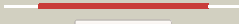
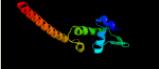


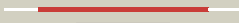


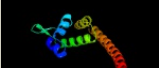









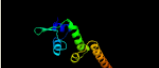





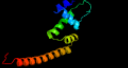
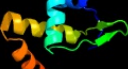
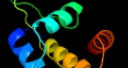

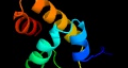





# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0353\_(hspR)\_423639\_424019  
 Date Tue Jul 23 14:50:42 BST 2019  
 Unique Job ID 950c3c45a4d4873e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3d6zA_</a>	 Alignment		99.8	20	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug-efflux transporter 1 regulator; <b>PDBTitle:</b> crystal structure of r275e mutant of bmrr bound to dna and rhodamine
2	<a href="#">c2zhhA_</a>	 Alignment		99.8	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensitive transcriptional activator soxr; <b>PDBTitle:</b> crystal structure of soxr
3	<a href="#">d1r8da_</a>	 Alignment		99.8	20	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
4	<a href="#">c3gpvA_</a>	 Alignment		99.8	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr2 family from bacillus thuringiensis
5	<a href="#">d1q06a_</a>	 Alignment		99.8	20	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
6	<a href="#">c3gp4B_</a>	 Alignment		99.8	18	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
7	<a href="#">c3qa0A_</a>	 Alignment		99.8	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> merr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
8	<a href="#">c3ucsB_</a>	 Alignment		99.8	18	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> chaperone-modulator protein cbpm; <b>PDBTitle:</b> crystal structure of the complex between cbpa j-domain and cbpm
9	<a href="#">c5xqlA_</a>	 Alignment		99.8	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug-efflux transporter 1 regulator; <b>PDBTitle:</b> crystal structure of a pseudomonas aeruginosa transcriptional2 regulator
10	<a href="#">c2vz4A_</a>	 Alignment		99.8	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional activator tipa; <b>PDBTitle:</b> the n-terminal domain of merr-like protein tipal bound to promoter dna
11	<a href="#">c3hh0C_</a>	 Alignment		99.8	22	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator, merr family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, merr family from2 bacillus cereus

12	<a href="#">d1r8ea1</a>	Alignment		99.8	21	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
13	<a href="#">c5gpeB</a>	Alignment		99.8	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator, merr-family; <b>PDBTitle:</b> crystal structure of the transcription regulator pbrr691 from 2 ralstonia metallidurans ch34 in complex with lead(ii)
14	<a href="#">c4r24B</a>	Alignment		99.8	27	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator tnra; <b>PDBTitle:</b> complete dissection of b. subtilis nitrogen homeostatic circuitry
15	<a href="#">c4r4eA</a>	Alignment		99.8	37	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator glnr; <b>PDBTitle:</b> structure of glnr-dna complex
16	<a href="#">c5criA</a>	Alignment		99.7	30	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric resistance operon regulatory protein; <b>PDBTitle:</b> crystal structure of the transcription activator tn501 merr in complex2 with mercury (ii)
17	<a href="#">c2jmlA</a>	Alignment		99.7	32	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> dna binding domain/transcriptional regulator; <b>PDBTitle:</b> solution structure of the n-terminal domain of cara repressor
18	<a href="#">c5i44E</a>	Alignment		99.7	20	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> E: <b>PDB Molecule:</b> chromosome-anchoring protein raca; <b>PDBTitle:</b> structure of raca-dna complex; p21 form
19	<a href="#">c5c8eC</a>	Alignment		99.6	27	<b>PDB header:</b> transcription regulator/dna <b>Chain:</b> C: <b>PDB Molecule:</b> light-dependent transcriptional regulator carh; <b>PDBTitle:</b> crystal structure of thermus thermophilus carh bound to adenosylcobalamin and a 26-bp dna segment
20	<a href="#">c5af3A</a>	Alignment		99.6	12	<b>PDB header:</b> dna binding <b>Chain:</b> A: <b>PDB Molecule:</b> vapbc49; <b>PDBTitle:</b> x-ray crystal structure of rv2018 from mycobacterium tuberculosis
21	<a href="#">c4ua2B</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> crystal structure of dual function transcriptional regulator merr from 2 bacillus megaterium mb1
22	<a href="#">c2dg6A</a>	Alignment	not modelled	99.5	28	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
23	<a href="#">c6amaO</a>	Alignment	not modelled	99.3	24	<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
24	<a href="#">c4j2nB</a>	Alignment	not modelled	98.0	24	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
25	<a href="#">c4j2nA</a>	Alignment	not modelled	97.9	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp37; <b>PDBTitle:</b> crystal structure of mycobacteriophage pukovnik xis
26	<a href="#">d1q08a</a>	Alignment	not modelled	97.6	16	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
27	<a href="#">c2ev2B</a>	Alignment	not modelled	96.8	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein rv1264/mt1302; <b>PDBTitle:</b> structure of rv1264n, the regulatory domain of the mycobacterial2 adenyllyl cylcase rv1264, at ph 8.5
28	<a href="#">c1z4hA</a>	Alignment	not modelled	96.6	9	<b>PDB header:</b> protein binding, dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> tor inhibition protein; <b>PDBTitle:</b> the response regulator tori belongs to a new family of2 atypical excisionase <b>PDB header:</b> transcription regulator

