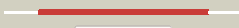
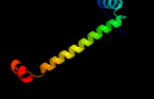





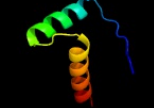

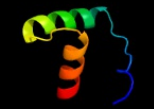
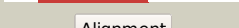

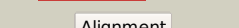

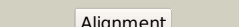
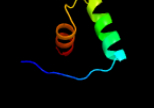
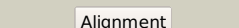
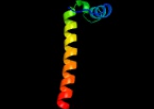
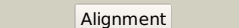

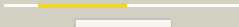

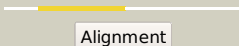
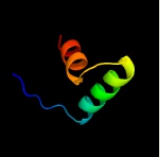
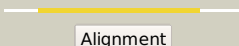
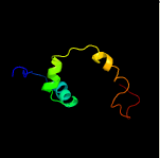
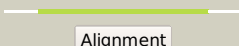
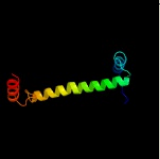
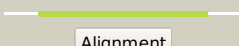
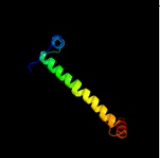
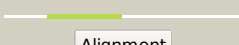

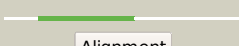
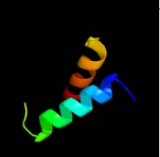

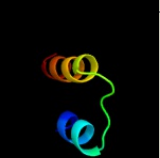

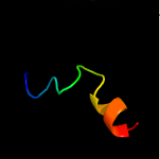

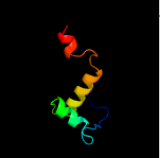


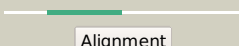

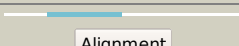


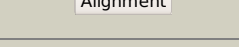


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1960c (-) _2203981_2204232
Date	Mon Aug 5 13:25:05 BST 2019
Unique Job ID	944df5e491f00662

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3kxeD_</a>	 Alignment		99.9	58	<b>PDB header:</b> protein binding <b>Chain:</b> D; <b>PDB Molecule:</b> antitoxin protein pard-1; <b>PDBTitle:</b> a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
2	<a href="#">c5cegC_</a>	 Alignment		99.9	30	<b>PDB header:</b> toxin <b>Chain:</b> C; <b>PDB Molecule:</b> addiction module antidote protein, cogp/arc/metj family; <b>PDBTitle:</b> x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
3	<a href="#">d2bj7a1</a>	 Alignment		98.5	23	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
4	<a href="#">d2hzaa1</a>	 Alignment		98.5	25	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
5	<a href="#">c1q5vB_</a>	 Alignment		98.2	26	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> apo-nikr
6	<a href="#">c2ca9B_</a>	 Alignment		98.2	23	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> putative nickel-responsive regulator; <b>PDBTitle:</b> apo-nikr from helicobacter pylori in closed trans-2 conformation
7	<a href="#">c2bj3D_</a>	 Alignment		98.1	23	<b>PDB header:</b> transcription <b>Chain:</b> D; <b>PDB Molecule:</b> nickel responsive regulator; <b>PDBTitle:</b> nikr-apo
8	<a href="#">d2hzab1</a>	 Alignment		98.0	27	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> CopG-like
9	<a href="#">c4me7E_</a>	 Alignment		95.9	28	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> E; <b>PDB Molecule:</b> antitoxin endoai; <b>PDBTitle:</b> crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
10	<a href="#">c2k5jB_</a>	 Alignment		90.8	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein yiif; <b>PDBTitle:</b> solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
11	<a href="#">c6qeqD_</a>	 Alignment		79.4	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> D; <b>PDB Molecule:</b> pcfff; <b>PDBTitle:</b> pcfff from enterococcus faecalis pcf10

12	<a href="#">c5x3tA_</a>	 Alignment		78.8	24	<b>PDB header:</b> antitoxin/toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin vapb26; <b>PDBTitle:</b> vapbc from mycobacterium tuberculosis
13	<a href="#">c2an7A_</a>	 Alignment		78.4	8	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein pard; <b>PDBTitle:</b> solution structure of the bacterial antidote pard
14	<a href="#">c5xe3E_</a>	 Alignment		69.7	20	<b>PDB header:</b> hydrolase/antitoxin <b>Chain:</b> E: <b>PDB Molecule:</b> probable antitoxin maze4; <b>PDBTitle:</b> endoribonuclease in complex with its cognate antitoxin from 2 mycobacterial species
15	<a href="#">c5xe3F_</a>	 Alignment		69.7	20	<b>PDB header:</b> hydrolase/antitoxin <b>Chain:</b> F: <b>PDB Molecule:</b> probable antitoxin maze4; <b>PDBTitle:</b> endoribonuclease in complex with its cognate antitoxin from 2 mycobacterial species
16	<a href="#">c3mb3A_</a>	 Alignment		66.1	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ph-interacting protein; <b>PDBTitle:</b> crystal structure of the second bromodomain of pleckstrin homology 2 domain interacting protein (phip)
17	<a href="#">c4p9fA_</a>	 Alignment		54.0	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hth-type transcriptional regulator mcbr; <b>PDBTitle:</b> e. coli mcbr/yncc
18	<a href="#">c4lz2A_</a>	 Alignment		53.6	22	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> bromodomain adjacent to zinc finger domain protein 2a; <b>PDBTitle:</b> crystal structure of the bromodomain of human baz2a
19	<a href="#">c6oitG_</a>	 Alignment		52.3	17	<b>PDB header:</b> plant protein <b>Chain:</b> G: <b>PDB Molecule:</b> protein chromatin remodeling 35; <b>PDBTitle:</b> cryoem structure of arabidopsis ddr' complex (drd1 peptide-dms3-rdm1)
20	<a href="#">c6a7vU_</a>	 Alignment		49.9	15	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> U: <b>PDB Molecule:</b> antitoxin vapb11; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis vapbc11 toxin-2 antitoxin complex
21	<a href="#">c5czgA_</a>	 Alignment	not modelled	43.9	24	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical bromodomain; <b>PDBTitle:</b> crystal structure analysis of hypothetical bromodomain tb427.10.74202 from trypanosoma brucei in complex with bromosporine
22	<a href="#">c5n17B_</a>	 Alignment	not modelled	41.1	20	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> bromodomain-containing factor 1; <b>PDBTitle:</b> first bromodomain (bd1) from candida albicans bdf1 bound to a2 dibenzothiazepinone (compound 3)
23	<a href="#">c3lqiA_</a>	 Alignment	not modelled	40.7	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ml11 phd3-bromo; <b>PDBTitle:</b> crystal structure of ml11 phd3-bromo complexed with h3(1-9)k4me22 peptide
24	<a href="#">c2nxbB_</a>	 Alignment	not modelled	39.4	22	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> bromodomain-containing protein 3; <b>PDBTitle:</b> crystal structure of human bromodomain containing protein 3 (brd3)
25	<a href="#">d3d7ca1</a>	 Alignment	not modelled	38.7	7	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bromodomain <b>Family:</b> Bromodomain
26	<a href="#">c2e3kC_</a>	 Alignment	not modelled	38.4	15	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> bromodomain-containing protein 2; <b>PDBTitle:</b> crystal structure of the human brd2 second bromodomain in2 complexed with the acetylated histone h4 peptide
27	<a href="#">c3daiA_</a>	 Alignment	not modelled	38.1	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> atpase family aaa domain-containing protein 2; <b>PDBTitle:</b> crystal structure of the bromodomain of the human atad2
28	<a href="#">c4p7dA_</a>	 Alignment	not modelled	37.9	16	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> antitoxin hicb3; <b>PDBTitle:</b> antitoxin hicb3 crystal structure

29	<a href="#">c2dkwA</a>	Alignment	not modelled	36.9	12	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein kiaa1240; <b>PDBTitle:</b> solution structure of the bromodomain of human protein2 kiaa1240
30	<a href="#">c2yekA</a>	Alignment	not modelled	34.4	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> bromodomain-containing protein 2; <b>PDBTitle:</b> crystal structure of the first bromodomain of human brd22 with the inhibitor gsk525762 (ibet)
31	<a href="#">c4ldfA</a>	Alignment	not modelled	34.4	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> gcn5 like acetylase + bromodomain; <b>PDBTitle:</b> crystal structure of cpbrd2 from cryptosporidium, cgd3_3190
32	<a href="#">c3iu5A</a>	Alignment	not modelled	33.8	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein polybromo-1; <b>PDBTitle:</b> crystal structure of the first bromodomain of human poly-bromodomain2 containing protein 1 (pb1)
33	<a href="#">c5c4qB</a>	Alignment	not modelled	33.8	30	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> bromodomain; <b>PDBTitle:</b> crystal structure analysis of bromodomain from leishmania donovani2 complexed with bromosporine
34	<a href="#">d1eqfa1</a>	Alignment	not modelled	33.3	11	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bromodomain <b>Family:</b> Bromodomain
35	<a href="#">c5uiyA</a>	Alignment	not modelled	33.3	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bromodomain adjacent to zinc finger domain protein 1a; <b>PDBTitle:</b> structure of bromodomain from human baz1a
36	<a href="#">c5n18B</a>	Alignment	not modelled	32.7	15	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> bromodomain-containing factor 1; <b>PDBTitle:</b> second bromodomain (bd2) from candida albicans bdf1 bound to an2 imidazopyridine (compound 2)
37	<a href="#">c2e7oA</a>	Alignment	not modelled	32.3	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> bromodomain adjacent to zinc finger domain 2b; <b>PDBTitle:</b> solution structure of the bromodomain from human2 bromodomain adjacent to zinc finger domain 2b
38	<a href="#">c4n4hA</a>	Alignment	not modelled	32.2	33	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> zinc finger mynd domain-containing protein 11; <b>PDBTitle:</b> crystal structure of the bromo-pwpp of the mouse zinc finger mynd-type2 containing 11 isoform alpha in complex with histone h3.1k36me3
39	<a href="#">c3hmhA</a>	Alignment	not modelled	31.8	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription initiation factor tfiid 210 kda subunit; <b>PDBTitle:</b> crystal structure of the second bromodomain of human tbp-associated2 factor rna polymerase 1-like (taf1)
40	<a href="#">c3hmfA</a>	Alignment	not modelled	31.3	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein polybromo-1; <b>PDBTitle:</b> crystal structure of the second bromodomain of human poly-bromodomain2 containing protein 1 (pb1)
41	<a href="#">c2yqdA</a>	Alignment	not modelled	30.7	12	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> polybromo-1; <b>PDBTitle:</b> solution structure of the fifth bromodomain from mouse2 polybromo-1
42	<a href="#">c6mr4B</a>	Alignment	not modelled	29.6	22	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear protein sth1/nps1; <b>PDBTitle:</b> crystal structure of the sth1 bromodomain from s.cerevisiae
43	<a href="#">c3hmeB</a>	Alignment	not modelled	29.6	19	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> bromodomain-containing protein 9; <b>PDBTitle:</b> crystal structure of human bromodomain containing 9 isoform 1 (brd9)
44	<a href="#">c6cw0A</a>	Alignment	not modelled	28.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> cgd2_2690 protein; <b>PDBTitle:</b> crystal structure of cryptosporidium parvum bromodomain cgd2_2690
45	<a href="#">c2yynA</a>	Alignment	not modelled	28.7	8	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription intermediary factor 1-alpha; <b>PDBTitle:</b> crystal structure of human bromodomain protein
46	<a href="#">c3rcwF</a>	Alignment	not modelled	27.8	12	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> bromodomain-containing protein 1; <b>PDBTitle:</b> crystal structure of the bromodomain of human brd1
47	<a href="#">c4rgwB</a>	Alignment	not modelled	27.2	12	<b>PDB header:</b> transferase/transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 7; <b>PDBTitle:</b> crystal structure of a taf1-taf7 complex in human transcription factor2 iid
48	<a href="#">c3zbeA</a>	Alignment	not modelled	27.2	13	<b>PDB header:</b> toxin-antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> paaa2; <b>PDBTitle:</b> e. coli o157 pare2-associated antitoxin 2 (paaa2)
49	<a href="#">c4hlxD</a>	Alignment	not modelled	26.0	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> k9; <b>PDBTitle:</b> the crystal structure of the dna binding domain of virf-1 from the2 oncogenic kshv
50	<a href="#">c4uetA</a>	Alignment	not modelled	25.9	12	<b>PDB header:</b> retinol-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> nematode fatty acid retinoid binding protein; <b>PDBTitle:</b> diversity in the structures and ligand binding sites among2 the fatty acid and retinol binding proteins of nematodes3 revealed by na-far-1 from necator americanus
51	<a href="#">d1e6ia</a>	Alignment	not modelled	25.4	12	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bromodomain <b>Family:</b> Bromodomain
52	<a href="#">c5ko4A</a>	Alignment	not modelled	25.3	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> bromodomain from trypanosoma brucei tb427.10.8150
53	<a href="#">c3hla</a>	Alignment	not modelled	25.1	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein polybromo-1;

53	<a href="#">c3upA</a>	Alignment	not modelled	23.1	10	<b>PDBTitle:</b> crystal structure of the fourth bromodomain of human poly-bromodomain2 containing protein 1 (pb1) <b>PDB header:</b> signaling protein
54	<a href="#">c6nimB</a>	Alignment	not modelled	25.0	24	<b>Chain:</b> B: <b>PDB Molecule:</b> bromodomain factor 2 protein; <b>PDBTitle:</b> trypanosoma cruzi - bdf2, tcclb.506553.20, solved with bromosporine
55	<a href="#">d2pi0a1</a>	Alignment	not modelled	24.5	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Interferon regulatory factor
56	<a href="#">c6g1nB</a>	Alignment	not modelled	24.3	14	<b>PDB header:</b> antitoxin <b>Chain:</b> B: <b>PDB Molecule:</b> antitoxin hicb; <b>PDBTitle:</b> crystal structure of the burkholderia pseudomallei antitoxin hicb
57	<a href="#">c4eqzA</a>	Alignment	not modelled	24.2	14	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> arabinose metabolism transcriptional repressor; <b>PDBTitle:</b> crystal structure of arar(dbd) in complex with operator orr3
58	<a href="#">d1ifya</a>	Alignment	not modelled	23.7	14	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> UBA-like <b>Family:</b> UBA domain
59	<a href="#">c6sbsB</a>	Alignment	not modelled	23.6	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> ytra from sulfobolus acidocaldarius, a gntr-family transcription2 factor
60	<a href="#">c3qu3A</a>	Alignment	not modelled	23.5	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> interferon regulatory factor 7; <b>PDBTitle:</b> crystal structure of irf-7 dbd apo form
61	<a href="#">d3dwya1</a>	Alignment	not modelled	22.1	11	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bromodomain <b>Family:</b> Bromodomain
62	<a href="#">c3fkmX</a>	Alignment	not modelled	21.7	20	<b>PDB header:</b> signaling protein <b>Chain:</b> X: <b>PDB Molecule:</b> signaling protein; <b>PDBTitle:</b> plasmodium falciparum bromodomain-containing protein pf10_0328
63	<a href="#">c4nxC</a>	Alignment	not modelled	21.6	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> bromodomain protein; <b>PDBTitle:</b> crystal structure of pf3d7_1475600, a bromodomain from plasmodium2 falciparum
64	<a href="#">d2irfg</a>	Alignment	not modelled	21.4	7	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Interferon regulatory factor
65	<a href="#">c2i7kA</a>	Alignment	not modelled	20.5	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bromodomain-containing protein 7; <b>PDBTitle:</b> solution structure of the bromodomain of human brd7 protein
66	<a href="#">c2d9eA</a>	Alignment	not modelled	19.9	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> peregrin; <b>PDBTitle:</b> solution structure of the bromodomain of peregrin
67	<a href="#">c6ep3B</a>	Alignment	not modelled	19.6	29	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> lmo0651 protein; <b>PDBTitle:</b> lar controls the expression of the listeria monocytogenes agr system2 and mediates virulence.
68	<a href="#">c6mf9B</a>	Alignment	not modelled	19.3	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> znkn (c2hc)+athook+bromo domain protein, taf250, <b>PDBTitle:</b> crystal structure of cgd4-650 with compound bi2536
69	<a href="#">d1wuma1</a>	Alignment	not modelled	19.3	11	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bromodomain <b>Family:</b> Bromodomain
70	<a href="#">c2di3A</a>	Alignment	not modelled	19.2	37	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bacterial regulatory proteins, gntr family; <b>PDBTitle:</b> crystal structure of the transcriptional factor cgl29152 from corynebacterium glutamicum
71	<a href="#">c2dlIA</a>	Alignment	not modelled	18.3	21	<b>PDB header:</b> cytokine <b>Chain:</b> A: <b>PDB Molecule:</b> interferon regulatory factor 4; <b>PDBTitle:</b> solution structure of the irf domain of human interferon2 regulator factors 4
72	<a href="#">c3nxbB</a>	Alignment	not modelled	17.9	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cat eye syndrome critical region protein 2; <b>PDBTitle:</b> crystal structure of the bromodomain of human cecr2
73	<a href="#">c2h34B</a>	Alignment	not modelled	17.7	21	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein kinase pkne; <b>PDBTitle:</b> apoenzyme crystal structure of the tuberculosis serine/threonine2 kinase, pkne
74	<a href="#">c3k2jB</a>	Alignment	not modelled	17.7	12	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> protein polybromo-1; <b>PDBTitle:</b> crystal structure of the 3rd bromodomain of human poly-bromodomain2 containing protein 1 (pb1)
75	<a href="#">d1eqfa2</a>	Alignment	not modelled	17.3	19	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bromodomain <b>Family:</b> Bromodomain
76	<a href="#">c2f6nA</a>	Alignment	not modelled	17.2	11	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bromodomain phd finger transcription factor; <b>PDBTitle:</b> crystal structure of phd finger-linker-bromodomain fragment of human2 bptf in the free form
77	<a href="#">c3mqmB</a>	Alignment	not modelled	17.0	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> probable histone-lysine n-methyltransferase ash11; <b>PDBTitle:</b> crystal structure of the bromodomain of human ash11
78	<a href="#">c2hs5A</a>	Alignment	not modelled	16.6	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator gntr; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 transcriptional regulator gntr from rhodococcus sp. rha1
						<b>PDB header:</b> protein binding

79	<a href="#">c6akmB_</a>	Alignment	not modelled	16.3	26	<b>Chain:</b> B: <b>PDB Molecule:</b> sarcolemmal membrane-associated protein; <b>PDBTitle:</b> crystal structure of slmap-sike1 complex
80	<a href="#">c3ihuA_</a>	Alignment	not modelled	16.2	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, gntr family; <b>PDBTitle:</b> crystal structure of dna binding protein (yp_298823.1) from ralstonia2 eutropha jmp134 at 1.92 a resolution
81	<a href="#">c3qztA_</a>	Alignment	not modelled	16.2	11	<b>PDB header:</b> transcription/nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nucleosome-remodeling factor subunit bptf; <b>PDBTitle:</b> crystal structure of bptf bromo in complex with histone h4k16ac - form2 ii
82	<a href="#">c6g8rB_</a>	Alignment	not modelled	15.5	7	<b>PDB header:</b> peptide binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> nuclear body protein sp140; <b>PDBTitle:</b> sp140 phd-bromodomain complex with scfv
83	<a href="#">c4ptbA_</a>	Alignment	not modelled	14.8	4	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear autoantigen sp-100; <b>PDBTitle:</b> crystal structure of human sp100 phd-bromodomain in the free state
84	<a href="#">d1rz4a2</a>	Alignment	not modelled	14.3	14	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> ARM repeat <b>Family:</b> Eukaryotic translation initiation factor 3 subunit 12, eIF3k, N-terminal domain
85	<a href="#">c1rxrD_</a>	Alignment	not modelled	13.8	20	<b>PDB header:</b> replication inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> seqa protein; <b>PDBTitle:</b> crystal structure of a dna-binding protein
86	<a href="#">d1rxra1</a>	Alignment	not modelled	13.8	20	<b>Fold:</b> Ribbon-helix-helix <b>Superfamily:</b> Ribbon-helix-helix <b>Family:</b> SeqA N-terminal domain-like
87	<a href="#">c2h5xA_</a>	Alignment	not modelled	13.6	32	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruva; <b>PDBTitle:</b> ruva from mycobacterium tuberculosis
88	<a href="#">c1ixrB_</a>	Alignment	not modelled	13.1	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction dna helicase ruva; <b>PDBTitle:</b> ruva-ruvb complex
89	<a href="#">d2hs5a1</a>	Alignment	not modelled	12.4	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> GntR-like transcriptional regulators
90	<a href="#">c1tu3H_</a>	Alignment	not modelled	12.2	27	<b>PDB header:</b> protein transport <b>Chain:</b> H: <b>PDB Molecule:</b> rab gtpase binding effector protein 1; <b>PDBTitle:</b> crystal structure of rab5 complex with rabaptin5 c-terminal2 domain
91	<a href="#">c5u7gB_</a>	Alignment	not modelled	11.8	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> creb-binding protein; <b>PDBTitle:</b> crystal structure of the catalytic core of cbp
92	<a href="#">c3iu6A_</a>	Alignment	not modelled	11.0	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> protein polybromo-1; <b>PDBTitle:</b> crystal structure of the sixth bromodomain of human poly-bromodomain2 containing protein 1 (pb1)
93	<a href="#">c1zxaB_</a>	Alignment	not modelled	10.8	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> cgmp-dependent protein kinase 1, alpha isozyme; <b>PDBTitle:</b> solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
94	<a href="#">c1eqfA_</a>	Alignment	not modelled	10.3	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase ii transcription initiation <b>PDBTitle:</b> crystal structure of the double bromodomain module from2 human tafii250
95	<a href="#">d2bl8a1</a>	Alignment	not modelled	10.1	18	<b>Fold:</b> Bromodomain-like <b>Superfamily:</b> Bacteriocin immunity protein-like <b>Family:</b> EntA-Im
96	<a href="#">c6iyaD_</a>	Alignment	not modelled	10.0	27	<b>PDB header:</b> antitoxin <b>Chain:</b> D: <b>PDB Molecule:</b> transcriptional regulator copg family; <b>PDBTitle:</b> structure of the dna binding domain of antitoxin copaso
97	<a href="#">c4ypiF_</a>	Alignment	not modelled	9.8	25	<b>PDB header:</b> rna binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> structure of ebola virus nucleoprotein n-terminal fragment bound to a2 peptide derived from ebola vp35
98	<a href="#">c4ypiG_</a>	Alignment	not modelled	9.8	25	<b>PDB header:</b> rna binding protein <b>Chain:</b> G: <b>PDB Molecule:</b> polymerase cofactor vp35; <b>PDBTitle:</b> structure of ebola virus nucleoprotein n-terminal fragment bound to a2 peptide derived from ebola vp35
99	<a href="#">c1nhgD_</a>	Alignment	not modelled	9.5	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> enoyl-acyl carrier reductase; <b>PDBTitle:</b> crystal structure analysis of plasmodium falciparum enoyl-2 acyl-carrier-protein reductase with triclosan