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Description	RVBD1956 (- )_2202145_2202594
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Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1y9qA_</a>	 Alignment		99.7	26	<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
2	<a href="#">c3ivpD_</a>	 Alignment		99.6	18	<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.
3	<a href="#">c3op9A_</a>	 Alignment		99.6	14	<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
4	<a href="#">c2bnoA_</a>	 Alignment		99.6	17	<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.
5	<a href="#">d1rioa_</a>	 Alignment		99.6	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
6	<a href="#">c5d4zF_</a>	 Alignment		99.5	15	<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
7	<a href="#">c1b0nA_</a>	 Alignment		99.5	17	<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
8	<a href="#">c2kpiA_</a>	 Alignment		99.5	20	<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="#">d1y9qa1</a>	 Alignment		99.5	25	<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
10	<a href="#">c5woqA_</a>	 Alignment		99.5	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
11	<a href="#">c2o38A_</a>	 Alignment		99.5	27	<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

12	<a href="#">d2o38a1</a>	Alignment		99.5	27	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
13	<a href="#">c3zhiA</a>	Alignment		99.5	15	<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
14	<a href="#">c3f52A</a>	Alignment		99.5	23	<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
15	<a href="#">d2b5aa1</a>	Alignment		99.5	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
16	<a href="#">c2mezA</a>	Alignment		99.5	21	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> multi-protein bridging factor (mbp-like); <b>PDBTitle:</b> flexible anchoring of archaeal mbf1 on ribosomes suggests role as 2 recruitment factor
17	<a href="#">c3lisB</a>	Alignment		99.5	15	<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)
18	<a href="#">c2ewtA</a>	Alignment		99.5	23	<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 bidd
19	<a href="#">c3vk0B</a>	Alignment		99.5	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 from 2 neisseria
20	<a href="#">c3clcC</a>	Alignment		99.5	13	<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
21	<a href="#">c3kxaD</a>	Alignment	not modelled	99.5	22	<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
22	<a href="#">d1y7ya1</a>	Alignment	not modelled	99.5	25	<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	99.5	23	<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="#">c3m1fC</a>	Alignment	not modelled	99.5	21	<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.
25	<a href="#">c3bs3A</a>	Alignment	not modelled	99.5	20	<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
26	<a href="#">d1x57a1</a>	Alignment	not modelled	99.5	17	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> EDF1-like
27	<a href="#">d2r1j1</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
28	<a href="#">d1lmb3</a>	Alignment	not modelled	99.5	25	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
29	<a href="#">c5iubA</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator;

29	<a href="#">c2juaA</a>	Alignment	not modelled	99.5	10	<b>PDBTitle:</b> crystal structure of comr from s.thermophilus in complex with dna and2 its signalling peptide coms.
30	<a href="#">d1adra</a>	Alignment	not modelled	99.5	20	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
31	<a href="#">c2ebyA</a>	Alignment	not modelled	99.5	20	<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
32	<a href="#">d2ofya1</a>	Alignment	not modelled	99.5	31	<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	99.4	22	<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="#">d1lib</a>	Alignment	not modelled	99.4	21	<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="#">c4o8bA</a>	Alignment	not modelled	99.4	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
36	<a href="#">c3omtA</a>	Alignment	not modelled	99.4	19	<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="#">c3b7hA</a>	Alignment	not modelled	99.4	24	<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
38	<a href="#">d2icta1</a>	Alignment	not modelled	99.4	12	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
39	<a href="#">c6b9tH</a>	Alignment	not modelled	99.4	19	<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="#">d1b0na2</a>	Alignment	not modelled	99.4	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
41	<a href="#">d1utxa</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> SinR domain-like
42	<a href="#">d2a6ca1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> NE1354
43	<a href="#">c3eusB</a>	Alignment	not modelled	99.4	20	<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
44	<a href="#">c5fd4B</a>	Alignment	not modelled	99.4	15	<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
45	<a href="#">c2jvIA</a>	Alignment	not modelled	99.4	23	<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
46	<a href="#">c4pu4C</a>	Alignment	not modelled	99.4	26	<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)
47	<a href="#">c3dnvB</a>	Alignment	not modelled	99.4	29	<b>PDB header:</b> transcription/dna <b>Chain:</b> B: <b>PDB Molecule:</b> hth-type transcriptional regulator hipb; <b>PDBTitle:</b> mdt protein
48	<a href="#">d1r69a</a>	Alignment	not modelled	99.4	22	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
49	<a href="#">d2croa</a>	Alignment	not modelled	99.4	24	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
50	<a href="#">d1sq8a</a>	Alignment	not modelled	99.4	26	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
51	<a href="#">c4mcxE</a>	Alignment	not modelled	99.4	22	<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
52	<a href="#">c3bdnB</a>	Alignment	not modelled	99.4	25	<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
53	<a href="#">c4yv9C</a>	Alignment	not modelled	99.4	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
54	<a href="#">c3cecA</a>	Alignment	not modelled	99.4	17	<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
55	<a href="#">c4rykA</a>	Alignment	not modelled	99.4	20	<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 <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
56	<a href="#">c3trbA_</a>	Alignment	not modelled	99.4	17	<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.
