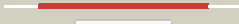
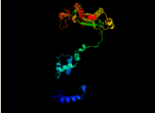


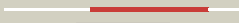




















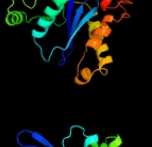
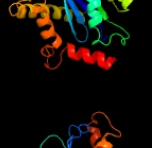


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2167c_(-)_2430167_2431051
Date	Mon Aug 5 13:25:29 BST 2019
Unique Job ID	7c32641478b31598

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4fcyA_	 Alignment		99.9	14	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
2	c3f9kV_	 Alignment		99.9	17	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
3	c5cz1B_	 Alignment		99.8	21	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase
4	d1bcoa2	 Alignment		99.8	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
5	d1c0ma2	 Alignment		99.8	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
6	d1asua_	 Alignment		99.8	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
7	c1c0mA_	 Alignment		99.8	23	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
8	c3nf9A_	 Alignment		99.7	18	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: integrase; PDBTitle: structural basis for a new mechanism of inhibition of hiv integrase2 identified by fragment screening and structure based design
9	c3jcaE_	 Alignment		99.7	20	PDB header: viral protein Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
10	c1bcoA_	 Alignment		99.7	16	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
11	d1lexqa_	 Alignment		99.7	17	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain

12	c5u1cA_	Alignment		99.7	15	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
13	c3kksB_	Alignment		99.7	17	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal2 form ii
14	c4mq3A_	Alignment		99.7	20	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of fiv integrase
15	c1ex4A_	Alignment		99.7	16	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
16	c3hpgC_	Alignment		99.7	16	PDB header: transferase Chain: C: PDB Molecule: integrase; PDBTitle: visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
17	c1k6yB_	Alignment		99.7	16	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
18	d1hyva_	Alignment		99.6	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
19	c5m0rF_	Alignment		99.6	17	PDB header: hydrolase Chain: F: PDB Molecule: integrase; PDBTitle: cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
20	d1cxqa_	Alignment		99.6	23	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
21	d1c6va_	Alignment	not modelled	99.6	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
22	c5ejkG_	Alignment	not modelled	99.5	19	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
23	c3hosA_	Alignment	not modelled	99.5	11	PDB header: transferase, dna binding protein/dna Chain: A: PDB Molecule: transposable element mariner, complete cds; PDBTitle: crystal structure of the mariner mos1 paired end complex with mg
24	c3l2tB_	Alignment	not modelled	99.4	16	PDB header: recombination/dna Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the prototype foamy virus (pfv) intasome in2 complex with magnesium and mk0518 (raltegravir)
25	c5u1cD_	Alignment	not modelled	99.1	16	PDB header: viral protein Chain: D: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
26	c3dlrA_	Alignment	not modelled	99.0	18	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv integrase
27	c3l2uA_	Alignment	not modelled	98.7	12	PDB header: recombination/dna Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the prototype foamy virus (pfv)2 intasome in complex with magnesium and gs91373 (elvitegravir)
28	c1u78A_	Alignment	not modelled	98.1	12	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposable element tc3 transposase; PDBTitle: structure of the bipartite dna-binding domain of tc32 transposase bound to transposon dna

29	c6paxA	Alignment	not modelled	98.0	17	PDB header: gene regulation/dna Chain: A: PDB Molecule: homeobox protein pax-6; PDBTitle: crystal structure of the human pax-6 paired domain-dna2 complex reveals a general model for pax protein-dna3 interactions
30	d1pdnc	Alignment	not modelled	98.0	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
31	c5cr4B	Alignment	not modelled	97.6	10	PDB header: hydrolase Chain: B: PDB Molecule: sleeping beauty transposase, sb100x; PDBTitle: crystal structure of the sleeping beauty transposase catalytic domain
32	c2f7tA	Alignment	not modelled	97.3	15	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
33	c2k27A	Alignment	not modelled	97.2	15	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
34	c3f2kB	Alignment	not modelled	96.5	16	PDB header: transferase Chain: B: PDB Molecule: histone-lysine n-methyltransferase setmar; PDBTitle: structure of the transposase domain of human histone-lysine2 n-methyltransferase setmar
35	c5byhM	Alignment	not modelled	95.8	23	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
36	c5ui5I	Alignment	not modelled	95.5	25	PDB header: transcription/dna Chain: I: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: crystal structure of aquifex aeolicus sigman bound to promoter dna
37	c6gh5M	Alignment	not modelled	95.5	19	PDB header: transcription Chain: M: PDB Molecule: rna polymerase sigma-54 factor,rna polymerase sigma-54 PDBTitle: cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex
38	c5nwtM	Alignment	not modelled	94.1	22	PDB header: transferase Chain: M: PDB Molecule: rna polymerase sigma-54 factor,rna polymerase sigma-54 PDBTitle: crystal structure of escherichia coli rna polymerase - sigma542 holoenzyme complex
39	d2jn6a1	Alignment	not modelled	94.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
40	c1hlvA	Alignment	not modelled	93.1	20	PDB header: dna binding protein/dna Chain: A: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
41	c2ahqA	Alignment	not modelled	89.9	30	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: solution structure of the c-terminal rpon domain of sigma-2 54 from aquifex aeolicus
42	c2ao9H	Alignment	not modelled	89.8	13	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: phage protein; PDBTitle: structural genomics, the crystal structure of a phage protein2 (phbc6a51) from bacillus cereus atcc 14579
43	c1b4aA	Alignment	not modelled	89.4	11	PDB header: repressor Chain: A: PDB Molecule: arginine repressor; PDBTitle: structure of the arginine repressor from bacillus stearothermophilus
44	c4i7hA	Alignment	not modelled	88.6	17	PDB header: transcription Chain: A: PDB Molecule: peroxide stress sensing regulator; PDBTitle: structural basis for peroxide sensing and gene regulation by perr from2 streptococcus pyogenes
45	c5unkA	Alignment	not modelled	88.4	25	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the red subdomain of the sleeping beauty transposase
46	c2o03A	Alignment	not modelled	88.3	21	PDB header: gene regulation Chain: A: PDB Molecule: probable zinc uptake regulation protein furb; PDBTitle: crystal structure of furb from m. tuberculosis- a zinc uptake2 regulator
47	c3mwmA	Alignment	not modelled	88.1	19	PDB header: transcription Chain: A: PDB Molecule: putative metal uptake regulation protein; PDBTitle: graded expression of zinc-responsive genes through two regulatory2 zinc-binding sites in zur
48	c3hefB	Alignment	not modelled	88.0	9	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
49	d2ao9a1	Alignment	not modelled	87.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
50	c1z4hA	Alignment	not modelled	87.7	20	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
51	d1aoya	Alignment	not modelled	87.6	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
52	c2fe3B	Alignment	not modelled	87.6	13	PDB header: dna binding protein Chain: B: PDB Molecule: peroxide operon regulator; PDBTitle: the crystal structure of bacillus subtilis perr-zn reveals a novel2 zn(cys)4 structural redox switch
53	c2mt3A	Alignment	not modelled	86.8	20	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma-54 factor; PDBTitle: structure of -24 dna binding domain of sigma 54 from e.coli

54	c4mtdA	Alignment	not modelled	86.6	18	PDB header: dna binding protein/dna Chain: A: PDB Molecule: zinc uptake regulation protein; PDBTitle: zinc uptake regulator complexed with zinc and dna
55	c5n9B	Alignment	not modelled	86.4	11	PDB header: dna binding protein Chain: B: PDB Molecule: transcriptional regulator (fur family); PDBTitle: crystal structure of a peroxide stress regulator from leptospira2 interrogans
56	c2xigA	Alignment	not modelled	86.3	9	PDB header: transcription Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
57	d1b4aa1	Alignment	not modelled	86.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
58	c4j2nB	Alignment	not modelled	86.1	17	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
59	c5fd6A	Alignment	not modelled	86.0	13	PDB header: transcription Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: zinc-bound manganese uptake regulator
60	d1mzba	Alignment	not modelled	86.0	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FUR-like
61	c4razB	Alignment	not modelled	85.7	11	PDB header: metal binding protein Chain: B: PDB Molecule: dna-binding transcriptional dual regulator of siderophore PDBTitle: crystal structure of magnetospirillum gryphiswaldense msr-1 holo-fur
62	d2p5ka1	Alignment	not modelled	85.3	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
63	d1umqa	Alignment	not modelled	84.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
64	c1umqA	Alignment	not modelled	84.8	14	PDB header: dna-binding protein Chain: A: PDB Molecule: photosynthetic apparatus regulatory protein; PDBTitle: solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
65	c4j2nA	Alignment	not modelled	84.7	18	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
66	c6fkgC	Alignment	not modelled	84.3	9	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
67	c2w57A	Alignment	not modelled	83.1	19	PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the vibrio cholerae ferric uptake2 regulator (fur) reveals structural rearrangement of the3 dna-binding domains
68	c5nbcD	Alignment	not modelled	82.5	19	PDB header: dna binding protein Chain: D: PDB Molecule: ferric uptake regulation protein; PDBTitle: structure of prokaryotic transcription factors
69	c3ereD	Alignment	not modelled	82.5	15	PDB header: dna binding protein/dna Chain: D: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator
70	c2o8kA	Alignment	not modelled	81.2	25	PDB header: transcription/dna Chain: A: PDB Molecule: rna polymerase sigma factor rpon; PDBTitle: nmr structure of the sigma-54 rpon domain bound to the-242 promoter element
71	c3eyyA	Alignment	not modelled	81.1	10	PDB header: transport Chain: A: PDB Molecule: putative iron uptake regulatory protein; PDBTitle: structural basis for the specialization of nur, a nickel-2 specific fur homologue, in metal sensing and dna3 recognition
72	d1etxa	Alignment	not modelled	79.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
73	c6dk4A	Alignment	not modelled	78.8	10	PDB header: metal transport Chain: A: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni peroxide stress regulator
74	c2rn7A	Alignment	not modelled	77.5	19	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpε protein from shigella2 flexneri. northeast structural genomics target sfr125
75	d1fipa	Alignment	not modelled	77.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
76	c4l5eA	Alignment	not modelled	76.1	21	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
77	c2fu4B	Alignment	not modelled	75.9	19	PDB header: dna binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of the dna binding domain of e.coli fur (ferric2 uptake regulator)
78	c3v4gA	Alignment	not modelled	75.0	17	PDB header: dna binding protein Chain: A: PDB Molecule: arginine repressor; PDBTitle: 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
79	c4etsB	Alignment	not modelled	74.6	15	PDB header: metal binding protein Chain: B: PDB Molecule: ferric uptake regulation protein; PDBTitle: crystal structure of campylobacter jejuni ferric uptake

						regulator
80	d1f9na1	Alignment	not modelled	72.6	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
81	d1rzsa_	Alignment	not modelled	72.5	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
82	c6amaO_	Alignment	not modelled	72.0	13	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
83	c3e7ID_	Alignment	not modelled	70.9	20	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
84	c1g2hA_	Alignment	not modelled	69.6	8	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein tyrr homolog; PDBTitle: solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
85	d1g2ha_	Alignment	not modelled	69.6	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
86	c3o60A_	Alignment	not modelled	68.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin0861 protein; PDBTitle: the crystal structure of lin0861 from listeria innocua to 2.8a
87	d2id3a1	Alignment	not modelled	68.4	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
88	c2lvsA_	Alignment	not modelled	68.0	23	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein
89	c2lcvA_	Alignment	not modelled	68.0	10	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
90	c2m8gX_	Alignment	not modelled	67.9	12	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator; PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
91	d1t56a1	Alignment	not modelled	66.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
92	c2r0qF_	Alignment	not modelled	66.0	19	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
93	d1stza1	Alignment	not modelled	64.8	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
94	c3f1bA_	Alignment	not modelled	64.4	16	PDB header: transcription regulator Chain: A: PDB Molecule: tetr-like transcriptional regulator; PDBTitle: the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1.
95	c5syszA_	Alignment	not modelled	63.9	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
96	c2elhA_	Alignment	not modelled	63.3	15	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
97	d2bjca1	Alignment	not modelled	61.9	7	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
98	d2g3ba1	Alignment	not modelled	61.8	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
99	c5i0pA_	Alignment	not modelled	61.4	20	PDB header: de novo protein Chain: A: PDB Molecule: transcription factor etv6, transcription factor etv6, PDBTitle: symmetry-based assembly of a two-dimensional protein lattice
100	d1jt6a1	Alignment	not modelled	61.2	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
101	d1qpza1	Alignment	not modelled	61.0	13	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
102	c1bdhA_	Alignment	not modelled	60.8	12	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
103	c2i0kA_	Alignment	not modelled	60.5	14	PDB header: transcription Chain: A: PDB Molecule: stage iii sporulation protein d; PDBTitle: nmr solution structure of a transcription factor spoiiid in complex2 with dna
104	d2vkva1	Alignment	not modelled	59.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
105	c3kxD_	Alignment	not modelled	59.7	5	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
106	d2fq4a1	Alignment	not modelled	59.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
107	c2l8nA_	Alignment	not modelled	59.3	5	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
108	c4mk6A_	Alignment	not modelled	59.1	15	PDB header: transcription regulator Chain: A: PDB Molecule: probable dihydroxyacetone kinase regulator dhsk_reg; PDBTitle: crystal structure of probable dihydroxyacetone kinase regulator2 dhsk_reg from listeria monocytogenes egd-e
109	c2guhA_	Alignment	not modelled	57.4	11	PDB header: transcription regulator Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
110	d1r8da_	Alignment	not modelled	57.3	8	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
111	d1k78a2	Alignment	not modelled	57.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
112	d1vi0a1	Alignment	not modelled	56.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
113	c4ac6A_	Alignment	not modelled	56.5	11	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional repressor acnr; PDBTitle: corynebacterium glutamicum acnr au derivative structure
114	c3ni7A_	Alignment	not modelled	56.0	8	PDB header: transcription regulator Chain: A: PDB Molecule: bacterial regulatory proteins, tetr family; PDBTitle: crystal structure of the tetr transcriptional regulator from2 nitrosomonas europaea atcc 19718
115	c3ppbB_	Alignment	not modelled	55.7	16	PDB header: transcription regulator Chain: B: PDB Molecule: putative tetr family transcription regulator; PDBTitle: crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
116	c2dg7A_	Alignment	not modelled	55.3	21	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
117	c3b81A_	Alignment	not modelled	55.3	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, acrr family; PDBTitle: crystal structure of predicted dna-binding transcriptional regulator2 of tetr/acrr family (np_350189.1) from clostridium acetobutylicum at3 2.10 a resolution
118	d1rkta1	Alignment	not modelled	55.1	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
119	c5dajB_	Alignment	not modelled	55.1	21	PDB header: transcription regulator Chain: B: PDB Molecule: nald; PDBTitle: crystal structure of nald, the secondary repressor of mexab-oprm2 multidrug efflux pump in pseudomonas aeruginosa
120	c1efaA_	Alignment	not modelled	55.0	7	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