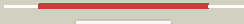



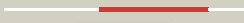







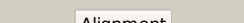











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1990c (-) _2233304_2233645
Date	Mon Aug 5 13:25:09 BST 2019
Unique Job ID	d2b144b984114097

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6fkqC_</a>	 Alignment		100.0	100	<b>PDB header:</b> toxin <b>Chain:</b> C: <b>PDB Molecule:</b> rv1990c (mbca); <b>PDBTitle:</b> crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
2	<a href="#">c6gw6B_</a>	 Alignment		99.9	19	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> xre antitoxin; <b>PDBTitle:</b> structure of the pseudomonas putida res-xre toxin-antitoxin complex
3	<a href="#">c6d0hB_</a>	 Alignment		99.2	20	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> pars: cog5642 (duf2384) antitoxin; <b>PDBTitle:</b> part: prs adp-ribosylating toxin bound to cognate antitoxin pars
4	<a href="#">c3ivpD_</a>	 Alignment		99.1	22	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> putative transposon-related dna-binding protein; <b>PDBTitle:</b> the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
5	<a href="#">c1y9qA_</a>	 Alignment		99.1	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family; <b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
6	<a href="#">d1adra_</a>	 Alignment		99.0	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
7	<a href="#">c3eusB_</a>	 Alignment		99.0	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein; <b>PDBTitle:</b> the crystal structure of the dna binding protein from silicibacter2 pomeroyi
8	<a href="#">c2kpiA_</a>	 Alignment		99.0	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> sos-response transcriptional repressor, lexa; <b>PDBTitle:</b> solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
9	<a href="#">c3vk0B_</a>	 Alignment		99.0	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of hypothetical transcription factor nhf from2 neisseria
10	<a href="#">c3f52A_</a>	 Alignment		99.0	16	<b>PDB header:</b> transcription activator <b>Chain:</b> A: <b>PDB Molecule:</b> clp gene regulator (clgr); <b>PDBTitle:</b> crystal structure of the clp gene regulator clgr from c. glutamicum
11	<a href="#">c3op9A_</a>	 Alignment		99.0	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> pli0006 protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator from listeria innocua

12	<a href="#">c5j9iH_</a>	Alignment		98.9	15	<b>PDB header:</b> antitoxin <b>Chain:</b> H: <b>PDB Molecule:</b> antitoxin iga-2; <b>PDBTitle:</b> crystal structure of the higa2 antitoxin c-terminal domain
13	<a href="#">c1b0nA_</a>	Alignment		98.9	9	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> protein (sinr protein); <b>PDBTitle:</b> sinr protein/sini protein complex
14	<a href="#">d1rioa_</a>	Alignment		98.9	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
15	<a href="#">c3clcC_</a>	Alignment		98.9	6	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
16	<a href="#">d2r1j1</a>	Alignment		98.9	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
17	<a href="#">c5jaaB_</a>	Alignment		98.9	15	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin iga-2; <b>PDBTitle:</b> crystal structure of the higa2 toxin-antitoxin complex
18	<a href="#">c5d4zF_</a>	Alignment		98.9	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> repressor; <b>PDBTitle:</b> crystal structure of repressor from salmonella-temperate phage
19	<a href="#">c4ghjA_</a>	Alignment		98.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
20	<a href="#">d1x57a1</a>	Alignment		98.9	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
21	<a href="#">c5woqA_</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator clgr; <b>PDBTitle:</b> crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
22	<a href="#">d2b5aa1</a>	Alignment	not modelled	98.9	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
23	<a href="#">c3f6wE_</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> xre-family like protein; <b>PDBTitle:</b> xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
24	<a href="#">d1y9qa1</a>	Alignment	not modelled	98.9	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Probable transcriptional regulator VC1968, N-terminal domain
25	<a href="#">c2mezA_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> multiprotein bridging factor (mbp-like); <b>PDBTitle:</b> flexible anchoring of archaeal mbf1 on ribosomes suggests role as2 recruitment factor
26	<a href="#">c3omtA_</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
27	<a href="#">c3m1fC_</a>	Alignment	not modelled	98.8	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> putative transcriptional regulator from staphylococcus aureus.
28	<a href="#">c4pu4C_</a>	Alignment	not modelled	98.8	9	<b>PDB header:</b> toxin/antitoxin/dna <b>Chain:</b> C: <b>PDB Molecule:</b> toxin-antitoxin system antidote transcriptional repressor <b>PDBTitle:</b> shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)

29	<a href="#">d1y7ya1</a>	Alignment	not modelled	98.8	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
30	<a href="#">c3dnvB</a>	Alignment	not modelled	98.8	9	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator hipb; <b>PDBTitle:</b> mdt protein
31	<a href="#">d2ppxa1</a>	Alignment	not modelled	98.8	20	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
32	<a href="#">c2ppxA</a>	Alignment	not modelled	98.8	20	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein atu1735; <b>PDBTitle:</b> crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
33	<a href="#">c4ybaA</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein c; <b>PDBTitle:</b> the structure of the c.kpn2i controller protein
34	<a href="#">c2bnoA</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
35	<a href="#">d1b0na2</a>	Alignment	not modelled	98.8	8	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
36	<a href="#">c2jvIA</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> trmbf1; <b>PDBTitle:</b> nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
37	<a href="#">c2ewtA</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of the dna-binding domain of bldd
38	<a href="#">c3bs3A</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> crystal structure of a putative dna-binding protein from bacteroides2 fragilis
39	<a href="#">c3fmyA</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
40	<a href="#">d1llib</a>	Alignment	not modelled	98.8	18	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
41	<a href="#">c3zhiA</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ci; <b>PDBTitle:</b> n-terminal domain of the ci repressor from bacteriophage tp901-1
42	<a href="#">c2ef8A</a>	Alignment	not modelled	98.8	13	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription factor; <b>PDBTitle:</b> crystal structure of c.ecot38is
43	<a href="#">c3lisB</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> csp231i c protein; <b>PDBTitle:</b> crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
44	<a href="#">c2xcjB</a>	Alignment	not modelled	98.8	6	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> c protein; <b>PDBTitle:</b> crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
45	<a href="#">d1lmb3</a>	Alignment	not modelled	98.8	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
46	<a href="#">c4o8bA</a>	Alignment	not modelled	98.8	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of transcriptional regulator bswr
47	<a href="#">d2icta1</a>	Alignment	not modelled	98.7	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
48	<a href="#">d1lutxA</a>	Alignment	not modelled	98.7	8	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
49	<a href="#">c2o38A</a>	Alignment	not modelled	98.7	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> putative xre family transcriptional regulator
50	<a href="#">d2o38a1</a>	Alignment	not modelled	98.7	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
51	<a href="#">d1sq8a</a>	Alignment	not modelled	98.7	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
52	<a href="#">c2ebyA</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ybaq; <b>PDBTitle:</b> crystal structure of a hypothetical protein from e. coli
53	<a href="#">c3kxaD</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of ngo0477 from neisseria gonorrhoeae
54	<a href="#">c5uk3J</a>	Alignment	not modelled	98.7	18	<b>PDB header:</b> lyase <b>Chain:</b> J: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of cyanase from t. urticae
55	<a href="#">c5fd4B</a>	Alignment	not modelled	98.7	25	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> comr; <b>PDBTitle:</b> crystal structure of comr from streptococcus suis

56	<a href="#">c5jubA</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> crystal structure of comr from s.thermophilus in complex with dna and2 its signalling peptide coms.
57	<a href="#">d1r69a</a>	Alignment	not modelled	98.7	21	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
58	<a href="#">c3gn5B</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator mqsa (ygit/b3021); <b>PDBTitle:</b> structure of the e. coli protein mqsa (ygit/b3021)
59	<a href="#">c3b7hA</a>	Alignment	not modelled	98.7	11	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> prophage lp1 protein 11; <b>PDBTitle:</b> crystal structure of the prophage lp1 protein 11
60	<a href="#">c4mcxE</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> toxin <b>Chain:</b> E: <b>PDB Molecule:</b> antidote protein; <b>PDBTitle:</b> p. vulgaris higa structure, crystal form 2
61	<a href="#">d2a6ca1</a>	Alignment	not modelled	98.6	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
62	<a href="#">c3cecA</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative antidote protein of plasmid maintenance system; <b>PDBTitle:</b> crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
63	<a href="#">d2croa</a>	Alignment	not modelled	98.6	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
64	<a href="#">c3t76A</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator vanug; <b>PDBTitle:</b> crystal structure of transcriptional regulator vanug, form ii
65	<a href="#">c3trbA</a>	Alignment	not modelled	98.6	7	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> virulence-associated protein i; <b>PDBTitle:</b> structure of an addition module antidote protein of a higa (higa)2 family from coxiella burnetii
66	<a href="#">c3bdnB</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> lambda repressor; <b>PDBTitle:</b> crystal structure of the lambda repressor
67	<a href="#">c6f8sA</a>	Alignment	not modelled	98.5	7	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> xre family transcriptional regulator; <b>PDBTitle:</b> toxin-antitoxin complex grata
68	<a href="#">c4yv9C</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> dna binding protein/inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> x-ray crystal structure of streptococcus dysgalactiae shp pheromone2 receptor rgg2
69	<a href="#">d2ofya1</a>	Alignment	not modelled	98.5	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
70	<a href="#">c2grmB</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> prgx; <b>PDBTitle:</b> crystal structure of prgx/icf10 complex
71	<a href="#">c4rykA</a>	Alignment	not modelled	98.5	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0325 protein; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator from2 listeria monocytogenes egd-e
72	<a href="#">c2axzC</a>	Alignment	not modelled	98.3	14	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> prgx; <b>PDBTitle:</b> crystal structure of prgx/ccf10 complex
73	<a href="#">c3pxpA</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> helix-turn-helix domain protein; <b>PDBTitle:</b> crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
74	<a href="#">c2fjrB</a>	Alignment	not modelled	98.3	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> repressor protein ci; <b>PDBTitle:</b> crystal structure of bacteriophage 186
75	<a href="#">c6b9rD</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> hydroxyethylphosphonate dioxygenase; <b>PDBTitle:</b> streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
76	<a href="#">c6b9tH</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> methylphosphonate synthase; <b>PDBTitle:</b> crystal structure of mpns with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
77	<a href="#">c2qfcB</a>	Alignment	not modelled	98.2	20	<b>PDB header:</b> transcription regulation <b>Chain:</b> B: <b>PDB Molecule:</b> plcr protein; <b>PDBTitle:</b> crystal structure of bacillus thuringiensis plcr complexed with papr
78	<a href="#">c2kfsA</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical regulatory protein; <b>PDBTitle:</b> nmr structure of rv2175c
79	<a href="#">c2mqkA</a>	Alignment	not modelled	98.2	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent target dna activator b; <b>PDBTitle:</b> solution structure of n terminal domain of the mub aaa+ atpase
80	<a href="#">c3qyxD</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> D: <b>PDB Molecule:</b> esx-1 secretion-associated regulator espr; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment
81	<a href="#">c5d50I</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> repressor; <b>PDBTitle:</b> crystal structure of rep-ant complex from salmonella-temperate phage

82	<a href="#">c3fymA</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the 1a structure of ymfM, a putative dna-binding membrane2 protein from staphylococcus aureus
83	<a href="#">c2wusR</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> structural protein <b>Chain:</b> R: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> bacterial actin mreB assembles in complex with cell shape protein rodZ
84	<a href="#">c4gqmA</a>	Alignment	not modelled	97.8	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ct009; <b>PDBTitle:</b> crystal structure of a helix-turn-helix containing hypothetical2 protein (ct009) from chlamydia trachomatis in a sub-domain swap3 conformation
85	<a href="#">d2hsga1</a>	Alignment	not modelled	96.9	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
86	<a href="#">d1lcda</a>	Alignment	not modelled	96.9	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
87	<a href="#">d2bjca1</a>	Alignment	not modelled	96.9	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
88	<a href="#">c1efaA</a>	Alignment	not modelled	96.7	12	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> lac repressor; <b>PDBTitle:</b> crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpF
89	<a href="#">d1qpza1</a>	Alignment	not modelled	96.7	10	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
90	<a href="#">c3bd1B</a>	Alignment	not modelled	96.6	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cro protein; <b>PDBTitle:</b> structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
91	<a href="#">d1efaa1</a>	Alignment	not modelled	96.6	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
92	<a href="#">c2l8nA</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor cytr; <b>PDBTitle:</b> nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
93	<a href="#">d1dwka1</a>	Alignment	not modelled	96.5	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Cyanase N-terminal domain
94	<a href="#">c2lcvA</a>	Alignment	not modelled	96.5	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor cytr; <b>PDBTitle:</b> structure of the cytidine repressor dna-binding domain; an alternate2 calculation
95	<a href="#">c1bdhA</a>	Alignment	not modelled	96.4	10	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (purine repressor); <b>PDBTitle:</b> purine repressor mutant-hypoxanthine-palindromic operator2 complex
96	<a href="#">d1luxca</a>	Alignment	not modelled	96.4	8	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
97	<a href="#">c2auwB</a>	Alignment	not modelled	96.3	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein ne0471; <b>PDBTitle:</b> crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
98	<a href="#">c5yszA</a>	Alignment	not modelled	96.3	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> transcriptional regulator celr-cellobiose complex
99	<a href="#">d1ic8a2</a>	Alignment	not modelled	96.3	11	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
100	<a href="#">c3kxD</a>	Alignment	not modelled	96.3	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
101	<a href="#">c1lbgB</a>	Alignment	not modelled	96.3	12	<b>PDB header:</b> <b>PDB COMPND:</b>
102	<a href="#">d1s4ka</a>	Alignment	not modelled	96.2	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> YdiL-like
103	<a href="#">c2iv1J</a>	Alignment	not modelled	96.1	15	<b>PDB header:</b> lyase <b>Chain:</b> J: <b>PDB Molecule:</b> cyanate hydratase; <b>PDBTitle:</b> site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
104	<a href="#">c3h5tA</a>	Alignment	not modelled	96.1	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
105	<a href="#">d1luxda</a>	Alignment	not modelled	96.0	8	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
106	<a href="#">c1zvva</a>	Alignment	not modelled	95.9	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-resistance amylase regulator; <b>PDBTitle:</b> crystal structure of a ccpA-crh-dna complex
107	<a href="#">c4go1A</a>	Alignment	not modelled	95.7	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lsrR; <b>PDBTitle:</b> crystal structure of full length transcription repressor lsrR from e.2 coli.
108	<a href="#">c2w49D</a>	Alignment	not modelled	95.4	9	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator;



108	<a href="#">c2w46U_</a>	Alignment	not modelled	95.4	9	<b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
109	<a href="#">c4j2nB_</a>	Alignment	not modelled	95.4	14	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
110	<a href="#">c5j2yA_</a>	Alignment	not modelled	95.3	11	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> molecular insight into the regulatory mechanism of the quorum-sensing2 repressor rsal in pseudomonas aeruginosa
111	<a href="#">d1rzsA_</a>	Alignment	not modelled	95.1	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
112	<a href="#">c4j2nA_</a>	Alignment	not modelled	94.9	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
113	<a href="#">c1ic8B_</a>	Alignment	not modelled	94.8	11	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hepatocyte nuclear factor 1-alpha; <b>PDBTitle:</b> hepatocyte nuclear factor 1a bound to dna : mody3 gene product
114	<a href="#">d2auwa1</a>	Alignment	not modelled	94.7	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE0471 C-terminal domain-like
115	<a href="#">d2bnma1</a>	Alignment	not modelled	94.7	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
116	<a href="#">c2h8rA_</a>	Alignment	not modelled	94.1	12	<b>PDB header:</b> transcription activator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> hepatocyte nuclear factor 1-beta; <b>PDBTitle:</b> hepatocyte nuclear factor 1b bound to dna: mody5 gene2 product
117	<a href="#">c6amaO_</a>	Alignment	not modelled	93.9	29	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> O: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
118	<a href="#">d2ao9a1</a>	Alignment	not modelled	93.7	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Nanomeric phage protein-like
119	<a href="#">c3vwbA_</a>	Alignment	not modelled	93.5	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> virulence regulon transcriptional activator virb; <b>PDBTitle:</b> crystal structure of virb core domain (se-met derivative) complexed2 with the cis-acting site (5-bru modifications) upstream icsb promoter
120	<a href="#">c3mkyP_</a>	Alignment	not modelled	93.5	9	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> P: <b>PDB Molecule:</b> protein sobp; <b>PDBTitle:</b> structure of sobp(155-323)-18mer dna complex, i23 form