

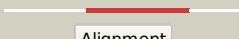

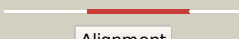










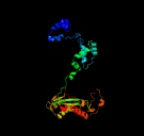
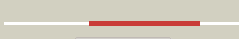
















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3430c_(-)_3847822_3848985
Date	Fri Aug 9 18:20:10 BST 2019
Unique Job ID	4734c2d5af61c3c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5cz1B_	 Alignment		100.0	18	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase
2	c1c0mA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
3	c3f9kV_	 Alignment		100.0	19	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
4	d1c0mA2	 Alignment		100.0	22	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	d1asua_	 Alignment		99.9	20	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
6	c5u1cA_	 Alignment		99.9	15	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
7	c3jcaE_	 Alignment		99.9	17	PDB header: viral protein Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
8	c4fcyA_	 Alignment		99.9	11	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
9	c1ex4A_	 Alignment		99.9	15	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
10	c3nf9A_	 Alignment		99.9	19	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
11	d1exqa_	 Alignment		99.9	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain

12	d1bcoa2	Alignment		99.9	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
13	d1cxqa	Alignment		99.9	21	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
14	c3kksB	Alignment		99.9	21	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal2 form ii
15	c3hpgC	Alignment		99.9	19	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
16	c5m0rF	Alignment		99.9	18	PDB header: hydrolase Chain: F: PDB Molecule: integrase; PDBTitle: cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
17	c4mq3A	Alignment		99.9	19	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of fiv integrase
18	c5ejkG	Alignment		99.9	16	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
19	c1k6yB	Alignment		99.9	18	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
20	d1c6va	Alignment		99.9	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
21	c3l2tB	Alignment	not modelled	99.9	15	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)
22	d1hyva	Alignment	not modelled	99.8	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
23	c1bcoA	Alignment	not modelled	99.8	15	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
24	c3dlrA	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv integrase
25	c3l2uA	Alignment	not modelled	99.8	13	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)
26	c5u1cD	Alignment	not modelled	99.7	19	PDB header: viral protein Chain: D: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
27	c3hosA	Alignment	not modelled	99.4	15	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
28	c5cr4B	Alignment	not modelled	97.9	15	PDB header: hydrolase Chain: B: PDB Molecule: sleeping beauty transposase, sb100x; PDBTitle: crystal structure of the sleeping beauty transposase catalytic domain

29	c6paxA	Alignment	not modelled	97.4	12	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	c1u78A	Alignment	not modelled	97.3	13	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
31	c2f7tA	Alignment	not modelled	97.2	15	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
32	d1pdnc	Alignment	not modelled	97.1	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
33	c3f2kB	Alignment	not modelled	96.9	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
34	c2k27A	Alignment	not modelled	93.5	13	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
35	c4j2nB	Alignment	not modelled	92.1	11	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
36	c3hefB	Alignment	not modelled	91.7	14	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
37	c4j2nA	Alignment	not modelled	91.6	12	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
38	d1rzsa	Alignment	not modelled	88.6	15	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
39	d2g3ba1	Alignment	not modelled	87.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
40	d2fq4a1	Alignment	not modelled	87.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
41	d2jn6a1	Alignment	not modelled	87.0	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
42	c1z4hA	Alignment	not modelled	86.7	22	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of 2 atypical excisionase
43	d2fbqa1	Alignment	not modelled	86.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
44	d1vi0a1	Alignment	not modelled	85.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
45	c2g7gA	Alignment	not modelled	85.8	13	PDB header: transcription Chain: A: PDB Molecule: rha04620, putative transcriptional regulator; PDBTitle: the crystal structure of the putative transcriptional regulator2 rha04620 from rhodococcus sp. rha1
46	d1umqa	Alignment	not modelled	85.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
47	c1umqA	Alignment	not modelled	85.8	17	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
48	c4mk6A	Alignment	not modelled	85.1	13	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
49	d1g2ha	Alignment	not modelled	84.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
50	c1g2hA	Alignment	not modelled	84.8	15	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
51	c6fkgC	Alignment	not modelled	84.7	15	PDB header: toxin Chain: C: PDB Molecule: rv1990c (mbca); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
52	c2guhA	Alignment	not modelled	84.3	6	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
53	c3nxC	Alignment	not modelled	84.1	23	PDB header: dna binding protein Chain: A: PDB Molecule: hth-type protein slma; PDBTitle: molecular mechanism by which the escherichia coli nucleoid occlusion2 factor, slma, keeps cytokinesis in check