57	<a href="#">c4ghjA_</a>	Alignment	not modelled	99.4	30	<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
58	<a href="#">c5uk3J_</a>	Alignment	not modelled	99.4	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
59	<a href="#">c2ef8A_</a>	Alignment	not modelled	99.4	30	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> xre family transcriptional regulator; <b>PDBTitle:</b> toxin-antitoxin complex grata
60	<a href="#">c6f8sA_</a>	Alignment	not modelled	99.3	23	<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
61	<a href="#">c2xcjB_</a>	Alignment	not modelled	99.3	19	<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
62	<a href="#">c4ybaA_</a>	Alignment	not modelled	99.3	25	<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
63	<a href="#">c3t76A_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> prgx; <b>PDBTitle:</b> crystal structure of prgx/ccf10 complex
64	<a href="#">c2axzC_</a>	Alignment	not modelled	99.3	9	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> prgx; <b>PDBTitle:</b> crystal structure of prgx/icf10 complex
65	<a href="#">c2grmB_</a>	Alignment	not modelled	99.3	12	<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
66	<a href="#">c3qyxD_</a>	Alignment	not modelled	99.2	12	<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
67	<a href="#">c3pxpA_</a>	Alignment	not modelled	99.2	24	<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
68	<a href="#">c2qfcB_</a>	Alignment	not modelled	99.2	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
69	<a href="#">c2wusR_</a>	Alignment	not modelled	99.2	11	<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
70	<a href="#">c3fymA_</a>	Alignment	not modelled	99.2	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)
71	<a href="#">c3fmyA_</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
72	<a href="#">d2ppxa1</a>	Alignment	not modelled	99.1	18	<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
73	<a href="#">c2ppxA_</a>	Alignment	not modelled	99.1	18	<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
74	<a href="#">c4gqmA_</a>	Alignment	not modelled	99.1	21	<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
75	<a href="#">c5j9iH_</a>	Alignment	not modelled	99.1	14	<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="#">c2fjrB_</a>	Alignment	not modelled	99.1	14	<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
77	<a href="#">c5jaaB_</a>	Alignment	not modelled	99.1	20	<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
78	<a href="#">c5d50L_</a>	Alignment	not modelled	98.9	11	<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)
79	<a href="#">c3gn5B_</a>	Alignment	not modelled	98.9	20	<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.
