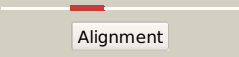

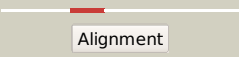

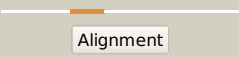

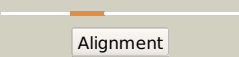

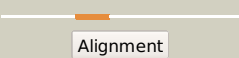

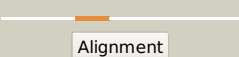

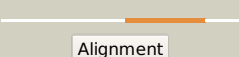






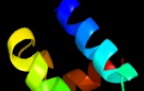
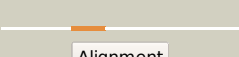



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0920c_(-)_1025501_1026820
Date	Fri Jul 26 01:50:51 BST 2019
Unique Job ID	7aa89a3b61a079b3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1k78a1	 Alignment		91.6	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
2	d6paxa1	 Alignment		91.2	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
3	d1pdnc_	 Alignment		89.7	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
4	c6paxA_	 Alignment		88.6	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
5	d1e3oc2	 Alignment		87.8	28	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
6	d1au7a2	 Alignment		86.6	25	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
7	c3q5xA_	 Alignment		85.7	17	PDB header: cell cycle Chain: A; PDB Molecule: protein cut8; PDBTitle: structure of proteasome tether
8	c1au7B_	 Alignment		85.2	26	PDB header: transcription/dna Chain: B; PDB Molecule: protein pit-1; PDBTitle: pit-1 mutant/dna complex
9	c1u78A_	 Alignment		84.5	9	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
10	c2r0qF_	 Alignment		83.9	24	PDB header: recombination/dna Chain: F; PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
11	c1rp3G_	 Alignment		83.1	22	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

12	c3d1nK_	Alignment		82.0	23	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
13	c3l1pA_	Alignment		80.8	25	PDB header: transcription/dna Chain: A: PDB Molecule: pou domain, class 5, transcription factor 1; PDBTitle: pou protein:dna complex
14	c3zeyG_	Alignment		80.8	33	PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s13, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
15	c4fcyA_	Alignment		80.6	17	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome
16	c2k27A_	Alignment		80.2	24	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
17	c3u5cN_	Alignment		78.5	28	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
18	c3izbO_	Alignment		78.2	28	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
19	c3korD_	Alignment		78.1	20	PDB header: transcription Chain: D: PDB Molecule: possible trp repressor; PDBTitle: crystal structure of a putative trp repressor from staphylococcus2 aureus
20	c2m8eA_	Alignment		77.7	21	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase
21	c2xzmO_	Alignment	not modelled	77.6	28	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
22	c3frwF_	Alignment	not modelled	77.1	18	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative trp repressor protein; PDBTitle: crystal structure of putative trp protein from ruminococcus obeum
23	d1trra_	Alignment	not modelled	77.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR
24	c1hf0A_	Alignment	not modelled	76.8	38	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
25	c2gm4B_	Alignment	not modelled	75.8	18	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
26	c1zljE_	Alignment	not modelled	75.4	27	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
27	c2xsdC_	Alignment	not modelled	75.3	23	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
28	d1jhga_	Alignment	not modelled	74.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Trp repressor, TrpR

29	c1iufA_	Alignment	not modelled	74.3	13	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
30	d1l3la1	Alignment	not modelled	71.4	20	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)
31	c3j20Q_	Alignment	not modelled	70.5	27	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)
32	c1x3uA_	Alignment	not modelled	69.3	30	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
33	c2jpcA_	Alignment	not modelled	68.9	23	PDB header: dna binding protein Chain: A: PDB Molecule: ssrb; PDBTitle: ssrb dna binding protein
34	c6jqsA_	Alignment	not modelled	68.9	17	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
35	d1fsea_	Alignment	not modelled	68.8	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)
36	d1yioa1	Alignment	not modelled	66.0	20	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)
37	c2bw3A_	Alignment	not modelled	66.0	19	PDB header: dna recombination Chain: A: PDB Molecule: transposase; PDBTitle: three-dimensional structure of the hermes dna transposase
38	c3cloC_	Alignment	not modelled	65.8	24	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
39	c2rniA_	Alignment	not modelled	64.5	23	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
40	d1xsva_	Alignment	not modelled	64.2	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
41	c5xyiN_	Alignment	not modelled	63.0	17	PDB header: ribosome Chain: N: PDB Molecule: 40s ribosomal protein s13, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
42	d1a04a1	Alignment	not modelled	62.0	27	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)
43	c3mzyA_	Alignment	not modelled	61.8	22	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
44	d1p4wa_	Alignment	not modelled	60.7	28	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)
45	c2krfB_	Alignment	not modelled	59.0	25	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
46	d1bcoa2	Alignment	not modelled	58.9	19	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: mu transposase, core domain
47	d1yb3a1	Alignment	not modelled	58.9	15	Fold: YktB/PF0168-like Superfamily: YktB/PF0168-like Family: PF0168-like
48	c3sztB_	Alignment	not modelled	58.2	26	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
49	c5ipmF_	Alignment	not modelled	56.0	11	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
50	c3c3wB_	Alignment	not modelled	55.0	26	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
51	d1iufa1	Alignment	not modelled	54.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
52	c3kinC_	Alignment	not modelled	53.9	20	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst
53	c3ut7A_	Alignment	not modelled	52.6	7	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structural view of a non pfam singleton and crystal packing analysis
54	c2lvsA_	Alignment	not modelled	51.1	28	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein;

						PDBTitle: nmr solution structure of a crispr repeat binding protein
55	c5o8yG_	Alignment	not modelled	49.7	30	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
56	c4mubA_	Alignment	not modelled	49.5	15	PDB header: transferase Chain: A: PDB Molecule: sulfotransferase; PDBTitle: schistosoma mansoni (blood fluke) sulfotransferase/oxamniquine complex
57	c5f64C_	Alignment	not modelled	49.4	15	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
58	c6jnyA_	Alignment	not modelled	49.1	21	PDB header: transcription Chain: A: PDB Molecule: antiterminator q protein; PDBTitle: crystal structure of bacteriophage 21 q protein
59	c3geiB_	Alignment	not modelled	48.0	7	PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
60	d2g9wa1	Alignment	not modelled	47.2	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
61	c3qyxD_	Alignment	not modelled	46.9	22	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
62	c3nvbA_	Alignment	not modelled	42.5	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal part of the protein bf1531 from2 bacteroides fragilis containing phosphatase domain complexed with mg3 and tungstate
63	c4kisA_	Alignment	not modelled	41.3	3	PDB header: recombination/dna Chain: A: PDB Molecule: putative integrase [bacteriophage a118]; PDBTitle: crystal structure of a lsr-dna complex
64	c4if4A_	Alignment	not modelled	40.6	22	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the magnesium and beryll fluoride-activated vvar2 from staphylococcus aureus
65	c6ez8A_	Alignment	not modelled	39.2	19	PDB header: protein binding Chain: A: PDB Molecule: shuntingtin; PDBTitle: human huntingtin-hap40 complex structure
66	c3gehA_	Alignment	not modelled	38.4	13	PDB header: hydrolase Chain: A: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from nostoc in complex with gdp, folinic2 acid and zn
67	c2khqA_	Alignment	not modelled	38.1	11	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
68	d2bw3a2	Alignment	not modelled	37.6	16	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Hermes transposase-like
69	c5hevC_	Alignment	not modelled	36.3	18	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vvar; PDBTitle: crystal structure of the beryll fluoride-activated liar from2 enterococcus faecium
70	c3lysC_	Alignment	not modelled	35.7	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
71	c5l87A_	Alignment	not modelled	35.0	36	PDB header: membrane protein Chain: A: PDB Molecule: peroxin 14; PDBTitle: targeting the pex14-pex5 interaction by small molecules provides novel2 therapeutic routes to treat trypanosomiasis.
72	d1hyva_	Alignment	not modelled	34.8	10	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
73	c4r3uB_	Alignment	not modelled	34.8	14	PDB header: isomerase Chain: B: PDB Molecule: 2-hydroxyisobutyryl-coa mutase large subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
74	c4yn8A_	Alignment	not modelled	34.2	15	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
75	c4go1A_	Alignment	not modelled	34.1	29	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr from e.2 coli.
76	c2w48D_	Alignment	not modelled	33.6	27	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
77	d1s7oa_	Alignment	not modelled	33.2	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
78	c4mq3A_	Alignment	not modelled	31.9	25	PDB header: viral protein Chain: A: PDB Molecule: integrase; PDBTitle: the 1.1 angstrom structure of catalytic core domain of hiv integrase
79	c5uxxC_	Alignment	not modelled	31.9	22	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

80	c1xzqA_	Alignment	not modelled	31.6	13	PDB header: hydrolase Chain: A: PDB Molecule: probable trna modification gtpase trme; PDBTitle: structure of the gtp-binding protein trme from thermotoga2 maritima complexed with 5-formyl-thf
81	d1z6ra1	Alignment	not modelled	31.3	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ROK associated domain
82	d1v9sa1	Alignment	not modelled	31.3	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
83	c1rnlA_	Alignment	not modelled	31.1	27	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
84	d1g3wa1	Alignment	not modelled	30.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
85	d1r6ta2	Alignment	not modelled	30.8	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
86	c2mqkA_	Alignment	not modelled	30.6	27	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
87	d1x2ga1	Alignment	not modelled	30.5	22	Fold: SufE/NifU Superfamily: SufE/NifU Family: SP1160 C-terminal domain-like
88	c3iayA_	Alignment	not modelled	30.0	21	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase delta catalytic subunit; PDBTitle: ternary complex of dna polymerase delta
89	d2p5ka1	Alignment	not modelled	28.5	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
90	d3ctaa1	Alignment	not modelled	28.3	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
91	c4ycsC_	Alignment	not modelled	27.6	13	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
92	c2q0oA_	Alignment	not modelled	27.4	21	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional activator protein trar; PDBTitle: crystal structure of an anti-activation complex in bacterial quorum2 sensing
93	c6ideA_	Alignment	not modelled	27.4	21	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional regulator luxr family; PDBTitle: crystal structure of the vibrio cholera vqma-ligand-dna complex2 provides molecular mechanisms for drug design
94	d2isya1	Alignment	not modelled	27.2	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Iron-dependent repressor protein
95	d2fnaa1	Alignment	not modelled	27.1	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain
96	d1smyf2	Alignment	not modelled	27.0	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
97	d1f9na1	Alignment	not modelled	26.9	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
98	c5zx3F_	Alignment	not modelled	25.7	17	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
99	c1h0mD_	Alignment	not modelled	25.0	20	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
100	c3femB_	Alignment	not modelled	24.4	23	PDB header: biosynthetic protein, transferase Chain: B: PDB Molecule: pyridoxine biosynthesis protein snz1; PDBTitle: structure of the synthase subunit pdx1.1 (snz1) of plp synthase from2 saccharomyces cerevisiae
101	d1r71a_	Alignment	not modelled	24.2	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
102	d1b4aa1	Alignment	not modelled	24.1	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Arginine repressor (ArgR), N-terminal DNA-binding domain
103	c2ogfD_	Alignment	not modelled	23.9	27	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein mj0408; PDBTitle: crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
104	c3hugA_	Alignment	not modelled	23.0	20	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
105	d1stza1	Alignment	not modelled	22.9	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain

106	c5cz1B_	Alignment	not modelled	22.7	9	PDB header: hydrolase Chain: B: PDB Molecule: integrage; PDBTitle: crystal structure of the catalytic core domain of mmtv integrase
107	c4lfuA_	Alignment	not modelled	22.5	22	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
108	c4n1vA_	Alignment	not modelled	22.3	21	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein hu-beta; PDBTitle: structure of dna-binding protein hu from micoplasma spiroplasma2 melliferum
109	c6jf1A_	Alignment	not modelled	22.1	12	PDB header: transport protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure of the substrate binding protein of a methionine2 transporter from streptococcus pneumoniae
110	d1yaca_	Alignment	not modelled	22.0	7	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
111	c2x4hA_	Alignment	not modelled	22.0	15	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
112	c3nrwA_	Alignment	not modelled	21.9	13	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
113	c3fdjA_	Alignment	not modelled	21.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: degv family protein; PDBTitle: the structure of a degv family protein from eubacterium eligens.
114	c5unkA_	Alignment	not modelled	21.8	26	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the red subdomain of the sleeping beauty transposase
115	c4j8sA_	Alignment	not modelled	21.7	22	PDB header: protein binding Chain: A: PDB Molecule: ccr4-not transcription complex subunit 1; PDBTitle: crystal structure of human cnot1 mif4g domain in complex with a ttp2 peptide
116	c3leqA_	Alignment	not modelled	21.5	38	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein cvnb5; PDBTitle: the crystal structure of the roadblock/lc7 domain from streptomyces2 avermitillis to 1.85a
117	d1bw6a_	Alignment	not modelled	21.5	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
118	c4firB_	Alignment	not modelled	21.4	24	PDB header: lyase Chain: B: PDB Molecule: pyridoxal biosynthesis lyase pdxs; PDBTitle: crystal structure of pyridoxal biosynthesis lyase pdxs from pyrococcus
119	c1zn2A_	Alignment	not modelled	20.7	18	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
120	c2ehjA_	Alignment	not modelled	20.4	22	PDB header: transferase Chain: A: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structure of uracil phosphoribosyl transferase