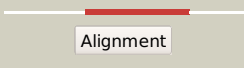
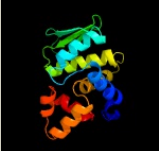
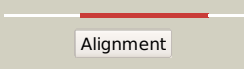

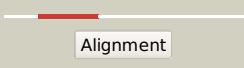

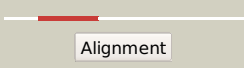

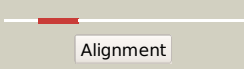

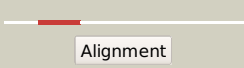

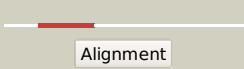

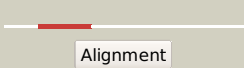

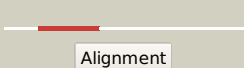

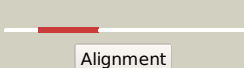

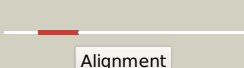



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2017 (- )_2264006_2265046
Date	Mon Aug 5 13:25:12 BST 2019
Unique Job ID	5c1068a14449180f

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6cz6D_</a>	 Alignment		99.9	14	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator prpr; <b>PDBTitle:</b> mycobacterium tuberculosis transcriptional regulator
2	<a href="#">c3dtkA_</a>	 Alignment		99.9	24	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> irre protein; <b>PDBTitle:</b> crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae
3	<a href="#">c3ivpD_</a>	 Alignment		99.5	15	<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.
4	<a href="#">c3op9A_</a>	 Alignment		99.4	17	<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
5	<a href="#">c1y9qA_</a>	 Alignment		99.4	23	<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="#">c2bnoA_</a>	 Alignment		99.4	21	<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.
7	<a href="#">c3lisB_</a>	 Alignment		99.4	21	<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)
8	<a href="#">c3mIfC_</a>	 Alignment		99.4	18	<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.
9	<a href="#">c1b0nA_</a>	 Alignment		99.3	20	<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
10	<a href="#">c4o8bA_</a>	 Alignment		99.3	24	<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
11	<a href="#">d2croa_</a>	 Alignment		99.3	29	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors

12	<a href="#">d1adra_</a>	Alignment		99.3	23	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
13	<a href="#">c2mezA_</a>	Alignment		99.3	23	<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 archaean mbf1 on ribosomes suggests role as2 recruitment factor
14	<a href="#">d1y9qa1</a>	Alignment		99.3	23	<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
15	<a href="#">c5woqA_</a>	Alignment		99.3	21	<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
16	<a href="#">d2r1jl1</a>	Alignment		99.3	25	<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="#">c3clcC_</a>	Alignment		99.3	22	<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
18	<a href="#">c3vk0B_</a>	Alignment		99.3	25	<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 nhtf from2 neisseria
19	<a href="#">c3zhiA_</a>	Alignment		99.3	25	<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
20	<a href="#">c3cecA_</a>	Alignment		99.3	18	<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
21	<a href="#">c2ewtA_</a>	Alignment	not modelled	99.3	32	<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
22	<a href="#">c2kpiA_</a>	Alignment	not modelled	99.3	21	<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
23	<a href="#">c2ebyA_</a>	Alignment	not modelled	99.3	23	<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
24	<a href="#">c3f52A_</a>	Alignment	not modelled	99.3	25	<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
25	<a href="#">d1y7ya1</a>	Alignment	not modelled	99.3	32	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
26	<a href="#">c4mcxE_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> toxin <b>Chain:</b> E: <b>PDB Molecule:</b> antidote protein; <b>PDBTitle:</b> p. vulgaris higba structure, crystal form 2
27	<a href="#">d2icta1</a>	Alignment	not modelled	99.3	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
28	<a href="#">d2b5aa1</a>	Alignment	not modelled	99.2	30	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like

29	<a href="#">d1sq8a_</a>	Alignment	not modelled	99.2	38	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
30	<a href="#">c5d4zF_</a>	Alignment	not modelled	99.2	13	<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
31	<a href="#">d1x57a1</a>	Alignment	not modelled	99.2	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
32	<a href="#">d1b0na2</a>	Alignment	not modelled	99.2	23	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
33	<a href="#">c6b9rD_</a>	Alignment	not modelled	99.2	26	<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
34	<a href="#">d1rioa_</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
35	<a href="#">d1r69a_</a>	Alignment	not modelled	99.2	35	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
36	<a href="#">c3omtA_</a>	Alignment	not modelled	99.2	21	<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.
37	<a href="#">c3trbA_</a>	Alignment	not modelled	99.2	18	<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 addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
38	<a href="#">c3bs3A_</a>	Alignment	not modelled	99.2	29	<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="#">c6b9tH_</a>	Alignment	not modelled	99.2	15	<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
40	<a href="#">c5fd4B_</a>	Alignment	not modelled	99.2	16	<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
41	<a href="#">c5jubA_</a>	Alignment	not modelled	99.2	19	<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.
42	<a href="#">c3f6wE_</a>	Alignment	not modelled	99.2	30	<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
43	<a href="#">c6f8sA_</a>	Alignment	not modelled	99.2	20	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> xre family transcriptional regulator; <b>PDBTitle:</b> toxin-antitoxin complex grata
44	<a href="#">c2jvIA_</a>	Alignment	not modelled	99.2	28	<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
45	<a href="#">c2xcjB_</a>	Alignment	not modelled	99.2	17	<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
46	<a href="#">c3qyxD_</a>	Alignment	not modelled	99.2	18	<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
47	<a href="#">c3kxaD_</a>	Alignment	not modelled	99.1	33	<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
48	<a href="#">d1utxa_</a>	Alignment	not modelled	99.1	22	<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="#">c4rykA_</a>	Alignment	not modelled	99.1	19	<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
50	<a href="#">c4yv9C_</a>	Alignment	not modelled	99.1	18	<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
51	<a href="#">c3b7hA_</a>	Alignment	not modelled	99.1	22	<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
52	<a href="#">c2o38A_</a>	Alignment	not modelled	99.1	17	<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
53	<a href="#">d2o38a1</a>	Alignment	not modelled	99.1	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
54	<a href="#">d1lmb3_</a>	Alignment	not modelled	99.1	23	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
55	<a href="#">d1llib_</a>	Alignment	not modelled	99.1	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors

56	<a href="#">c2grmB_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> prgx; <b>PDBTitle:</b> crystal structure of prgx/icf10 complex
57	<a href="#">c3eusB_</a>	Alignment	not modelled	99.1	31	<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
58	<a href="#">c2ef8A_</a>	Alignment	not modelled	99.1	38	<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
59	<a href="#">c5uk3J_</a>	Alignment	not modelled	99.1	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
60	<a href="#">c4ybaA_</a>	Alignment	not modelled	99.1	22	<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
61	<a href="#">d2ofya1</a>	Alignment	not modelled	99.1	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
62	<a href="#">c3dvnB_</a>	Alignment	not modelled	99.1	25	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator hipb; <b>PDBTitle:</b> mdt protein
63	<a href="#">c4pu4C_</a>	Alignment	not modelled	99.0	34	<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)
64	<a href="#">c4ghjA_</a>	Alignment	not modelled	99.0	34	<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.
65	<a href="#">d2a6ca1</a>	Alignment	not modelled	99.0	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
66	<a href="#">c3bdnB_</a>	Alignment	not modelled	99.0	23	<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="#">c3pxpA_</a>	Alignment	not modelled	99.0	32	<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
68	<a href="#">c2axzC_</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> prgx; <b>PDBTitle:</b> crystal structure of prgx/ccf10 complex
69	<a href="#">c5j9iH_</a>	Alignment	not modelled	98.9	18	<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
70	<a href="#">c3t76A_</a>	Alignment	not modelled	98.9	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
71	<a href="#">c2wusR_</a>	Alignment	not modelled	98.9	22	<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
72	<a href="#">c2qfcB_</a>	Alignment	not modelled	98.9	31	<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
73	<a href="#">c3fymA_</a>	Alignment	not modelled	98.8	23	<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 yfmf, a putative dna-binding membrane2 protein from staphylococcus aureus
74	<a href="#">c4gqmA_</a>	Alignment	not modelled	98.8	16	<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
75	<a href="#">c2fjrB_</a>	Alignment	not modelled	98.8	21	<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
76	<a href="#">c5d50I_</a>	Alignment	not modelled	98.8	19	<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
77	<a href="#">c3fmyA_</a>	Alignment	not modelled	98.8	32	<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)
78	<a href="#">d2ppxa1</a>	Alignment	not modelled	98.7	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
79	<a href="#">c2ppxA_</a>	Alignment	not modelled	98.7	27	<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
80	<a href="#">c5jaaB_</a>	Alignment	not modelled	98.7	18	<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
81	<a href="#">c6fkqC_</a>	Alignment	not modelled	98.6	25	<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.

82	<a href="#">c3gn5B_</a>	Alignment	not modelled	98.4	34	<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)
83	<a href="#">c3r1fO_</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> transcription <b>Chain:</b> O: <b>PDB Molecule:</b> esx-1 secretion-associated regulator espr; <b>PDBTitle:</b> crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
84	<a href="#">c2mqkA_</a>	Alignment	not modelled	98.0	15	<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
85	<a href="#">d1dwka1</a>	Alignment	not modelled	97.1	18	<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
86	<a href="#">c3bd1B_</a>	Alignment	not modelled	97.0	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
87	<a href="#">d1nera_</a>	Alignment	not modelled	96.9	15	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
88	<a href="#">c2iv1J_</a>	Alignment	not modelled	96.8	17	<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
89	<a href="#">d2bnma1</a>	Alignment	not modelled	96.7	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
90	<a href="#">c3c37B_</a>	Alignment	not modelled	96.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> peptidase, m48 family; <b>PDBTitle:</b> x-ray structure of the putative zn-dependent peptidase q74d82 at the2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
91	<a href="#">d2hsqa1</a>	Alignment	not modelled	96.1	17	<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="#">c3ce2A_</a>	Alignment	not modelled	96.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative peptidase; <b>PDBTitle:</b> crystal structure of putative peptidase from chlamydomphila abortus
93	<a href="#">c2auwB_</a>	Alignment	not modelled	96.0	13	<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
94	<a href="#">d1lcda_</a>	Alignment	not modelled	95.8	15	<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
95	<a href="#">c3sksA_</a>	Alignment	not modelled	95.8	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oligoendopeptidase f; <b>PDBTitle:</b> crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
96	<a href="#">d2bjca1</a>	Alignment	not modelled	95.8	15	<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="#">d1efaa1</a>	Alignment	not modelled	95.8	15	<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
98	<a href="#">c2h1jA_</a>	Alignment	not modelled	95.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oligoendopeptidase f; <b>PDBTitle:</b> 3.1 a x-ray structure of putative oligoendopeptidase f: crystals grown2 by microfluidic seeding
99	<a href="#">c4aw6B_</a>	Alignment	not modelled	95.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> caax prenyl protease 1 homolog; <b>PDBTitle:</b> crystal structure of the human nuclear membrane zinc metalloprotease2 zmpste24 (face1)
100	<a href="#">d1ic8a2</a>	Alignment	not modelled	95.5	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
101	<a href="#">c1efaA_</a>	Alignment	not modelled	95.5	16	<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
102	<a href="#">c5u57B_</a>	Alignment	not modelled	95.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> (s)-2-hydroxypropylphosphonic acid epoxidase; <b>PDBTitle:</b> psf4 in complex with fe2+ and (s)-2-hpp
103	<a href="#">c3kxD_</a>	Alignment	not modelled	95.1	26	<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
104	<a href="#">c4il3B_</a>	Alignment	not modelled	94.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ste24p; <b>PDBTitle:</b> crystal structure of s. mikatae ste24p
105	<a href="#">c1lbgB_</a>	Alignment	not modelled	94.8	16	<b>PDB header:</b> <b>PDB COMPND:</b>
106	<a href="#">d1qpza1</a>	Alignment	not modelled	94.8	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
107	<a href="#">d1j7na2</a>	Alignment	not modelled	94.7	18	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Anthrax toxin lethal factor, N- and C-terminal domains
						<b>PDB header:</b> transcription regulator



108	<a href="#">c2lcvA_</a>	Alignment	not modelled	94.7	11	<b>Chain:</b> A: <b>PDB Molecule:</b> nth-type transcriptional repressor cytr; <b>PDBTitle:</b> structure of the cytidine repressor dna-binding domain; an alternate2 calculation
109	<a href="#">d2awia1</a>	Alignment	not modelled	94.7	25	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> PrgX N-terminal domain-like
110	<a href="#">c2k9qB_</a>	Alignment	not modelled	94.6	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.
111	<a href="#">c5j2yA_</a>	Alignment	not modelled	94.6	23	<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
112	<a href="#">c2l8nA_</a>	Alignment	not modelled	94.6	11	<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
113	<a href="#">d1au7a2</a>	Alignment	not modelled	94.6	30	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
114	<a href="#">c6aitD_</a>	Alignment	not modelled	94.5	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> beta-barrel assembly-enhancing protease; <b>PDBTitle:</b> crystal structure of e. coli bepa
115	<a href="#">d1e3oc2</a>	Alignment	not modelled	94.4	26	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
116	<a href="#">d1luxda_</a>	Alignment	not modelled	94.4	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
117	<a href="#">c5syszA_</a>	Alignment	not modelled	94.3	16	<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
118	<a href="#">c1bdhA_</a>	Alignment	not modelled	94.3	8	<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
119	<a href="#">d1luxca_</a>	Alignment	not modelled	94.3	18	<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
120	<a href="#">d2ajfa1</a>	Alignment	not modelled	94.3	15	<b>Fold:</b> Zincin-like <b>Superfamily:</b> Metalloproteases ("zincins"), catalytic domain <b>Family:</b> Neurolysin-like