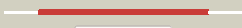
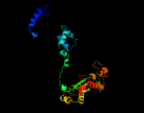
























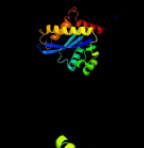
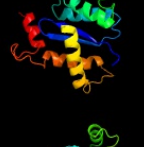

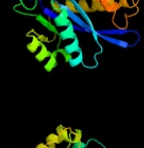
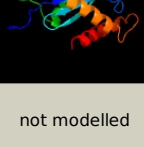


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3187 (-) _3553138_3554022
Date	Thu Aug 8 16:20:37 BST 2019
Unique Job ID	cc4a01f5888c9278

Detailed template information

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

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

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

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

						regulator
80	<a href="#">d1f9na1</a>	Alignment	not modelled	72.6	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Arginine repressor (ArgR), N-terminal DNA-binding domain
81	<a href="#">d1rzsa_</a>	Alignment	not modelled	72.5	16	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> Phage repressors
82	<a href="#">c6amaO_</a>	Alignment	not modelled	72.0	13	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> O: <b>PDB Molecule:</b> putative dna-binding protein; <b>PDBTitle:</b> structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
83	<a href="#">c3e7ID_</a>	Alignment	not modelled	70.9	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4's dna binding2 domain
84	<a href="#">c1g2hA_</a>	Alignment	not modelled	69.6	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein tyrr homolog; <b>PDBTitle:</b> solution structure of the dna-binding domain of the tyrr2 protein of haemophilus influenzae
85	<a href="#">d1g2ha_</a>	Alignment	not modelled	69.6	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> FIS-like
86	<a href="#">c3o60A_</a>	Alignment	not modelled	68.5	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin0861 protein; <b>PDBTitle:</b> the crystal structure of lin0861 from listeria innocua to 2.8a
87	<a href="#">d2id3a1</a>	Alignment	not modelled	68.4	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
88	<a href="#">c2lvsA_</a>	Alignment	not modelled	68.0	23	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of a crispr repeat binding protein
89	<a href="#">c2lcvA_</a>	Alignment	not modelled	68.0	10	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor cytr; <b>PDBTitle:</b> structure of the cytidine repressor dna-binding domain; an alternate2 calculation
90	<a href="#">c2m8gX_</a>	Alignment	not modelled	67.9	12	<b>PDB header:</b> transcription <b>Chain:</b> X: <b>PDB Molecule:</b> transcriptional regulator; <b>PDBTitle:</b> structure, function, and tethering of dna-binding domains in 542 transcriptional activators
91	<a href="#">d1t56a1</a>	Alignment	not modelled	66.9	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
92	<a href="#">c2r0qF_</a>	Alignment	not modelled	66.0	19	<b>PDB header:</b> recombination/dna <b>Chain:</b> F: <b>PDB Molecule:</b> putative transposon tn552 dna-invertase bin3; <b>PDBTitle:</b> crystal structure of a serine recombinase- dna regulatory2 complex
93	<a href="#">d1stza1</a>	Alignment	not modelled	64.8	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Heat-inducible transcription repressor HrcA, N-terminal domain
94	<a href="#">c3f1bA_</a>	Alignment	not modelled	64.4	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> tetr-like transcriptional regulator; <b>PDBTitle:</b> the crystal structure of a tetr-like transcriptional regulator from2 rhodococcus sp. rha1.
95	<a href="#">c5syszA_</a>	Alignment	not modelled	63.9	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> transcriptional regulator celr-cellobiose complex
96	<a href="#">c2elhA_</a>	Alignment	not modelled	63.3	15	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cg11849-pa; <b>PDBTitle:</b> solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
97	<a href="#">d2bjca1</a>	Alignment	not modelled	61.9	7	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
98	<a href="#">d2g3ba1</a>	Alignment	not modelled	61.8	22	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
99	<a href="#">c5i0pA_</a>	Alignment	not modelled	61.4	20	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcription factor etv6, transcription factor etv6, <b>PDBTitle:</b> symmetry-based assembly of a two-dimensional protein lattice
100	<a href="#">d1jt6a1</a>	Alignment	not modelled	61.2	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
101	<a href="#">d1qpza1</a>	Alignment	not modelled	61.0	13	<b>Fold:</b> lambda repressor-like DNA-binding domains <b>Superfamily:</b> lambda repressor-like DNA-binding domains <b>Family:</b> GalR/LacI-like bacterial regulator
102	<a href="#">c1bdhA_</a>	Alignment	not modelled	60.8	12	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (purine repressor); <b>PDBTitle:</b> purine repressor mutant-hypoxanthine-palindromic operator2 complex
103	<a href="#">c2i0kA_</a>	Alignment	not modelled	60.5	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> stage iii sporulation protein d; <b>PDBTitle:</b> nmr solution structure of a transcription factor spoiiid in complex2 with dna
104	<a href="#">d2vkva1</a>	Alignment	not modelled	59.8	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
105	<a href="#">c3kxD_</a>	Alignment	not modelled	59.7	5	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator, lacI family; <b>PDBTitle:</b> crystal structure of a transcriptional regulator, lacI2

						family protein from silicibacter pomeroyi
106	<a href="#">d2fq4a1</a>	Alignment	not modelled	59.7	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
107	<a href="#">c2l8nA_</a>	Alignment	not modelled	59.3	5	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional repressor cytr; <b>PDBTitle:</b> nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
108	<a href="#">c4mk6A_</a>	Alignment	not modelled	59.1	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> probable dihydroxyacetone kinase regulator dhsk_reg; <b>PDBTitle:</b> crystal structure of probable dihydroxyacetone kinase regulator2 dhsk_reg from listeria monocytogenes egd-e
109	<a href="#">c2guhA_</a>	Alignment	not modelled	57.4	11	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative tetr-family transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative tetr-family transcriptional2 regulator from rhodococcus sp. rha1
110	<a href="#">d1r8da_</a>	Alignment	not modelled	57.3	8	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> DNA-binding N-terminal domain of transcription activators
111	<a href="#">d1k78a2</a>	Alignment	not modelled	57.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Paired domain
112	<a href="#">d1vi0a1</a>	Alignment	not modelled	56.9	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
113	<a href="#">c4ac6A_</a>	Alignment	not modelled	56.5	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional repressor acnr; <b>PDBTitle:</b> corynebacterium glutamicum acnr au derivative structure
114	<a href="#">c3ni7A_</a>	Alignment	not modelled	56.0	8	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory proteins, tetr family; <b>PDBTitle:</b> crystal structure of the tetr transcriptional regulator from2 nitrosomonas europaea atcc 19718
115	<a href="#">c3ppbB_</a>	Alignment	not modelled	55.7	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative tetr family transcription regulator; <b>PDBTitle:</b> crystal structure of a putative tetr family transcription regulator2 (shew_3104) from shewanella sp. pv-4 at 2.10 a resolution
116	<a href="#">c2dg7A_</a>	Alignment	not modelled	55.3	21	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator; <b>PDBTitle:</b> crystal structure of the putative transcriptional regulator sco03372 from streptomyces coelicolor a3(2)
117	<a href="#">c3b81A_</a>	Alignment	not modelled	55.3	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, acrr family; <b>PDBTitle:</b> crystal structure of predicted dna-binding transcriptional regulator2 of tetr/acrr family (np_350189.1) from clostridium acetobutylicum at3 2.10 a resolution
118	<a href="#">d1rkta1</a>	Alignment	not modelled	55.1	8	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
119	<a href="#">c5dajB_</a>	Alignment	not modelled	55.1	21	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> nald; <b>PDBTitle:</b> crystal structure of nald, the secondary repressor of mexab-oprm2 multidrug efflux pump in pseudomonas aeruginosa
120	<a href="#">c1efaA_</a>	Alignment	not modelled	55.0	7	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> lac repressor; <b>PDBTitle:</b> crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf