: **PDB Molecule:**sigma factor siga; **PDBTitle:** thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
4	c1ku2A_	Alignment		100.0	60	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sigma factor siga; **PDBTitle:** crystal structure of thermus aquaticus rna polymerase sigma2 subunit fragment containing regions 1.2 to 3.1
5	d1siga_	Alignment		100.0	86	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
6	c1rp3G_	Alignment		100.0	25	**PDB header:**transcription **Chain:** G: **PDB Molecule:**rna polymerase sigma factor sigma-28 (flia); **PDBTitle:** cocrystal structure of the flagellar sigma/anti-sigma2 complex, sigma-28/flgm
7	d1ku2a2	Alignment		100.0	60	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
8	d1smyf3	Alignment		100.0	60	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
9	d1rp3a3	Alignment		99.8	28	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
10	c3t72o_	Alignment		99.7	95	**PDB header:**transcription/dna **Chain:** O: **PDB Molecule:**pho box dna (strand 1); **PDBTitle:** phob(e)-sigma70(4)-(rnap-betha-flap-tip-helix)-dna transcription2 activation sub-complex
11	d1smyf2	Alignment		99.7	56	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain

12	d1ku7a_	Alignment		99.6	56	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
13	d2p7vb1	Alignment		99.6	100	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
14	d1ttya_	Alignment		99.5	62	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
15	c1or7A_	Alignment		99.4	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma-e factor; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
16	c3mzyA_	Alignment		99.4	31	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**rna polymerase sigma-h factor; **PDBTitle:** the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
17	d1ku3a_	Alignment		99.4	56	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
18	c2q1zA_	Alignment		99.3	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rpoe, ecf sige; **PDBTitle:** crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
19	d1ku2a1	Alignment		99.2	59	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
20	d1l0oc_	Alignment		98.9	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
21	c1l0oC_	Alignment	not modelled	98.9	18	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**sigma factor; **PDBTitle:** crystal structure of the bacillus stearothermophilus anti-2 sigma factor spoiiab with the sporulation sigma factor3 sigmaf
22	d1rp3a2	Alignment	not modelled	98.9	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
23	c3hugA_	Alignment	not modelled	98.8	19	**PDB header:**transcription/membrane protein **Chain:** A: **PDB Molecule:**rna polymerase sigma factor; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
24	d1rp3a1	Alignment	not modelled	98.7	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma3 domain
25	d1or7a1	Alignment	not modelled	98.3	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
26	c2o8xA_	Alignment	not modelled	98.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
27	d1xsva_	Alignment	not modelled	98.2	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**YlxM/p13-like
28	d1s7oa_	Alignment	not modelled	98.1	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors

						Family: YlxM/p13-like
29	c1c1gA_	Alignment	not modelled	98.0	8	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**tropomyosin; **PDBTitle:** crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
30	c1ciiA_	Alignment		97.9	12	**PDB header:**transmembrane protein **Chain:** A: **PDB Molecule:**colicin ia; **PDBTitle:** colicin ia
31	d1or7b2	Alignment	not modelled	97.8	23	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
32	d1or7a2	Alignment	not modelled	97.8	21	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
33	d1yioa1	Alignment	not modelled	97.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
34	c3ojaB_	Alignment	not modelled	97.4	13	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**anopheles plasmodium-responsive leucine-rich repeat protein **PDBTitle:** crystal structure of lrim1/apl1c complex
35	c1x3uA_	Alignment	not modelled	97.2	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulatory protein fixj; **PDBTitle:** solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
36	c2k6xA_	Alignment		97.1	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase sigma factor rpod; **PDBTitle:** autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
37	c1yvlB_	Alignment	not modelled	97.0	7	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** structure of unphosphorylated stat1
38	c1zljE_	Alignment	not modelled	97.0	18	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dormancy survival regulator; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
39	c3qp5C_	Alignment	not modelled	97.0	24	**PDB header:**transcription **Chain:** C: **PDB Molecule:**cvir transcriptional regulator; **PDBTitle:** crystal structure of cvir bound to antagonist chlorolactone (cl)
40	d1a04a1	Alignment	not modelled	97.0	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
41	c2o7gA_	Alignment	not modelled	96.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable rna polymerase sigma-c factor; **PDBTitle:** crystal structure of the pribnow box recognition region of sigc from2 mycobacterium tuberculosis
42	c2rnjA_	Alignment	not modelled	96.9	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**response regulator protein vrar; **PDBTitle:** nmr structure of the s. aureus vrar dna binding domain
43	d1fsea_	Alignment	not modelled	96.8	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
44	c2krfB_	Alignment	not modelled	96.8	22	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcriptional regulatory protein coma; **PDBTitle:** nmr solution structure of the dna binding domain of competence protein2 a
45	c2q0oA_	Alignment	not modelled	96.8	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**probable transcriptional activator protein trar; **PDBTitle:** crystal structure of an anti-activation complex in bacterial quorum2 sensing
46	d1l3la1	Alignment	not modelled	96.7	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
47	c3sztB_	Alignment	not modelled	96.7	26	**PDB header:**transcription **Chain:** B: **PDB Molecule:**quorum-sensing control repressor; **PDBTitle:** quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
48	c1h0mD_	Alignment	not modelled	96.7	26	**PDB header:**transcription/dna **Chain:** D: **PDB Molecule:**transcriptional activator protein trar; **PDBTitle:** three-dimensional structure of the quorum sensing protein2 trar bound to its autoinducer and to its target dna
49	d1p4wa_	Alignment	not modelled	96.5	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**C-terminal effector domain of the bipartite response regulators **Family:**GerE-like (LuxR/UhpA family of transcriptional regulators)
50	c3cloC_	Alignment	not modelled	96.5	21	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
51	c2w48D_	Alignment	not modelled	96.0	15	**PDB header:**transcription **Chain:** D: **PDB Molecule:**sorbitol operon regulator; **PDBTitle:** crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
						PDB header:transcription

52	c3cwgA_	Alignment	not modelled	95.9	8	**Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** unphosphorylated mouse stat3 core fragment
53	c3n0rA_	Alignment	not modelled	95.5	19	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**response regulator; **PDBTitle:** structure of the phyr stress response regulator at 1.25 angstrom2 resolution
54	d1h3la_	Alignment	not modelled	95.5	16	**Fold:**Sigma2 domain of RNA polymerase sigma factors **Superfamily:**Sigma2 domain of RNA polymerase sigma factors **Family:**Sigma2 domain of RNA polymerase sigma factors
55	c3klnC_	Alignment	not modelled	95.4	17	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, luxr family; **PDBTitle:** vibrio cholerae vpst
56	c3c3wB_	Alignment	not modelled	95.4	20	**PDB header:**transcription **Chain:** B: **PDB Molecule:**two component transcriptional regulatory protein devr; **PDBTitle:** crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
57	c1bg1A_	Alignment	not modelled	95.4	8	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protein (transcription factor stat3b); **PDBTitle:** transcription factor stat3b/dna complex
58	c2jpcA_	Alignment	not modelled	95.3	22	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**ssrb; **PDBTitle:** ssrb dna binding protein
59	c1ei3C_	Alignment	not modelled	94.9	4	**PDB header:** **PDB COMPND:**
60	c1bf5A_	Alignment	not modelled	94.6	7	**PDB header:**gene regulation/dna **Chain:** A: **PDB Molecule:**signal transducer and activator of transcription **PDBTitle:** tyrosine phosphorylated stat-1/dna complex
61	c2efrB_	Alignment	not modelled	94.5	12	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 alpha chain; **PDBTitle:** crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
62	c1hciB_	Alignment	not modelled	94.3	9	**PDB header:**triple-helix coiled coil **Chain:** B: **PDB Molecule:**alpha-actinin 2; **PDBTitle:** crystal structure of the rod domain of alpha-actinin
63	c1deqF_	Alignment	not modelled	94.3	9	**PDB header:** **PDB COMPND:**
64	c1zn2A_	Alignment	not modelled	94.1	13	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**response regulatory protein; **PDBTitle:** low resolution structure of response regulator styr
65	c1rnlA_	Alignment	not modelled	93.7	22	**PDB header:**signal transduction protein **Chain:** A: **PDB Molecule:**nitrate/nitrite response regulator protein narl; **PDBTitle:** the nitrate/nitrite response regulator protein narl from narl
66	c3na7A_	Alignment	not modelled	93.6	9	**PDB header:**gene regulation, chaperone **Chain:** A: **PDB Molecule:**hp0958; **PDBTitle:** 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
67	c2oevA_	Alignment	not modelled	93.3	8	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**programmed cell death 6-interacting protein; **PDBTitle:** crystal structure of alix/aip1
68	d1jhfa1	Alignment	not modelled	92.9	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
69	c1u78A_	Alignment	not modelled	92.9	22	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**transposable element tc3 transposase; **PDBTitle:** structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
70	c2d3eD_	Alignment	not modelled	92.7	15	**PDB header:**contractile protein **Chain:** D: **PDB Molecule:**general control protein gcn4 and tropomyosin 1 **PDBTitle:** crystal structure of the c-terminal fragment of rabbit2 skeletal alpha-tropomyosin
71	c1jchC_	Alignment	not modelled	92.3	11	**PDB header:**ribosome inhibitor, hydrolase **Chain:** C: **PDB Molecule:**colicin e3; **PDBTitle:** crystal structure of colicin e3 in complex with its immunity protein
72	d2o38a1	Alignment	not modelled	92.0	11	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
73	c2o38A_	Alignment	not modelled	92.0	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative xre family transcriptional regulator
74	c2v71A_	Alignment	not modelled	91.3	10	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear distribution protein nude-like 1; **PDBTitle:** coiled-coil region of nudel
75	c3f2hA_	Alignment	not modelled	91.2	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alkylmercury lyase; **PDBTitle:** crystal structure of the mercury-bound form of merb mutant2 c160s, the organomercurial lyase involved in a bacterial3 mercury resistance system
76	c3mkyP_	Alignment	not modelled	89.9	16	**PDB header:**dna binding protein/dna **Chain:** P: **PDB Molecule:**protein sopb; **PDBTitle:** structure of sopb(155-323)-18mer dna complex, i23 form
						Fold:lambda repressor-like DNA-binding domains

77	d2a6ca1	Alignment	not modelled	89.9	15	**Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
78	d1trra_	Alignment	not modelled	89.8	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
79	c1deqO_	Alignment	not modelled	89.7	10	**PDB header:** **PDB COMPND:**
80	c3r0aB_	Alignment	not modelled	89.2	11	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
81	c3ghgK_	Alignment	not modelled	88.8	4	**PDB header:**blood clotting **Chain:** K: **PDB Molecule:**fibrinogen beta chain; **PDBTitle:** crystal structure of human fibrinogen
82	d2d1ha1	Alignment	not modelled	88.8	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**TrmB-like
83	c2x4hA_	Alignment	not modelled	88.7	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hypothetical protein sso2273; **PDBTitle:** crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
84	c3ojaA_	Alignment	not modelled	88.3	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**leucine-rich immune molecule 1; **PDBTitle:** crystal structure of lrim1/apl1c complex
85	c1ei3E_	Alignment	not modelled	88.0	5	**PDB header:** **PDB COMPND:**
86	c1deqD_	Alignment	not modelled	87.8	5	**PDB header:** **PDB COMPND:**
87	c3hnwB_	Alignment	not modelled	87.5	8	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a basic coiled-coil protein of unknown function2 from eubacterium eligens atcc 27750
88	c3fmyA_	Alignment	not modelled	87.4	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)
89	d1vz0a1	Alignment	not modelled	87.0	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
90	c2w7nA_	Alignment	not modelled	87.0	9	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**trfb transcriptional repressor protein; **PDBTitle:** crystal structure of kora bound to operator dna: insight2 into repressor cooperation in rp4 gene regulation
91	c2bnoA_	Alignment	not modelled	86.9	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**epoxidase; **PDBTitle:** the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorenis.