54	d3c07a1	Alignment	not modelled	84.1	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
55	d2iu5a1	Alignment	not modelled	83.9	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
56	d2np5a1	Alignment	not modelled	83.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
57	d1t56a1	Alignment	not modelled	83.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
58	c3f1bA_	Alignment	not modelled	83.4	13	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.
59	d2d6ya1	Alignment	not modelled	83.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
60	c3lj1B_	Alignment	not modelled	83.1	9	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator luxt; PDBTitle: the crystal structure of the full-length transcriptional regulator2 luxt from vibrio parahaemolyticus rimd 2210633.
61	c5vl9D_	Alignment	not modelled	82.9	19	PDB header: transcription/dna Chain: D: PDB Molecule: regulatory protein tetr; PDBTitle: crystal structure of eilr in complex with eilo dna element
62	d1jt6a1	Alignment	not modelled	82.8	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
63	c5nbcD_	Alignment	not modelled	82.7	22	PDB header: dna binding protein Chain: D: PDB Molecule: ferric uptake regulation protein; PDBTitle: structure of prokaryotic transcription factors
64	d2coba1	Alignment	not modelled	82.7	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
65	d2vkea1	Alignment	not modelled	82.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
66	d1pb6a1	Alignment	not modelled	82.3	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
67	d2fx0a1	Alignment	not modelled	82.1	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
68	c3fiwB_	Alignment	not modelled	82.0	19	PDB header: transcription regulator Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structure of sco0253, a tetr-family transcriptional regulator from2 streptomyces coelicolor
69	d1rktA1	Alignment	not modelled	82.0	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
70	c3gziA_	Alignment	not modelled	81.8	22	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a transcriptional regulator of the tetr family2 (shew_3567) from shewanella loihica pv-4 at 2.05 a resolution
71	c4ac6A_	Alignment	not modelled	81.6	19	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional repressor acnr; PDBTitle: corynebacterium glutamicum acnr au derivative structure
72	d1etxa_	Alignment	not modelled	81.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
73	c2iu5A_	Alignment	not modelled	81.6	13	PDB header: transcription Chain: A: PDB Molecule: hth-type dhaklm operon transcriptional activator dhas; PDBTitle: dihydroxyacetone kinase operon activator dhas
74	d2hya1	Alignment	not modelled	81.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
75	c2nx4A_	Alignment	not modelled	81.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: transcriptional regulator, tetr family protein; PDBTitle: the crystal structure of athe putative tetr-family transcriptional2 regulator rha06780 from rhodococcus sp. rha1.
76	d2i10a1	Alignment	not modelled	81.0	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
77	c1h1vA_	Alignment	not modelled	80.9	7	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
78	c2w57A_	Alignment	not modelled	80.8	27	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
79	c3vibD_	Alignment	not modelled	80.7	16	PDB header: dna binding protein Chain: D: PDB Molecule: mtrr; PDBTitle: structural basis for multidrug recognition and antimicrobial2 resistance by mtrr, an efflux pump regulator from

