


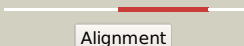


















Phyre2

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Description	RVBD3191c (-)_3557308_3558342
Date	Thu Aug 8 16:20:38 BST 2019
Unique Job ID	dbc7f151a3bcb2dd

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f9kV_	 Alignment		99.9	16	PDB header: viral protein, recombination Chain: V: PDB Molecule: integrase; PDBTitle: two domain fragment of hiv-2 integrase in complex with ledgf ibd
2	d1exqa_	 Alignment		99.9	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
3	c1ex4A_	 Alignment		99.9	13	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: hiv-1 integrase catalytic core and c-terminal domain
4	d1c6va_	 Alignment		99.9	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
5	c3kksB_	 Alignment		99.9	15	PDB header: dna binding protein Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of catalytic core domain of biv integrase in crystal2 form ii
6	c5cz1B_	 Alignment		99.9	9	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain of mmv integrase
7	c5u1cA_	 Alignment		99.9	12	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
8	c3nf9A_	 Alignment		99.9	10	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	c5m0rF_	 Alignment		99.9	16	PDB header: hydrolase Chain: F: PDB Molecule: integrase; PDBTitle: cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
10	d1c0ma2	 Alignment		99.9	11	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
11	c1c0mA_	 Alignment		99.8	11	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase

12	c4mq3A_	Alignment		99.8	19	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of fiv integrase
13	d1hyva_	Alignment		99.8	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
14	c3hpgC_	Alignment		99.8	15	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
15	d1asua_	Alignment		99.8	11	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
16	c3jcaE_	Alignment		99.8	9	PDB header: viral protein Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
17	c1k6yB_	Alignment		99.8	11	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
18	c4fcyA_	Alignment		99.8	11	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
19	c3l2tB_	Alignment		99.7	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)
20	c5u1cD_	Alignment		99.7	11	PDB header: viral protein Chain: D: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
21	d1bcoa2	Alignment	not modelled	99.7	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
22	d1cxqa_	Alignment	not modelled	99.7	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
23	c5ejkG_	Alignment	not modelled	99.6	7	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
24	c1bcoA_	Alignment	not modelled	99.6	13	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
25	c3dlrA_	Alignment	not modelled	99.5	14	PDB header: transferase Chain: A: PDB Molecule: integrase; PDBTitle: crystal structure of the catalytic core domain from pfv integrase
26	c3hosA_	Alignment	not modelled	99.1	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
27	c1u78A_	Alignment	not modelled	99.1	16	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
28	c3l2uA_	Alignment	not modelled	99.0	10	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)

29	c6paxA	Alignment	not modelled	98.7	20	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	98.7	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
31	c2k27A	Alignment	not modelled	98.2	23	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
32	d1k78a1	Alignment	not modelled	98.0	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
33	d6paxa1	Alignment	not modelled	97.9	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
34	c2elhA	Alignment	not modelled	97.7	21	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
35	c1hlvA	Alignment	not modelled	97.7	21	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
36	d2jn6a1	Alignment	not modelled	97.6	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
37	d1hlva1	Alignment	not modelled	97.4	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
38	d1bw6a	Alignment	not modelled	97.1	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
39	c2rn7A	Alignment	not modelled	97.1	28	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
40	d1tc3c	Alignment	not modelled	96.8	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
41	c2lvsA	Alignment	not modelled	96.7	41	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein
42	c3sztB	Alignment	not modelled	96.7	19	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
43	c5cr4B	Alignment	not modelled	96.7	14	PDB header: hydrolase Chain: B: PDB Molecule: sleeping beauty transposase, sb100x; PDBTitle: crystal structure of the sleeping beauty transposase catalytic domain
44	c3hefB	Alignment	not modelled	96.5	30	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
45	c2q0oA	Alignment	not modelled	96.5	24	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
46	d2ao9a1	Alignment	not modelled	96.4	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Nanomeric phage protein-like
47	c4lfuA	Alignment	not modelled	96.3	24	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
48	c4go1A	Alignment	not modelled	96.3	36	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
49	d1xsva	Alignment	not modelled	96.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
50	c2w48D	Alignment	not modelled	96.2	32	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
51	c2mqkA	Alignment	not modelled	96.1	21	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
52	c1r71B	Alignment	not modelled	96.1	20	PDB header: transcription/dna Chain: B: PDB Molecule: transcriptional repressor protein korb; PDBTitle: crystal structure of the dna binding domain of korb in complex with2 the operator dna
53	c1rp3G	Alignment	not modelled	96.0	24	PDB header: transcription Chain: G: PDB Molecule: rna polymerase sigma factor sigma-28 (flia); PDBTitle: cocrystal structure of the flagellar sigma/anti-sigma complex, sigma-2 28/flgm
54	d1g2ha	Alignment	not modelled	96.0	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like

55	c1g2hA	Alignment	not modelled	96.0	20	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
56	d1ntca	Alignment	not modelled	96.0	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
57	c3vdoA	Alignment	not modelled	96.0	23	PDB header: dna binding protein/protein binding Chain: A: PDB Molecule: rna polymerase sigma factor sigk; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
58	c5fgmA	Alignment	not modelled	96.0	33	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
59	c3hugA	Alignment	not modelled	96.0	38	PDB header: transcription/membrane protein Chain: A: PDB Molecule: rna polymerase sigma factor; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
60	d1umqa	Alignment	not modelled	96.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
61	c1umqA	Alignment	not modelled	96.0	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
62	c3frwF	Alignment	not modelled	96.0	21	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum
63	c2o8xA	Alignment	not modelled	95.9	21	PDB header: transcription Chain: A: PDB Molecule: probable rna polymerase sigma-c factor; PDBTitle: crystal structure of the "-35 element" promoter recognition domain of2 mycobacterium tuberculosis sigc
64	c2m8eA	Alignment	not modelled	95.9	33	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase
65	d1rp3a2	Alignment	not modelled	95.9	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
66	d1or7a1	Alignment	not modelled	95.9	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
67	d1ijwc	Alignment	not modelled	95.9	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
68	c6c03A	Alignment	not modelled	95.9	18	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
69	c5zx3F	Alignment	not modelled	95.8	28	PDB header: transcription Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigh; PDBTitle: mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
70	c6in7B	Alignment	not modelled	95.8	28	PDB header: transcription Chain: B: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of algu in complex with muca(cyto)
71	d1r71a	Alignment	not modelled	95.8	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
72	d1s7oa	Alignment	not modelled	95.8	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
73	d1l3la1	Alignment	not modelled	95.8	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
74	c5uxxC	Alignment	not modelled	95.7	30	PDB header: dna binding protein/unknown function Chain: C: PDB Molecule: rna polymerase sigma factor; PDBTitle: co-crystal structure of the sigma factor rpoe in complex with the2 anti-sigma factor nepr from bartonella quintana
75	d1fsea	Alignment	not modelled	95.7	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
76	c1zljE	Alignment	not modelled	95.7	34	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
77	d1a04a1	Alignment	not modelled	95.7	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
78	d1hcra	Alignment	not modelled	95.7	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
79	c5wurB	Alignment	not modelled	95.7	26	PDB header: metal binding protein Chain: B: PDB Molecule: ecf rna polymerase sigma factor sigw; PDBTitle: crystal structure of sigw in complex with its anti-sigma

						rsiw, an2 oxidized form
80	c1iufA_	Alignment	not modelled	95.7	15	PDB header: dna binding protein Chain: A: PDB Molecule: centromere abp1 protein; PDBTitle: low resolution solution structure of the two dna-binding2 domains in schizosaccharomyces pombe abp1 protein
81	c2krfB_	Alignment	not modelled	95.6	24	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
82	c3e7ID_	Alignment	not modelled	95.6	18	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4's dna binding2 domain
83	c3korD_	Alignment	not modelled	95.6	24	PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus
84	d1vz0a1	Alignment	not modelled	95.6	37	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
85	c1h0mD_	Alignment	not modelled	95.6	26	PDB header: transcription/dna Chain: D: PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
86	d1fipa_	Alignment	not modelled	95.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
87	c4I5eA_	Alignment	not modelled	95.5	16	PDB header: protein binding Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of a. aeolicus ntrc1 dna binding domain
88	c4cxfA_	Alignment	not modelled	95.5	25	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry
89	c6dvdF_	Alignment	not modelled	95.5	38	PDB header: transferase/dna Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigl; PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11
90	c6jqsA_	Alignment	not modelled	95.5	29	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
91	c2ia0A_	Alignment	not modelled	95.5	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)
92	d1yioa1	Alignment	not modelled	95.3	31	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
93	d1ku3a_	Alignment	not modelled	95.3	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
94	d1etxa_	Alignment	not modelled	95.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
95	c2ao9H_	Alignment	not modelled	95.2	16	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
96	c3vepA_	Alignment	not modelled	95.2	23	PDB header: membrane protein/transcription Chain: A: PDB Molecule: probable rna polymerase sigma-d factor; PDBTitle: crystal structure of sigd4 in complex with its negative regulator rsda
97	c3qp5C_	Alignment	not modelled	95.2	26	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
98	c5ipmF_	Alignment	not modelled	95.1	13	PDB header: transcription, transferase/dna/rna Chain: F: PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna
99	d1p4wa_	Alignment	not modelled	95.1	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
100	d1r69a_	Alignment	not modelled	95.0	17	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
101	d1jhga_	Alignment	not modelled	95.0	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
102	c2xcjB_	Alignment	not modelled	95.0	25	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
103	c1x3uA_	Alignment	not modelled	94.9	34	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
104	c4j2nB_	Alignment	not modelled	94.9	32	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
105	c2m8aY_	Alignment	not modelled	94.9	16	PDB header: transcription Chain: X: PDB Molecule: transcriptional regulator;

105	c2m0gA_	Alignment	not modelled	94.5	10	PDBTitle: structure, function, and tethering of dna-binding domains in 542 transcriptional activators
106	c2cg4B_	Alignment	not modelled	94.8	18	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
107	d2coba1	Alignment	not modelled	94.8	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
108	c3mzyA_	Alignment	not modelled	94.8	19	PDB header: rna binding protein Chain: A: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: the crystal structure of the rna polymerase sigma-h factor from2 fusobacterium nucleatum to 2.5a
109	c2fjrB_	Alignment	not modelled	94.7	17	PDB header: transcription regulator Chain: B: PDB Molecule: repressor protein ci; PDBTitle: crystal structure of bacteriophage 186
110	c4yn8A_	Alignment	not modelled	94.7	30	PDB header: dna binding protein Chain: A: PDB Molecule: response regulator chra; PDBTitle: crystal structure of response regulator chra in heme-sensing two2 component system
111	c1rnA_	Alignment	not modelled	94.7	34	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narl; PDBTitle: the nitrate/nitrite response regulator protein narl from narl
112	d1trra_	Alignment	not modelled	94.7	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
113	d2p7vb1	Alignment	not modelled	94.7	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
114	c2rnjA_	Alignment	not modelled	94.7	27	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
115	c4j2nA_	Alignment	not modelled	94.7	32	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
116	c5f64C_	Alignment	not modelled	94.7	26	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
117	d1ttya_	Alignment	not modelled	94.6	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
118	d1etob_	Alignment	not modelled	94.6	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: FIS-like
119	c3cloC_	Alignment	not modelled	94.5	33	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of putative transcriptional regulator containing a2 luxr dna binding domain (np_811094.1) from bacteroides3 thetaiotaomicron vpi-5482 at 2.04 a resolution
120	c4if4A_	Alignment	not modelled	94.5	26	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and berylliofluoride-activated vvar2 from staphylococcus aureus