80	<a href="#">c6fkgC_</a>	Alignment	not modelled	98.8	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 nub aaa+
81	<a href="#">c2mqkA_</a>	Alignment	not modelled	98.0	13	

					atpase
82	<a href="#">c3r1fO_</a>	Alignment	not modelled	97.6	13 <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
83	<a href="#">c3bd1B_</a>	Alignment	not modelled	97.3	20 <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
84	<a href="#">c5j2yA_</a>	Alignment	not modelled	97.2	26 <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
85	<a href="#">d2bnma1</a>	Alignment	not modelled	97.0	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
86	<a href="#">d1dwka1</a>	Alignment	not modelled	97.0	17 <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
87	<a href="#">c2iv1J_</a>	Alignment	not modelled	96.7	18 <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
88	<a href="#">c5u57B_</a>	Alignment	not modelled	96.5	13 <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
89	<a href="#">d1nera_</a>	Alignment	not modelled	96.5	20 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
90	<a href="#">d1lcda_</a>	Alignment	not modelled	96.5	24 <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
91	<a href="#">c3vwbA_</a>	Alignment	not modelled	96.5	27 <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 icbs promoter
92	<a href="#">c4go1A_</a>	Alignment	not modelled	96.4	25 <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.
93	<a href="#">c2w48D_</a>	Alignment	not modelled	96.3	24 <b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> sorbitol operon regulator; <b>PDBTitle:</b> crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
94	<a href="#">d2hsqa1</a>	Alignment	not modelled	96.3	23 <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="#">d2bjca1</a>	Alignment	not modelled	96.3	25 <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
96	<a href="#">c1efaA_</a>	Alignment	not modelled	96.1	25 <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
97	<a href="#">c3l1pA_</a>	Alignment	not modelled	96.1	28 <b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> pou domain, class 5, transcription factor 1; <b>PDBTitle:</b> pou protein:dna complex
98	<a href="#">c1ic8B_</a>	Alignment	not modelled	96.0	14 <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
99	<a href="#">c2k9qB_</a>	Alignment	not modelled	96.0	19 <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.
100	<a href="#">c1zx4B_</a>	Alignment	not modelled	96.0	26 <b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> plasmid partition par b protein; <b>PDBTitle:</b> structure of parb bound to dna
101	<a href="#">d1e3oc2</a>	Alignment	not modelled	95.9	24 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
102	<a href="#">d1ic8a2</a>	Alignment	not modelled	95.9	17 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
103	<a href="#">d1efaa1</a>	Alignment	not modelled	95.8	24 <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
104	<a href="#">c3kxD_</a>	Alignment	not modelled	95.8	27 <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
105	<a href="#">d1au7a2</a>	Alignment	not modelled	95.8	16 <b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> POU-specific domain
106	<a href="#">d1qpza1</a>	Alignment	not modelled	95.8	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
107	<a href="#">c1lbgB_</a>	Alignment	not modelled	95.6	25 <b>PDB header:</b> <b>PDB COMPND:</b>

108	<a href="#">c2l8nA_</a>	Alignment	not modelled	95.5	26	<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
109	<a href="#">d1luxca_</a>	Alignment	not modelled	95.5	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
110	<a href="#">d1luxda_</a>	Alignment	not modelled	95.4	23	<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
111	<a href="#">c1bdhA_</a>	Alignment	not modelled	95.4	27	<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
112	<a href="#">c2lcvA_</a>	Alignment	not modelled	95.4	27	<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
113	<a href="#">c2auwB_</a>	Alignment	not modelled	95.3	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
114	<a href="#">c1zvva_</a>	Alignment	not modelled	95.3	23	<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
115	<a href="#">c3k2zA_</a>	Alignment	not modelled	95.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lexa repressor; <b>PDBTitle:</b> crystal structure of a lexa protein from thermotoga maritima
116	<a href="#">c3h5tA_</a>	Alignment	not modelled	95.1	20	<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
117	<a href="#">d1r71a_</a>	Alignment	not modelled	95.1	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> KorB DNA-binding domain-like <b>Family:</b> KorB DNA-binding domain-like
118	<a href="#">c5sysA_</a>	Alignment	not modelled	95.1	26	<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="#">c4la3B_</a>	Alignment	not modelled	95.1	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dimethylsulphoniopropionate (dmsp) lyase dddq; <b>PDBTitle:</b> crystal structure of dimethylsulphoniopropionate (dmsp) lyase dddq2 y131a in complex with dmsp
120	<a href="#">d1k78a1</a>	Alignment	not modelled	95.0	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain