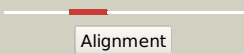

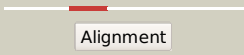


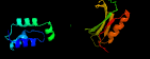
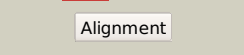

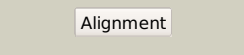

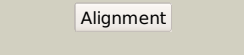

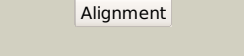

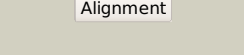

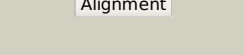

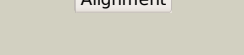

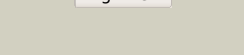
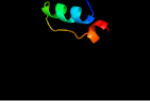






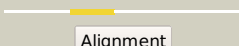

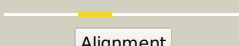

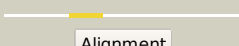

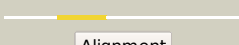






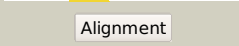
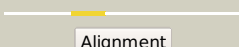
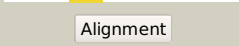
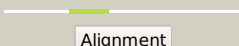


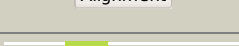
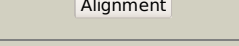


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3431c_(-)_3849474_3850319
Date	Fri Aug 9 18:20:10 BST 2019
Unique Job ID	1af5ca8fe850a97e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k78a1	 Alignment		94.2	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
2	d6paxa1	 Alignment		94.0	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
3	c4fcyA_	 Alignment		93.7	15	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
4	d1pdnc_	 Alignment		92.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
5	c6paxA_	 Alignment		92.4	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
6	c1u78A_	 Alignment		88.0	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
7	c1rp3G_	 Alignment		87.5	18	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
8	c2m8eA_	 Alignment		83.2	19	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase
9	d1bcoa2	 Alignment		83.1	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
10	d1trra_	 Alignment		82.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
11	d1au7a2	 Alignment		82.4	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain

12	c1au7B_	 Alignment		81.2	21	PDB header: transcription/dna Chain: B: PDB Molecule: protein pit-1; PDBTitle: pit-1 mutant/dna complex
13	c2r0qF_	 Alignment		80.7	18	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
14	d1jhga_	 Alignment		80.4	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
15	c3mzyA_	 Alignment		79.8	8	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
16	d1e3oc2	 Alignment		79.5	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
17	c2k27A_	 Alignment		79.3	23	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
18	c3korD_	 Alignment		78.5	19	PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus
19	c3frwF_	 Alignment		78.3	16	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trpr protein from ruminococcus obeum
20	d1l3la1	 Alignment		77.7	18	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)
21	d1xsva_	 Alignment	not modelled	76.5	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
22	c1zljE_	 Alignment	not modelled	75.7	10	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
23	c2gm4B_	 Alignment	not modelled	72.3	12	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
24	c3l1pA_	 Alignment	not modelled	70.4	19	PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex
25	c1x3uA_	 Alignment	not modelled	69.8	17	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
26	c2rniA_	 Alignment	not modelled	69.4	10	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar; PDBTitle: nmr structure of the s. aureus vrar dna binding domain
27	d1fsea_	 Alignment	not modelled	69.3	12	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)
28	c6jqsA_	 Alignment	not modelled	68.7	15	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
		 Alignment				PDB header: dna binding protein

29	c2jpcA_	Alignment	not modelled	68.6	8	Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
30	c3hosA_	Alignment	not modelled	67.2	13	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
31	d1a04a1	Alignment	not modelled	64.3	10	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)
32	c3sztB_	Alignment	not modelled	64.3	5	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
33	c1hf0A_	Alignment	not modelled	63.9	19	PDB header: transcription Chain: A: PDB Molecule: octamer-binding transcription factor 1; PDBTitle: crystal structure of the dna-binding domain of oct-1 bound to dna as a2 dimer
34	c2krfB_	Alignment	not modelled	63.3	13	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
35	d1yioa1	Alignment	not modelled	62.6	10	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)
36	c3d1nK_	Alignment	not modelled	61.9	27	PDB header: transcription regulator/dna Chain: K: PDB Molecule: pou domain, class 6, transcription factor 1; PDBTitle: structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter
37	c2lvsA_	Alignment	not modelled	61.3	24	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr solution structure of a crispr repeat binding protein
38	c2bw3A_	Alignment	not modelled	60.7	14	PDB header: dna recombination Chain: A: PDB Molecule: transposase; PDBTitle: three-dimensional structure of the hermes dna transposase
39	c3cloC_	Alignment	not modelled	60.5	20	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
40	d2jn6a1	Alignment	not modelled	60.2	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
41	d1p4wa_	Alignment	not modelled	59.8	7	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)
42	c3zeyG_	Alignment	not modelled	59.3	15	PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s13, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
43	c3izbO_	Alignment	not modelled	57.9	14	PDB header: ribosome Chain: O: PDB Molecule: 40s ribosomal protein rps13 (s15p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
44	c5f7pA_	Alignment	not modelled	55.8	13	PDB header: transcription Chain: A: PDB Molecule: lmo0178 protein; PDBTitle: rok repressor lmo0178 from listeria monocytogenes
45	d1yb3a1	Alignment	not modelled	55.4	12	Fold: YktB/PF0168-like Superfamily: YktB/PF0168-like Family: PF0168-like
46	c3hugA_	Alignment	not modelled	51.5	19	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
47	c1bcoA_	Alignment	not modelled	50.5	19	PDB header: transposase Chain: A: PDB Molecule: bacteriophage mu transposase; PDBTitle: bacteriophage mu transposase core domain
48	c2derA_	Alignment	not modelled	48.7	14	PDB header: transferase/rna Chain: A: PDB Molecule: trna-specific 2-thiouridylase mnma; PDBTitle: cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
49	c2xsdC_	Alignment	not modelled	48.4	15	PDB header: transcription/dna Chain: C: PDB Molecule: pou domain, class 3, transcription factor 1; PDBTitle: crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna
50	c3lysC_	Alignment	not modelled	48.4	8	PDB header: recombination Chain: C: PDB Molecule: prophage pi2 protein 01, integrase; PDBTitle: crystal structure of the n-terminal domain of the prophage pi2 protein2 01 (integrase) from lactococcus lactis, northeast structural genomics3 consortium target kr124f
51	c5uxxC_	Alignment	not modelled	48.2	10	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
52	d1c6va_	Alignment	not modelled	47.6	18	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
53	d1smyf2	Alignment	not modelled	46.1	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain PDB header: transcription, transferase/dna/rna

54	c5jpmF_	Alignment	not modelled	45.8	14	Chain: F: PDB Molecule: rna polymerase sigma factor rpos; PDBTitle: sigmas-transcription initiation complex with 4-nt nascent rna
55	c3nf9A_	Alignment	not modelled	45.7	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
56	c1c0mA_	Alignment	not modelled	44.9	13	PDB header: transferase Chain: A: PDB Molecule: protein (integrase); PDBTitle: crystal structure of rsv two-domain integrase
57	c2khqA_	Alignment	not modelled	44.8	5	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
58	c3qyxD_	Alignment	not modelled	44.5	14	PDB header: transcription/dna Chain: D: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of mycobacterium tuberculosis espr in complex with a2 small dna fragment
59	c3vepA_	Alignment	not modelled	43.8	15	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
60	d1s7oa_	Alignment	not modelled	43.6	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
61	c1iufA_	Alignment	not modelled	42.8	12	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
62	c2mqkA_	Alignment	not modelled	42.8	9	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent target dna activator b; PDBTitle: solution structure of n terminal domain of the mub aaa+ atpase
63	c5zx3F_	Alignment	not modelled	42.8	8	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
64	c2w48D_	Alignment	not modelled	41.3	18	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
65	c2xzmO_	Alignment	not modelled	41.2	8	PDB header: ribosome Chain: O: PDB Molecule: rps13e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
66	d1z6ra1	Alignment	not modelled	40.4	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
67	c3vdoA_	Alignment	not modelled	40.3	19	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
68	c6jnyA_	Alignment	not modelled	39.6	15	PDB header: transcription Chain: A: PDB Molecule: antiterminator q protein; PDBTitle: crystal structure of bacteriophage 21 q protein
69	d1g3wa1	Alignment	not modelled	38.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
70	c3u5cN_	Alignment	not modelled	38.5	10	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s13; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
71	c6in7B_	Alignment	not modelled	38.1	13	PDB header: transcription Chain: B: PDB Molecule: rna polymerase sigma-h factor; PDBTitle: crystal structure of algu in complex with muca(cyto)
72	d1or7a1	Alignment	not modelled	38.0	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
73	c4go1A_	Alignment	not modelled	37.8	26	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
74	c3j20O_	Alignment	not modelled	37.4	13	PDB header: ribosome Chain: Q: PDB Molecule: 30s ribosomal protein s15p/s13e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
75	c3t0yA_	Alignment	not modelled	37.1	18	PDB header: transcription regulator/protein binding Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr anti-anti-sigma domain bound to the anti-sigma2 factor, nepr
76	c2lfwA_	Alignment	not modelled	36.7	23	PDB header: signaling protein Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
77	c5fgmA_	Alignment	not modelled	36.6	14	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
78	c2o8xA_	Alignment	not modelled	35.5	13	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

79	c2f7tA_	Alignment	not modelled	35.1	11	PDB header: dna binding protein Chain: A: PDB Molecule: mos1 transposase; PDBTitle: crystal structure of the catalytic domain of mos1 mariner2 transposase
80	c4lfuA_	Alignment	not modelled	34.7	12	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
81	c2q0aA_	Alignment	not modelled	34.6	13	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
82	c5z7iC_	Alignment	not modelled	33.5	18	PDB header: dna binding protein/dna Chain: C: PDB Molecule: cell cycle regulatory protein gcra; PDBTitle: caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna
83	c3c65A_	Alignment	not modelled	33.3	26	PDB header: hydrolase Chain: A: PDB Molecule: uvrbc system protein c; PDBTitle: crystal structure of bacillus stearotheophilus uvrC 5' endonuclease2 domain
84	d1asua_	Alignment	not modelled	33.2	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
85	c6dvdF_	Alignment	not modelled	32.8	19	PDB header: transferase/dna Chain: F: PDB Molecule: ecf rna polymerase sigma factor sigI; PDBTitle: crystal structure of mycobacterium tuberculosis transcription2 initiation complex(ecf sigma factor I) with 6 nt spacer and bromine3 labelled in position "-11
86	c4a5pC_	Alignment	not modelled	32.7	12	PDB header: protein transport Chain: C: PDB Molecule: protein mxia; PDBTitle: structure of the shigella flexneri mxia protein
87	c2q1zA_	Alignment	not modelled	32.7	17	PDB header: transcription Chain: A: PDB Molecule: rpoe, ecf sigE; PDBTitle: crystal structure of rhodobacter sphaeroides sigE in complex with the2 anti-sigma chrr
88	d1hyva_	Alignment	not modelled	32.3	12	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
89	c1or7A_	Alignment	not modelled	31.9	13	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma-e factor; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
90	d2isya1	Alignment	not modelled	31.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
91	c1h0mD_	Alignment	not modelled	31.8	17	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
92	c3c3wB_	Alignment	not modelled	31.8	13	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
93	d2bw3a2	Alignment	not modelled	31.7	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Hermes transposase-like
94	d1rp3a2	Alignment	not modelled	29.5	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
95	c3nrwA_	Alignment	not modelled	29.3	14	PDB header: recombination Chain: A: PDB Molecule: phage integrase/site-specific recombinase; PDBTitle: crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a
96	c5u1cA_	Alignment	not modelled	29.1	19	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
97	d1c0ma2	Alignment	not modelled	28.6	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
98	d1cxqa_	Alignment	not modelled	28.3	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
99	c6c03A_	Alignment	not modelled	28.1	15	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
100	c3ut7A_	Alignment	not modelled	27.9	3	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structural view of a non pfam singleton and crystal packing analysis
101	c1z05A_	Alignment	not modelled	27.9	12	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, rok family; PDBTitle: crystal structure of the rok family transcriptional regulator, homolog2 of e.coli mlc protein.
102	c5o8yG_	Alignment	not modelled	27.8	7	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
103	c6g7oA_	Alignment	not modelled	27.2	13	PDB header: membrane protein Chain: A: PDB Molecule: alkaline ceramidase 3,soluble cytochrome b562;

						PDBTitle: crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution
104	c2keyA_	Alignment	not modelled	26.6	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative phage integrase; PDBTitle: solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
105	c5f64C_	Alignment	not modelled	26.5	13	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
106	c2kd1A_	Alignment	not modelled	26.5	7	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dna integration/recombination/inversion protein; PDBTitle: solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f
107	d1iufa1	Alignment	not modelled	26.0	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
108	d1vi0a1	Alignment	not modelled	25.6	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
109	c5xe7A_	Alignment	not modelled	25.6	11	PDB header: dna binding protein Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigj; PDBTitle: crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
110	c4kisA_	Alignment	not modelled	25.1	5	PDB header: recombination/dna Chain: A: PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a lsr-dna complex
111	c4cxfA_	Alignment	not modelled	25.0	20	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor cnrh; PDBTitle: structure of cnrh in complex with the cytosolic domain of cnry
112	c2nrrA_	Alignment	not modelled	24.7	20	PDB header: hydrolase Chain: A: PDB Molecule: uvrabc system protein c; PDBTitle: crystal structure of the c-terminal rnaseh endonuclease domain of uvrc
113	c5cr4B_	Alignment	not modelled	24.5	10	PDB header: hydrolase Chain: B: PDB Molecule: sleeping beauty transposase, sb100x; PDBTitle: crystal structure of the sleeping beauty transposase catalytic domain
114	c3iwfA_	Alignment	not modelled	24.3	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcription regulator rpir family; PDBTitle: the crystal structure of the n-terminal domain of a rpir2 transcriptional regulator from staphylococcus epidermidis to 1.4a
115	c2oxoA_	Alignment	not modelled	24.1	11	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
116	c2kiwA_	Alignment	not modelled	23.4	15	PDB header: dna binding protein Chain: A: PDB Molecule: int protein; PDBTitle: solution nmr structure of the domain n-terminal to the2 integrase domain of sh1003 from staphylococcus3 haemolyticus. northeast structural genomics consortium4 target shr105f (64-166).
117	c3qp5C_	Alignment	not modelled	22.4	13	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
118	c2rn7A_	Alignment	not modelled	21.8	8	PDB header: unknown function Chain: A: PDB Molecule: is629 orfa; PDBTitle: nmr solution structure of tnpe protein from shigella2 flexneri. northeast structural genomics target sfr125
119	c2x4hA_	Alignment	not modelled	21.3	12	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfobolus solfataricus
120	d1nera_	Alignment	not modelled	21.3	16	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors