

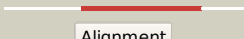
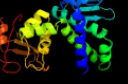
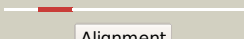


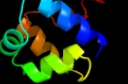
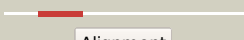
























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0465c (-)_554885_556309
Date	Tue Jul 23 14:50:54 BST 2019
Unique Job ID	6c1e1a2410377627

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6cz6D_	 Alignment		100.0	50	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator pprp; PDBTitle: mycobacterium tuberculosis transcriptional regulator
2	c3dtkA_	 Alignment		99.9	17	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	c2bnoA_	 Alignment		99.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: epoxidase; PDBTitle: the structure of hydroxypropylphosphonic acid epoxidase from s.2 wedmorenis.
4	c1y9qA_	 Alignment		99.5	30	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	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.
6	c1b0nA_	 Alignment		99.4	22	PDB header: transcription regulator Chain: A: PDB Molecule: protein (sinr protein); PDBTitle: sinr protein/sini protein complex
7	c3op9A_	 Alignment		99.4	13	PDB header: transcription regulator Chain: A: PDB Molecule: pli0006 protein; PDBTitle: crystal structure of transcriptional regulator from listeria innocua
8	c6b9rD_	 Alignment		99.4	15	PDB header: oxidoreductase Chain: D: PDB Molecule: hydroxyethylphosphonate dioxygenase; PDBTitle: streptomyces albus hepd with substrate 2-hydroxyethylphosphonate (2-2 hep) and fe(ii) bound
9	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)
10	c6b9tH_	 Alignment		99.4	15	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
11	d1adra_	 Alignment		99.3	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors

12	c5woqA	Alignment		99.3	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator clgr; PDBTitle: crystal structure of an xre family protein transcriptional regulator2 from mycobacterium smegmatis
13	c3f52A	Alignment		99.3	18	PDB header: transcription activator Chain: A: PDB Molecule: clp gene regulator (clgr); PDBTitle: crystal structure of the clp gene regulator clgr from c. glutamicum
14	c2mezA	Alignment		99.3	18	PDB header: rna binding protein Chain: A: PDB Molecule: multi-protein bridging factor (mbp-like); PDBTitle: flexible anchoring of archaean mbf1 on ribosomes suggests role as2 recruitment factor
15	c3mfc	Alignment		99.3	15	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: putative transcriptional regulator from staphylococcus aureus.
16	d1y9qa1	Alignment		99.3	30	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Probable transcriptional regulator VC1968, N-terminal domain
17	c2ewtA	Alignment		99.3	20	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of the dna-binding domain of bldd
18	c3vk0B	Alignment		99.3	21	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of hypothetical transcription factor nhft from2 neisseria
19	d2r1jl1	Alignment		99.3	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
20	d1rioa	Alignment		99.3	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
21	d2b5aa1	Alignment	not modelled	99.3	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
22	c4o8bA	Alignment	not modelled	99.3	20	PDB header: dna binding protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of transcriptional regulator bswr
23	d1b0na2	Alignment	not modelled	99.3	26	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
24	c4mcxE	Alignment	not modelled	99.3	19	PDB header: toxin Chain: E: PDB Molecule: antidote protein; PDBTitle: p. vulgaris higba structure, crystal form 2
25	d2icta1	Alignment	not modelled	99.3	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
26	d1y7ya1	Alignment	not modelled	99.3	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
27	c3clcC	Alignment	not modelled	99.3	28	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
28	c3f6wE	Alignment	not modelled	99.3	23	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
						PDB header: transcription