29	<a href="#">c5ydcA</a>	Alignment	not modelled	96.3	13	<b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator rv1828; <b>PDBTitle:</b> crystal structure of mercury soaked c-terminal domain of rv1828 from2 mycobacterium tuberculosis
30	<a href="#">c2kfsA</a>	Alignment	not modelled	96.1	21	<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
31	<a href="#">c3ezfA</a>	Alignment	not modelled	95.5	9	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> para; <b>PDBTitle:</b> partition protein
32	<a href="#">c1hlvA</a>	Alignment	not modelled	94.3	18	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> major centromere autoantigen b; <b>PDBTitle:</b> crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
33	<a href="#">c2wusR</a>	Alignment	not modelled	94.1	12	<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
34	<a href="#">d1j9ia</a>	Alignment	not modelled	93.7	21	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Terminase gpNU1 subunit domain
35	<a href="#">d1stza1</a>	Alignment	not modelled	92.9	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain
36	<a href="#">c6j05B</a>	Alignment	not modelled	92.7	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
37	<a href="#">c1u78A</a>	Alignment	not modelled	91.7	10	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> transposable element tc3 transposase; <b>PDBTitle:</b> structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna
38	<a href="#">d1biaa1</a>	Alignment	not modelled	91.7	12	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
39	<a href="#">c3fymA</a>	Alignment	not modelled	91.6	4	<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
40	<a href="#">c5dukA</a>	Alignment	not modelled	90.9	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna binding protein; <b>PDBTitle:</b> n-terminal structure of putative dna binding transcription factor from2 thermoplasmatales archaeon scgc ab-539-n05
41	<a href="#">c3cuoB</a>	Alignment	not modelled	90.9	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized hth-type transcriptional regulator ygav; <b>PDBTitle:</b> crystal structure of the predicted dna-binding transcriptional2 regulator from e. coli
42	<a href="#">c3by6C</a>	Alignment	not modelled	90.4	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> predicted transcriptional regulator; <b>PDBTitle:</b> crystal structure of a transcriptional regulator from oenococcus oeni
43	<a href="#">d1j5ya1</a>	Alignment	not modelled	89.1	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Biotin repressor-like
44	<a href="#">c6j0eB</a>	Alignment	not modelled	89.1	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> arsenic responsive repressor arsr; <b>PDBTitle:</b> structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
45	<a href="#">c6paxA</a>	Alignment	not modelled	89.0	12	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> homeobox protein pax-6; <b>PDBTitle:</b> crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
46	<a href="#">c5j9iH</a>	Alignment	not modelled	89.0	23	<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
47	<a href="#">c4gqmA</a>	Alignment	not modelled	88.7	9	<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
48	<a href="#">d2d1ha1</a>	Alignment	not modelled	87.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> TrmB-like
49	<a href="#">d2ppxa1</a>	Alignment	not modelled	87.6	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
50	<a href="#">c2ppxA</a>	Alignment	not modelled	87.6	14	<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
51	<a href="#">c3kxaD</a>	Alignment	not modelled	87.6	24	<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
52	<a href="#">c2oqgA</a>	Alignment	not modelled	87.3	21	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> arsr-like transcriptional regulator from rhodococcus sp. rha1
53	<a href="#">c5jaaB</a>	Alignment	not modelled	87.3	23	<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
54	<a href="#">c3jthA</a>	Alignment	not modelled	87.2	17	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription activator hlyu; <b>PDBTitle:</b> crystal structure of a transcriptional regulator hlyu from2

