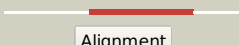





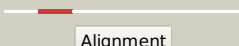

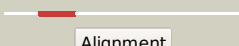

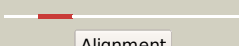

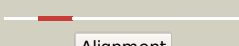

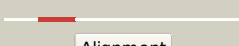
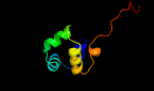

















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2515c_(-)_2831354_2832601
Date	Wed Aug 7 12:50:14 BST 2019
Unique Job ID	7917e38d2eb8620e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6cz6D_	 Alignment		99.9	19	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator ppr; PDBTitle: mycobacterium tuberculosis transcriptional regulator
2	c3dtkA_	 Alignment		99.9	25	PDB header: gene regulation Chain: A: PDB Molecule: irre protein; PDBTitle: crystal structure of the irre protein, a central regulator2 of dna damage repair in deinococcaceae
3	c3ivpD_	 Alignment		99.4	18	PDB header: dna binding protein Chain: D: PDB Molecule: putative transposon-related dna-binding protein; PDBTitle: the structure of a possible transposon-related dna-binding protein2 from clostridium difficile 630.
4	c1y9qA_	 Alignment		99.4	35	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, hth_3 family; PDBTitle: crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae
5	c4mcxE_	 Alignment		99.4	15	PDB header: toxin Chain: E: PDB Molecule: antidote protein; PDBTitle: p. vulgaris higba structure, crystal form 2
6	c2ebyA_	 Alignment		99.4	16	PDB header: transcription Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
7	c3lisB_	 Alignment		99.4	20	PDB header: transcription Chain: B: PDB Molecule: csp231i c protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.csp231i (monoclinic form)
8	c2bnoA_	 Alignment		99.4	30	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
9	c3op9A_	 Alignment		99.4	22	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
10	c3cecA_	 Alignment		99.3	10	PDB header: transcription Chain: A: PDB Molecule: putative antidote protein of plasmid maintenance system; PDBTitle: crystal structure of a putative antidote protein of plasmid2 maintenance system (npun_f2943) from nostoc punctiforme pcc 73102 at3 1.60 a resolution
11	d2icta1	 Alignment		99.3	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like

12	c4ybaA	Alignment		99.3	18	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
13	c2mezA	Alignment		99.3	22	PDB header: rna binding protein Chain: A: PDB Molecule: multiprotein bridging factor (mbp-like); PDBTitle: flexible anchoring of archaean mbf1 on ribosomes suggests role as2 recruitment factor
14	c3mfc	Alignment		99.3	17	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
15	c6b9tH	Alignment		99.3	18	PDB header: oxidoreductase Chain: H: PDB Molecule: methylphosphonate synthase; PDBTitle: crystal structure of mpns with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
16	d1y9qa1	Alignment		99.3	35	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
17	c1b0nA	Alignment		99.3	18	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
18	c3trbA	Alignment		99.3	16	PDB header: dna binding protein Chain: A: PDB Molecule: virulence-associated protein i; PDBTitle: structure of an addiction module antidote protein of a higa (higa)2 family from coxiella burnetii
19	c3bs3A	Alignment		99.3	16	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of a putative dna-binding protein from bacteroides2 fragilis
20	d1rioa	Alignment		99.3	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
21	c6b9rD	Alignment	not modelled	99.3	23	PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
22	c3f52A	Alignment	not modelled	99.3	19	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
23	d2r1j1	Alignment	not modelled	99.3	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
24	c2kpiA	Alignment	not modelled	99.3	13	PDB header: transcription regulator Chain: A: PDB Molecule: sos-response transcriptional repressor, lexa; PDBTitle: solution structure of protein sos-response transcriptional2 repressor, lexa from eubacterium rectale. northeast3 structural genomics consortium target err9a
25	c3vk0B	Alignment	not modelled	99.3	21	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhtf from2 neisseria
26	c6f8sA	Alignment	not modelled	99.3	15	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
27	c5woqA	Alignment	not modelled	99.3	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
28	c3zhiA	Alignment	not modelled	99.3	19	PDB header: transcription Chain: A: PDB Molecule: ci; PDBTitle: n-terminal domain of the ci repressor from bacteriophage

					tp901-1
29	c3omtA	Alignment	not modelled	99.3	20 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
30	d1adra	Alignment	not modelled	99.3	15 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
31	c4o8bA	Alignment	not modelled	99.3	18 PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of transcriptional regulator bswr
32	d2b5aa1	Alignment	not modelled	99.3	19 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
33	c2ewtA	Alignment	not modelled	99.3	25 PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
34	d1utxa	Alignment	not modelled	99.2	19 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
35	c3clcC	Alignment	not modelled	99.2	26 PDB header: transcription regulator/dna Chain: C: PDB Molecule: regulatory protein; PDBTitle: crystal structure of the restriction-modification controller protein2 c.esp1396i tetramer in complex with its natural 35 base-pair operator
36	d1y7ya1	Alignment	not modelled	99.2	24 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
37	d1x57a1	Alignment	not modelled	99.2	25 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
38	c3f6wE	Alignment	not modelled	99.2	21 PDB header: dna binding protein Chain: E: PDB Molecule: xre-family like protein; PDBTitle: xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
39	d1b0na2	Alignment	not modelled	99.2	19 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
40	c5uk3J	Alignment	not modelled	99.2	20 PDB header: lyase Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
41	d1lmb3	Alignment	not modelled	99.2	21 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
42	d1llib	Alignment	not modelled	99.2	21 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
43	c2o38A	Alignment	not modelled	99.2	16 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: putative xre family transcriptional regulator
44	d2o38a1	Alignment	not modelled	99.2	16 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
45	c2jvIA	Alignment	not modelled	99.2	21 PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
46	d1r69a	Alignment	not modelled	99.2	21 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
47	c5d4zF	Alignment	not modelled	99.2	18 PDB header: dna binding protein Chain: F: PDB Molecule: repressor; PDBTitle: crystal structure of repressor from salmonella-temperate phage
48	c3kxaD	Alignment	not modelled	99.1	19 PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
49	d1sq8a	Alignment	not modelled	99.1	18 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
50	c3b7hA	Alignment	not modelled	99.1	28 PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
51	d2croa	Alignment	not modelled	99.1	18 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
52	c5jubA	Alignment	not modelled	99.1	15 PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of comr from s.thermophilus in complex with dna and2 its signalling peptide coms.
53	c2ef8A	Alignment	not modelled	99.1	21 PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
54	d2ofya1	Alignment	not modelled	99.1	23 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
55	c4rykA	Alignment	not modelled	99.1	21 PDB header: dna binding protein Chain: A: PDB Molecule: lmo0325 protein; PDBTitle: crystal structure of a putative transcriptional regulator

						from2 listeria monocytogenes egd-e
56	c5fd4B	Alignment	not modelled	99.1	14	PDB header: transcription regulator Chain: B: PDB Molecule: comr; PDBTitle: crystal structure of comr from streptococcus suis
57	c3eusB	Alignment	not modelled	99.1	28	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
58	c2xcjB	Alignment	not modelled	99.1	15	PDB header: viral protein Chain: B: PDB Molecule: c protein; PDBTitle: crystal structure of p2 c, the immunity repressor of2 temperate e. coli phage p2
59	c3t76A	Alignment	not modelled	99.1	10	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
60	c5j9iH	Alignment	not modelled	99.1	18	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
61	c3dnvB	Alignment	not modelled	99.0	19	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
62	c3qyxD	Alignment	not modelled	99.0	18	PDB header: transcription/dna Chain: D: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment
63	c4yv9C	Alignment	not modelled	99.0	18	PDB header: dna binding protein/inhibitor Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of streptococcus dysgalactiae shp pheromone2 receptor rgg2
64	c3bdnB	Alignment	not modelled	99.0	21	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
65	c4pu4C	Alignment	not modelled	99.0	23	PDB header: toxin/antitoxin/dna Chain: C: PDB Molecule: toxin-antitoxin system antidote transcriptional repressor PDBTitle: shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)
66	c5d50I	Alignment	not modelled	99.0	15	PDB header: dna binding protein Chain: I: PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage
67	c2fjrB	Alignment	not modelled	99.0	12	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
68	c3fmyA	Alignment	not modelled	99.0	17	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqa (ygit/b3021)
69	d2a6ca1	Alignment	not modelled	99.0	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
70	c4ghjA	Alignment	not modelled	99.0	19	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator ftom2 vibrio vulnificus.
71	c2grmB	Alignment	not modelled	98.9	11	PDB header: transcription Chain: B: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/icf10 complex
72	c5jaaB	Alignment	not modelled	98.9	18	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex
73	c3fymA	Alignment	not modelled	98.9	18	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of yfmf, a putative dna-binding membrane2 protein from staphylococcus aureus
74	c2axzC	Alignment	not modelled	98.9	14	PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex
75	c3pxpA	Alignment	not modelled	98.9	16	PDB header: transcription regulator Chain: A: PDB Molecule: helix-turn-helix domain protein; PDBTitle: crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
76	c2wusR	Alignment	not modelled	98.8	17	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
77	c2ppxA	Alignment	not modelled	98.8	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
78	d2ppxa1	Alignment	not modelled	98.8	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
79	c2qfcB	Alignment	not modelled	98.8	23	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
80	c4gqmA	Alignment	not modelled	98.7	21	PDB header: unknown function Chain: A: PDB Molecule: ct009; PDBTitle: crystal structure of a helix-turn-helix containing hypothetical2 protein (ct009) from chlamydia trachomatis in a sub-domain swap3 conformation
81	c3gn5B	Alignment	not modelled	98.6	17	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqa

81	c3gn3B	Alignment	not modelled	98.8	17	(ygit/b3021); PDBTitle: structure of the e. coli protein mqsA (ygit/b3021)
82	c6fkqC	Alignment	not modelled	98.4	26	PDB header: toxin Chain: C; PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
83	c3r1fO	Alignment	not modelled	97.8	17	PDB header: transcription Chain: O; PDB Molecule: resx-1 secretion-associated regulator espr; PDBTitle: crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
84	c2mqkA	Alignment	not modelled	97.6	16	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
85	d1nera	Alignment	not modelled	97.2	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
86	c3bd1B	Alignment	not modelled	97.2	15	PDB header: transcription Chain: B; PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
87	d1dwka1	Alignment	not modelled	97.1	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
88	d2bnma1	Alignment	not modelled	96.8	35	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
89	c2iv1J	Alignment	not modelled	96.8	15	PDB header: lyase Chain: J; PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
90	c3c37B	Alignment	not modelled	96.7	17	PDB header: hydrolase Chain: B; PDB Molecule: peptidase, m48 family; PDBTitle: x-ray structure of the putative zn-dependent peptidase q74d82 at the2 resolution 1.7 a. northeast structural genomics consortium target3 gsr143a
91	c2auwB	Alignment	not modelled	96.2	14	PDB header: unknown function Chain: B; PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
92	c1y791	Alignment	not modelled	96.2	12	PDB header: hydrolase Chain: 1; PDB Molecule: peptidyl-dipeptidase dcp; PDBTitle: crystal structure of the e.coli dipeptidyl carboxypeptidase2 dcp in complex with a peptidic inhibitor
93	c3sksA	Alignment	not modelled	96.2	14	PDB header: hydrolase Chain: A; PDB Molecule: putative oligoendopeptidase f; PDBTitle: crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
94	c5i43B	Alignment	not modelled	95.9	10	PDB header: hydrolase Chain: B; PDB Molecule: k-26 dipeptidyl carboxypeptidase; PDBTitle: structure of k26-dcp
95	c5u57B	Alignment	not modelled	95.9	15	PDB header: oxidoreductase Chain: B; PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
96	c4ka8A	Alignment	not modelled	95.7	17	PDB header: hydrolase Chain: A; PDB Molecule: oligopeptidase a; PDBTitle: structure of organellar oligopeptidase
97	c2h1jA	Alignment	not modelled	95.6	11	PDB header: hydrolase Chain: A; PDB Molecule: oligoendopeptidase f; PDBTitle: 3.1 a x-ray structure of putative oligoendopeptidase f: crystals grown2 by microfluidic seeding
98	d1lcda	Alignment	not modelled	95.5	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
99	c4il3B	Alignment	not modelled	95.3	19	PDB header: hydrolase Chain: B; PDB Molecule: ste24p; PDBTitle: crystal structure of s. mikatae ste24p
100	d2hsqa1	Alignment	not modelled	95.3	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
101	c2c6nA	Alignment	not modelled	95.1	16	PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: angiotensin-converting enzyme, somatic isoform; PDBTitle: structure of human somatic angiotensin-i converting enzyme n domain2 with lisinopril
102	d1s4bp	Alignment	not modelled	94.9	13	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
103	d2bjca1	Alignment	not modelled	94.9	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
104	d1ic8a2	Alignment	not modelled	94.8	5	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
105	c3ce2A	Alignment	not modelled	94.8	20	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: putative peptidase; PDBTitle: crystal structure of putative peptidase from chlamydomphila abortus
106	d1i1ip	Alignment	not modelled	94.7	17	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
107	d1efaa1	Alianment	not modelled	94.5	12	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains

						Family: GalR/LacI-like bacterial regulator
108	d2ajfa1	Alignment	not modelled	94.5	11	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Neurolysin-like
109	c2k9qB	Alignment	not modelled	94.4	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of hth_xre family transcriptional2 regulator bt_p548217 from bacteroides thetaiotaomicron.3 northeast structural genomics consortium target btr244.
110	d1qpza1	Alignment	not modelled	94.3	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
111	c6aitD	Alignment	not modelled	94.3	16	PDB header: hydrolase Chain: D: PDB Molecule: beta-barrel assembly-enhancing protease; PDBTitle: crystal structure of e. coli bepa
112	c2lcvA	Alignment	not modelled	94.3	14	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation
113	c1efaA	Alignment	not modelled	94.2	13	PDB header: transcription/dna Chain: A: PDB Molecule: lac repressor; PDBTitle: crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf
114	c5j2yA	Alignment	not modelled	94.1	17	PDB header: gene regulation/dna Chain: A: PDB Molecule: regulatory protein; PDBTitle: molecular insight into the regulatory mechanism of the quorum-sensing2 repressor rsal in pseudomonas aeruginosa
115	c2l8nA	Alignment	not modelled	94.1	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
116	d1luxda	Alignment	not modelled	94.1	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
117	c3cqbB	Alignment	not modelled	93.9	11	PDB header: hydrolase Chain: B: PDB Molecule: probable protease htpx homolog; PDBTitle: crystal structure of heat shock protein htpx domain from vibrio parahaemolyticus rimd 2210633
118	c4go1A	Alignment	not modelled	93.9	30	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
119	d1luxca	Alignment	not modelled	93.8	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
120	d2auwa1	Alignment	not modelled	93.7	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like