92	c3mlfC_	Alignment	not modelled	86.7	26	**PDB header:**transcription regulator **Chain:** C: **PDB Molecule:**transcriptional regulator; **PDBTitle:** putative transcriptional regulator from staphylococcus aureus.
93	d1rioa_	Alignment	not modelled	86.6	8	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
94	c3k2zA_	Alignment	not modelled	85.7	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lexa repressor; **PDBTitle:** crystal structure of a lexa protein from thermotoga maritima
95	c1y9qA_	Alignment	not modelled	85.5	18	**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
96	c3dtpA_	Alignment	not modelled	85.3	11	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
97	d2cfxa1	Alignment	not modelled	85.0	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
98	c2p6tH_	Alignment	not modelled	85.0	16	**PDB header:**transcription **Chain:** H: **PDB Molecule:**transcriptional regulator, lrp/asnc family; **PDBTitle:** crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
99	c3kxaD_	Alignment	not modelled	83.9	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of ngo0477 from neisseria gonorrhoeae
100	d2cg4a1	Alignment	not modelled	83.7	28	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
101	d1biaa1	Alignment	not modelled	83.6	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Biotin repressor-like
102	c2l4aA_	Alignment	not modelled	83.4	11	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**leucine responsive regulatory protein; **PDBTitle:** nmr structure of the dna-binding domain of e.coli lrp
103	d1nr3a_	Alignment	not modelled	83.4	19	**Fold:**DNA-binding protein Tfx **Superfamily:**DNA-binding protein Tfx

						Family:DNA-binding protein Tfx
104	d2b5aa1	Alignment	not modelled	83.3	18	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
105	d1i1ga1	Alignment	not modelled	83.1	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Lrp/AsnC-like transcriptional regulator N-terminal domain
106	c2it0A_	Alignment	not modelled	83.1	13	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**iron-dependent repressor ider; **PDBTitle:** crystal structure of a two-domain ider-dna complex crystal2 form ii
107	c3nqoB_	Alignment	not modelled	83.0	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**marr-family transcriptional regulator; **PDBTitle:** crystal structure of a marr family transcriptional regulator (cd1569)2 from clostridium difficile 630 at 2.20 a resolution
108	c2jvlA_	Alignment	not modelled	82.8	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
109	c3trbA_	Alignment	not modelled	82.8	14	**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
110	d1r71a_	Alignment	not modelled	82.7	21	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
111	d1y7ya1	Alignment	not modelled	82.6	12	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
112	c2ef8A_	Alignment	not modelled	82.6	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**putative transcription factor; **PDBTitle:** crystal structure of c.ecot38is
113	d1lmb3_	Alignment	not modelled	82.4	9	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
114	c2vbzA_	Alignment	not modelled	82.0	14	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**transcriptional regulatory protein; **PDBTitle:** feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
115	d1jhga_	Alignment	not modelled	81.7	20	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Trp repressor, TrpR
116	c3f6wE_	Alignment	not modelled	81.6	15	**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
117	c1r71B_	Alignment	not modelled	81.6	21	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcriptional repressor protein korb; **PDBTitle:** crystal structure of the dna binding domain of korb in2 complex with the operator dna
118	c2gl2B_	Alignment	not modelled	81.5	11	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**adhesion a; **PDBTitle:** crystal structure of the tetra muntant (t66g,r67g,f68g,2 y69g) of bacterial adhesin fada
119	c2ppxA_	Alignment	not modelled	81.3	19	**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
120	d2ppxa1	Alignment	not modelled	81.3	19	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like