						vibrio vulnificus cmcp6
55	<a href="#">d2jn6a1</a>	Alignment	not modelled	87.1	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Cgl2762-like
56	<a href="#">c5jbrA</a>	Alignment	not modelled	86.8	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein bcav_2135; <b>PDBTitle:</b> crystal structure of uncharacterized protein bcav_2135 from2 beutenbergia cavernae
57	<a href="#">c1y6uA</a>	Alignment	not modelled	86.8	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> excisionase from transposon tn916; <b>PDBTitle:</b> the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
58	<a href="#">c3clcC</a>	Alignment	not modelled	86.5	11	<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
59	<a href="#">c5woqA</a>	Alignment	not modelled	86.4	14	<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
60	<a href="#">c3f6vA</a>	Alignment	not modelled	86.1	25	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> possible transcriptional regulator, arsr family protein; <b>PDBTitle:</b> crystal structure of possible transcriptional regulator for arsenical2 resistance
61	<a href="#">c2kpiA</a>	Alignment	not modelled	86.1	19	<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
62	<a href="#">c1b0nA</a>	Alignment	not modelled	85.8	26	<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
63	<a href="#">c3fmyA</a>	Alignment	not modelled	85.6	18	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mqa <b>PDBTitle:</b> structure of the c-terminal domain of the e. coli protein2 mqa (ygit/b3021)
64	<a href="#">d2ofya1</a>	Alignment	not modelled	84.6	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
65	<a href="#">c4r1hA</a>	Alignment	not modelled	84.4	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0741 protein; <b>PDBTitle:</b> gntr family transcriptional regulator from listeria monocytogenes
66	<a href="#">d1y7ya1</a>	Alignment	not modelled	84.4	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
67	<a href="#">d1pdnc</a>	Alignment	not modelled	84.2	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
68	<a href="#">c2ev5B</a>	Alignment	not modelled	84.2	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator mntr; <b>PDBTitle:</b> bacillus subtilis manganese transport regulator (mntr)2 bound to calcium
69	<a href="#">c2rn7A</a>	Alignment	not modelled	83.7	30	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> is629 orfa; <b>PDBTitle:</b> nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
70	<a href="#">c1r22B</a>	Alignment	not modelled	82.9	19	<b>PDB header:</b> transcription repressor <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional repressor smtb; <b>PDBTitle:</b> crystal structure of the cyanobacterial metallothionein2 repressor smtb (c14s/c61s/c121s mutant) in the zn2alpha5-3 form
71	<a href="#">c4omzG</a>	Alignment	not modelled	82.9	21	<b>PDB header:</b> transcription <b>Chain:</b> G: <b>PDB Molecule:</b> nolr; <b>PDBTitle:</b> crystal structure of nolr from sinorhizobium fredii
72	<a href="#">c3b7hA</a>	Alignment	not modelled	82.2	23	<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
73	<a href="#">c3eqxB</a>	Alignment	not modelled	81.7	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> fic domain containing transcriptional regulator; <b>PDBTitle:</b> crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
74	<a href="#">d1r1ua</a>	Alignment	not modelled	81.6	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> ArsR-like transcriptional regulators
75	<a href="#">c3izbV</a>	Alignment	not modelled	81.2	18	<b>PDB header:</b> ribosome <b>Chain:</b> V: <b>PDB Molecule:</b> 40s ribosomal protein rps25 (s25e); <b>PDBTitle:</b> localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
76	<a href="#">d1adra</a>	Alignment	not modelled	81.2	9	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
77	<a href="#">c2ebyA</a>	Alignment	not modelled	80.8	19	<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
78	<a href="#">c3op9A</a>	Alignment	not modelled	80.8	23	<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
						<b>Fold:</b> lambda repressor-like DNA-binding domains

79	<a href="#">d2b5aa1</a>	Alignment	not modelled	80.6	20	<b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
80	<a href="#">c3kxD</a>	Alignment	not modelled	80.6	18	<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
81	<a href="#">c3bd1B</a>	Alignment	not modelled	80.3	21	<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
82	<a href="#">c3omtA</a>	Alignment	not modelled	80.2	9	<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.
83	<a href="#">c4nb5D</a>	Alignment	not modelled	80.2	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> dna binding protein; <b>PDBTitle:</b> crystal structure of a transcriptional regulator
84	<a href="#">c3bs3A</a>	Alignment	not modelled	80.1	18	<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
85	<a href="#">d2bjca1</a>	Alignment	not modelled	79.7	22	<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="#">c2kkoB</a>	Alignment	not modelled	79.7	26	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> possible transcriptional regulatory protein <b>PDBTitle:</b> solution nmr structure of the homodimeric winged helix-turn-2 helix dna-binding domain (fragment 1-100) mb0332 from3 mycobacterium bovis, a possible arsr-family transcriptional4 regulator. northeast structural genomics consortium target5 mbr242e.
87	<a href="#">c5chhA</a>	Alignment	not modelled	79.6	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> arac family transcriptional regulator; <b>PDBTitle:</b> crystal structure of transcriptional regulator cdpr from pseudomonas2 aeruginosa
88	<a href="#">c3vk0B</a>	Alignment	not modelled	79.6	13	<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 heisseria
89	<a href="#">c1lbgB</a>	Alignment	not modelled	79.4	29	<b>PDB header:</b> <b>PDB COMPND:</b>
90	<a href="#">d1pm6a</a>	Alignment	not modelled	79.3	13	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Excisionase-like
91	<a href="#">c1b10A</a>	Alignment	not modelled	79.0	9	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (multiple antibiotic resistance protein); <b>PDBTitle:</b> multiple antibiotic resistance protein (mara)/dna complex
92	<a href="#">d1x57a1</a>	Alignment	not modelled	78.9	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
93	<a href="#">c1bdhA</a>	Alignment	not modelled	78.8	22	<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
94	<a href="#">c6fkGc</a>	Alignment	not modelled	78.7	6	<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.
95	<a href="#">c5wayB</a>	Alignment	not modelled	78.7	14	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional activator; <b>PDBTitle:</b> mgaspn protein, mga regulator from streptococcus pneumoniae
96	<a href="#">c2xzm8</a>	Alignment	not modelled	78.7	22	<b>PDB header:</b> ribosome <b>Chain:</b> 8: <b>PDB Molecule:</b> rps25e,; <b>PDBTitle:</b> crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
97	<a href="#">c3j3aZ</a>	Alignment	not modelled	78.6	14	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 40s ribosomal protein s25; <b>PDBTitle:</b> structure of the human 40s ribosomal proteins
98	<a href="#">d2coba1</a>	Alignment	not modelled	78.6	23	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Psq domain
99	<a href="#">d2p4wa1</a>	Alignment	not modelled	78.6	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> PF1790-like
100	<a href="#">c4ivnB</a>	Alignment	not modelled	78.4	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> the vibrio vulnificus nanr protein complexed with manna-6p
101	<a href="#">c4r6iA</a>	Alignment	not modelled	78.3	25	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> anthrax toxin expression trans-acting positive regulator; <b>PDBTitle:</b> atxa protein, a virulence regulator from bacillus anthracis.
102	<a href="#">d1qpza1</a>	Alignment	not modelled	78.2	21	<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
103	<a href="#">d1r69a</a>	Alignment	not modelled	78.2	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
104	<a href="#">d2htja1</a>	Alignment	not modelled	78.1	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> FaeA-like



105	<a href="#">c1luxca_</a>	Alignment	not modelled	78.0	26	<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="#">c6cmvA_</a>	Alignment	not modelled	77.8	20	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator Lrs14-like protein; <b>PDBTitle:</b> crystal structure of archaeal biofilm regulator (abfr2) from <i>Sulfolobus acidocaldarius</i>
107	<a href="#">c3k69A_</a>	Alignment	not modelled	77.7	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcription regulator; <b>PDBTitle:</b> crystal structure of a putative transcriptional regulator (lp_0360)2 from <i>Lactobacillus plantarum</i> at 1.95 Å resolution
108	<a href="#">c3dnvB_</a>	Alignment	not modelled	77.6	18	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator hipb; <b>PDBTitle:</b> mdt protein
109	<a href="#">c3f52A_</a>	Alignment	not modelled	77.5	18	<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 <i>C. glutamicum</i>
110	<a href="#">c2du9A_</a>	Alignment	not modelled	77.5	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> predicted transcriptional regulators; <b>PDBTitle:</b> crystal structure of the transcriptional factor from <i>C. glutamicum</i>
111	<a href="#">c3t76A_</a>	Alignment	not modelled	77.4	16	<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
112	<a href="#">d2hsga1</a>	Alignment	not modelled	77.4	20	<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
113	<a href="#">c3h5tA_</a>	Alignment	not modelled	77.3	13	<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 <i>Corynebacterium glutamicum</i>
114	<a href="#">c4ybaA_</a>	Alignment	not modelled	77.3	23	<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
115	<a href="#">c3m1fC_</a>	Alignment	not modelled	77.3	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> C: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> putative transcriptional regulator from <i>Staphylococcus aureus</i> .
116	<a href="#">d1sq8a_</a>	Alignment	not modelled	77.2	14	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
117	<a href="#">c4ghjA_</a>	Alignment	not modelled	77.1	27	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable transcriptional regulator; <b>PDBTitle:</b> 1.75 Å crystal structure of transcriptional regulator ftom2 from <i>Vibrio vulnificus</i> .
118	<a href="#">c5syszA_</a>	Alignment	not modelled	76.9	29	<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
119	<a href="#">c3zeyU_</a>	Alignment	not modelled	76.8	18	<b>PDB header:</b> ribosome <b>Chain:</b> U: <b>PDB Molecule:</b> 40S ribosomal protein s25, putative; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the <i>Trypanosoma brucei</i> ribosome
120	<a href="#">c5lcnwN_</a>	Alignment	not modelled	76.4	14	<b>PDB header:</b> cell cycle <b>Chain:</b> N: <b>PDB Molecule:</b> anaphase-promoting complex subunit 2; <b>PDBTitle:</b> cryo-em structure of the anaphase-promoting complex/cyclosome, in2 complex with the mitotic checkpoint complex (apc/c-mcc) at 4.23 Å resolution