						neisseria3 gonorrhoeae
80	c3b81A	Alignment	not modelled	80.7	13	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
81	c3cwrA	Alignment	not modelled	80.7	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of transcriptional regulator of tetr family2 (yp_425770.1) from rhodospirillum rubrum atcc 11170 at 1.50 a3 resolution
82	c6azhA	Alignment	not modelled	80.6	13	PDB header: transcription Chain: A: PDB Molecule: tetr family transcriptional regulator; PDBTitle: clostridium perfringens putative fatty acid metabolism regulator
83	d2id3a1	Alignment	not modelled	80.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
84	c5dajB	Alignment	not modelled	80.5	13	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
85	c1vi0B	Alignment	not modelled	80.4	16	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of a transcriptional regulator
86	d2fd5a1	Alignment	not modelled	80.3	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
87	d2id6a1	Alignment	not modelled	80.3	6	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
88	c3ppbB	Alignment	not modelled	80.1	6	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
89	c3pasA	Alignment	not modelled	79.9	19	PDB header: transcription regulator Chain: A: PDB Molecule: tetr family transcription regulator; PDBTitle: crystal structure of a tetr family transcriptional regulator (maqu_1417)2 from marinobacter aquaeolei vt8 at 1.90 a resolution
90	c3dcfB	Alignment	not modelled	79.9	10	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator of the tetr/acrr family; PDBTitle: crystal structure of transcriptional regulator of the tetr/acrr family2 (yp_290855.1) from thermobifida fusca yx-er1 at 2.50 a resolution
91	c4l5eA	Alignment	not modelled	79.9	13	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
92	c2jk3A	Alignment	not modelled	79.8	6	PDB header: transcription Chain: A: PDB Molecule: hemolysin ii regulatory protein; PDBTitle: crystal structure of the hlyii mutant protein with2 residues 169-186 substituted by gssgsg linker
93	c3cjdB	Alignment	not modelled	79.6	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of putative tetr transcriptional regulator2 (yp_510936.1) from jannaschia sp. ccs1 at 1.79 a resolution
94	c2of7A	Alignment	not modelled	79.5	10	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structural genomics, the crystal structure of a tetr-family2 transcriptional regulator from streptomyces coelicolor a3
95	c4za6A	Alignment	not modelled	79.4	25	PDB header: signaling protein Chain: A: PDB Molecule: tetr family transcriptional regulator; PDBTitle: structure of the r. erythropolis transcriptional repressor qsdR from2 tetr family
96	d2o7ta1	Alignment	not modelled	79.4	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
97	c3g56A	Alignment	not modelled	79.3	6	PDB header: dna binding protein Chain: A: PDB Molecule: regulator of macrolide 2'-phosphotransferase i; PDBTitle: structure of the macrolide biosensor protein, mpr(a)
98	c3anpD	Alignment	not modelled	79.3	3	PDB header: transcription Chain: D: PDB Molecule: transcriptional repressor, tetr family; PDBTitle: crystal structure of thermus thermophilus fadr, a tetr family2 transcriptional repressor, in complex with lauroyl-coa.
99	c3ni7A	Alignment	not modelled	79.3	6	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
100	d1ntca	Alignment	not modelled	79.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
101	c3kkcB	Alignment	not modelled	79.2	16	PDB header: transcription regulator Chain: B: PDB Molecule: tetr family transcriptional regulator; PDBTitle: the crystal structure of tetr transcriptional regulator from2 streptococcus agalactiae 2603v
102	c5k7fA	Alignment	not modelled	79.2	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of apo aibr
103	c2ibdB	Alignment	not modelled	79.2	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: possible transcriptional regulator; PDBTitle: crystal structure of probable transcriptional regulatory protein2 rha5900
104	c3c2bA	Alignment	not modelled	79.1	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, tetr family;

104	c3c2vA	Alignment	not modelled	79.1	19	PDBTitle: crystal structure of tetr transcriptional regulator from agrobacterium2 tumefaciens
105	d1v7ba1	Alignment	not modelled	79.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
106	d2vkva1	Alignment	not modelled	79.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
107	c2dg7A	Alignment	not modelled	79.0	19	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)
108	c3e7qB	Alignment	not modelled	78.9	16	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: the crystal structure of the putative transcriptional regulator from2 pseudomonas aeruginosa pao1
109	c3voxD	Alignment	not modelled	78.8	19	PDB header: transcription Chain: D: PDB Molecule: transcriptional regulator; PDBTitle: x-ray crystal structure of wild type hrtr in the apo form
110	d1fipa	Alignment	not modelled	78.8	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
111	c2f07A	Alignment	not modelled	78.7	16	PDB header: transcription Chain: A: PDB Molecule: yvdt; PDBTitle: crystal structure of yvdt from bacillus subtilis
112	d2gfna1	Alignment	not modelled	78.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
113	c5xazD	Alignment	not modelled	78.5	10	PDB header: dna binding protein Chain: D: PDB Molecule: gamma-butyrolactone receptor protein; PDBTitle: crystal structure of full length native tylp, a tetr regulator from2 streptomyces fradiae
114	c3vprA	Alignment	not modelled	78.5	19	PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: crystal structure of a tetr family transcriptional regulator pfmr from2 thermus thermophilus hb8
115	d1z0xa1	Alignment	not modelled	78.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
116	c3zqiB	Alignment	not modelled	78.3	25	PDB header: transcription Chain: B: PDB Molecule: tetracycline repressor protein class b from transposon PDBTitle: structure of tetracycline repressor in complex with inducer peptide-2 tip2
117	c3f0cA	Alignment	not modelled	78.2	19	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of transcriptional regulator from cytophaga2 hutchinsonii atcc 33406
118	c4r4eA	Alignment	not modelled	78.1	15	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
119	c1jumB	Alignment	not modelled	78.0	6	PDB header: transcription Chain: B: PDB Molecule: hypothetical transcriptional regulator in qaca 5' region; PDBTitle: crystal structure of the multidrug binding transcriptional repressor2 qacr bound to the natural drug berberine
120	c2eh3A	Alignment	not modelled	77.9	10	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of aq_1058, a transcriptional regulator (terr/acrr2 family) from aquifex aeolicus vf5