29	c2ebyA	Alignment	not modelled	99.3	19	Chain: A: PDB Molecule: putative hth-type transcriptional regulator ybaq; PDBTitle: crystal structure of a hypothetical protein from e. coli
30	c2kpiA	Alignment	not modelled	99.3	10	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
31	c3omtA	Alignment	not modelled	99.3	16	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.
32	c3bs3A	Alignment	not modelled	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
33	c3zhiA	Alignment	not modelled	99.2	20	PDB header: transcription Chain: A: PDB Molecule: ci; PDBTitle: n-terminal domain of the ci repressor from bacteriophage tp901-1
34	d1x57a1	Alignment	not modelled	99.2	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: EDF1-like
35	c3cecA	Alignment	not modelled	99.2	17	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
36	c5jubA	Alignment	not modelled	99.2	23	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.
37	c3kxuD	Alignment	not modelled	99.2	24	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ngo0477 from neisseria gonorrhoeae
38	d2o38a1	Alignment	not modelled	99.2	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
39	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
40	d2ofya1	Alignment	not modelled	99.2	19	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
41	c4ybaA	Alignment	not modelled	99.2	19	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein c; PDBTitle: the structure of the c.kpn2i controller protein
42	c5uk3J	Alignment	not modelled	99.2	16	PDB header: lyase Chain: J: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of cyanase from t. urticae
43	d1r69a	Alignment	not modelled	99.2	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
44	c3trbA	Alignment	not modelled	99.2	25	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
45	d1utxa	Alignment	not modelled	99.2	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
46	c2jvIA	Alignment	not modelled	99.2	18	PDB header: transcription Chain: A: PDB Molecule: trmbf1; PDBTitle: nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
47	c3qyxD	Alignment	not modelled	99.2	16	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
48	d1sq8a	Alignment	not modelled	99.2	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
49	d1lmb3	Alignment	not modelled	99.2	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
50	c5fd4B	Alignment	not modelled	99.2	24	PDB header: transcription regulator Chain: B: PDB Molecule: comr; PDBTitle: crystal structure of comr from streptococcus suis
51	d2croa	Alignment	not modelled	99.2	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
52	c3eusB	Alignment	not modelled	99.2	25	PDB header: dna binding protein Chain: B: PDB Molecule: dna-binding protein; PDBTitle: the crystal structure of the dna binding protein from silicibacter2 pomeroyi
53	c2xcjB	Alignment	not modelled	99.2	13	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
54	d1llib	Alignment	not modelled	99.2	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors

55	c6f8sA	Alignment	not modelled	99.2	24	PDB header: toxin Chain: A: PDB Molecule: xre family transcriptional regulator; PDBTitle: toxin-antitoxin complex grata
56	c3b7hA	Alignment	not modelled	99.2	12	PDB header: structural protein Chain: A: PDB Molecule: prophage lp1 protein 11; PDBTitle: crystal structure of the prophage lp1 protein 11
57	c4rykA	Alignment	not modelled	99.2	24	PDB header: dna binding protein Chain: A: PDB Molecule: lmo0325 protein; PDBTitle: crystal structure of a putative transcriptional regulator from <i>listeria monocytogenes</i> egd-e
58	c3pxpA	Alignment	not modelled	99.2	25	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 <i>chloroflexus aurantiacus</i> j-10-fl at 2.30 a3 resolution
59	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
60	c4pu4C	Alignment	not modelled	99.1	15	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)
61	c2ef8A	Alignment	not modelled	99.1	29	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of c.ecot38is
62	c3dnvB	Alignment	not modelled	99.1	18	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator hipb; PDBTitle: mdt protein
63	c4yv9C	Alignment	not modelled	99.1	23	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	c4ghjA	Alignment	not modelled	99.1	18	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: 1.75 angstrom crystal structure of transcriptional regulator from <i>vibrio vulnificus</i> .
65	c3bdnB	Alignment	not modelled	99.0	16	PDB header: transcription/dna Chain: B: PDB Molecule: lambda repressor; PDBTitle: crystal structure of the lambda repressor
66	d2a6ca1	Alignment	not modelled	99.0	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE1354
67	c2grmB	Alignment	not modelled	99.0	31	PDB header: transcription Chain: B: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/pcf10 complex
68	c2wusR	Alignment	not modelled	99.0	25	PDB header: structural protein Chain: R: PDB Molecule: putative uncharacterized protein; PDBTitle: bacterial actin mreB assembles in complex with cell shape protein rodz
69	c3t76A	Alignment	not modelled	99.0	18	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator vanug; PDBTitle: crystal structure of transcriptional regulator vanug, form ii
70	c3fymA	Alignment	not modelled	99.0	18	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the 1a structure of ymfM, a putative dna-binding membrane2 protein from <i>staphylococcus aureus</i>
71	c2axzC	Alignment	not modelled	98.9	31	PDB header: transcription Chain: C: PDB Molecule: prgx; PDBTitle: crystal structure of prgx/ccf10 complex
72	c2qfcB	Alignment	not modelled	98.9	22	PDB header: transcription regulation Chain: B: PDB Molecule: plcr protein; PDBTitle: crystal structure of bacillus thuringiensis plcr complexed with papr
73	c5j9iH	Alignment	not modelled	98.9	12	PDB header: antitoxin Chain: H: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 antitoxin c-terminal domain
74	c3fmyA	Alignment	not modelled	98.9	10	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type transcriptional regulator mqsa PDBTitle: structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
75	c5d50I	Alignment	not modelled	98.9	10	PDB header: dna binding protein Chain: I: PDB Molecule: repressor; PDBTitle: crystal structure of rep-ant complex from salmonella-temperate phage
76	c2fjrB	Alignment	not modelled	98.9	13	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
77	c4gqmA	Alignment	not modelled	98.9	22	PDB header: unknown function Chain: A: PDB Molecule: ct009; PDBTitle: crystal structure of a helix-turn-helix containing hypothetical2 protein (ct009) from <i>chlamydia trachomatis</i> in a sub-domain swap3 conformation
78	c2ppxA	Alignment	not modelled	98.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu1735; PDBTitle: crystal structure of a hth xre-family like protein from <i>agrobacterium tumefaciens</i>
79	d2ppxa1	Alignment	not modelled	98.9	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
80	c5jaaB	Alignment	not modelled	98.8	14	PDB header: toxin Chain: B: PDB Molecule: antitoxin iga-2; PDBTitle: crystal structure of the higa2 toxin-antitoxin complex

81	c3gn5B_	Alignment	not modelled	98.5	10	PDB header: dna binding protein Chain: B: PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
82	c6fkqC_	Alignment	not modelled	98.3	15	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	98.1	16	PDB header: transcription Chain: O: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
84	c2mqkA_	Alignment	not modelled	97.8	9	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	c3bd1B_	Alignment	not modelled	96.9	21	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
86	d1dwka1	Alignment	not modelled	96.9	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
87	c2iv1J_	Alignment	not modelled	96.7	10	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the catalytic2 mechanism of cyanase
88	d1nera_	Alignment	not modelled	96.6	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
89	c2auwB_	Alignment	not modelled	96.4	13	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
90	d2bnma1	Alignment	not modelled	96.2	24	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
91	c5u57B_	Alignment	not modelled	96.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: (s)-2-hydroxypropylphosphonic acid epoxidase; PDBTitle: psf4 in complex with fe2+ and (s)-2-hpp
92	c5j2yA_	Alignment	not modelled	95.9	24	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
93	d1lc8a2	Alignment	not modelled	95.5	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
94	d1lcda_	Alignment	not modelled	95.1	5	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
95	d2awia1	Alignment	not modelled	95.0	33	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: PrgX N-terminal domain-like
96	c4la3B_	Alignment	not modelled	94.9	7	PDB header: lyase Chain: B: PDB Molecule: dimethylsulphoniopropionate (dmsp) lyase dddq; PDBTitle: crystal structure of dimethylsulphoniopropionate (dmsp) lyase dddq2 y131a in complex with dmsp
97	d2hsqa1	Alignment	not modelled	94.9	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
98	d2bjca1	Alignment	not modelled	94.7	5	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
99	c5sysZ_	Alignment	not modelled	94.3	10	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
100	c1efaA_	Alignment	not modelled	94.1	5	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
101	d1efaa1	Alignment	not modelled	94.0	5	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
102	c1lc8B_	Alignment	not modelled	93.9	12	PDB header: transcription/dna Chain: B: PDB Molecule: hepatocyte nuclear factor 1-alpha; PDBTitle: hepatocyte nuclear factor 1a bound to dna : mody3 gene product
103	c2k9qB_	Alignment	not modelled	93.9	18	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.
104	c2lcvA_	Alignment	not modelled	93.8	11	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
105	d2auwa1	Alignment	not modelled	93.7	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: NE0471 C-terminal domain-like
106	c3kxD_	Alignment	not modelled	93.4	10	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi

107	d1qpza1	Alignment	not modelled	93.3	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LaCl-like bacterial regulator
108	c2l8nA_	Alignment	not modelled	93.2	11	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
109	c3sksA_	Alignment	not modelled	93.1	5	PDB header: hydrolase Chain: A: PDB Molecule: putative oligoendopeptidase f; PDBTitle: crystal structure of a putative oligoendopeptidase f from bacillus2 anthracis str. ames
110	c1lbgB_	Alignment	not modelled	93.1	5	PDB header: PDB COMPND:
111	d1luxda_	Alignment	not modelled	93.1	11	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LaCl-like bacterial regulator
112	c1bdhA_	Alignment	not modelled	93.1	8	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
113	d1luxca_	Alignment	not modelled	92.8	8	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GaIR/LaCl-like bacterial regulator
114	c3h5tA_	Alignment	not modelled	92.5	20	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
115	c2h8rA_	Alignment	not modelled	92.4	10	PDB header: transcription activator/dna Chain: A: PDB Molecule: hepatocyte nuclear factor 1-beta; PDBTitle: hepatocyte nuclear factor 1b bound to dna: mody5 gene2 product
116	c3vwbA_	Alignment	not modelled	92.2	19	PDB header: transcription/dna Chain: A: PDB Molecule: virulence regulon transcriptional activator virb; PDBTitle: crystal structure of virb core domain (se-met derivative) complexed2 with the cis-acting site (5-bru modifications) upstream icsb promoter
117	d1au7a2	Alignment	not modelled	92.2	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
118	c3ce2A_	Alignment	not modelled	92.2	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative peptidase; PDBTitle: crystal structure of putative peptidase from chlamydomophila abortus
119	c3l1pA_	Alignment	not modelled	92.0	24	PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex
120	d1e3oc2	Alignment	not modelled	91.9	20	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain