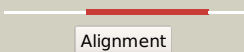

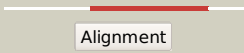



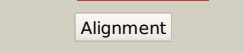



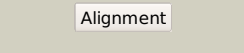

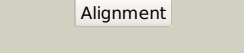


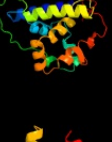
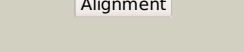

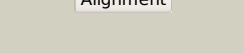

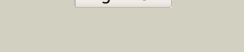



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2667_(clpC2)_2983906_2984664
Date	Wed Aug 7 12:50:31 BST 2019
Unique Job ID	0aa257c157746310

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4xbiA_</a>	 Alignment		100.0	22	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> clpb protein, putative,green fluorescent protein; <b>PDBTitle:</b> structure of a malarial protein involved in proteostasis
2	<a href="#">c4y0cB_</a>	 Alignment		100.0	18	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> clp protease-related protein at4g12060, chloroplastic; <b>PDBTitle:</b> the structure of arabidopsis clpt2
3	<a href="#">c3fh2A_</a>	 Alignment		100.0	38	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent protease (heat shock protein); <b>PDBTitle:</b> the crystal structure of the probable atp-dependent protease (heat2 shock protein) from corynebacterium glutamicum
4	<a href="#">c3zriA_</a>	 Alignment		100.0	14	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> n-domain of clpv from vibrio cholerae
5	<a href="#">c5guiA_</a>	 Alignment		100.0	33	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein clpc1, chloroplastic; <b>PDBTitle:</b> crystal structure of the n-terminal domain of caseinolytic protease2 associated chaperone clpc1 from arabidopsis thaliana
6	<a href="#">c4y0bA_</a>	 Alignment		100.0	17	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> double clp-n motif protein; <b>PDBTitle:</b> the structure of arabidopsis clpt1
7	<a href="#">c2k77A_</a>	 Alignment		100.0	33	<b>PDB header:</b> chaperone, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> negative regulator of genetic competence <b>PDBTitle:</b> nmr solution structure of the bacillus subtilis clpc n-2 domain
8	<a href="#">c5u2IA_</a>	 Alignment		100.0	23	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> crystal structure of the hsp104 n-terminal domain from candida2 albicans
9	<a href="#">c5gkmA_</a>	 Alignment		100.0	27	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> at5g51070/k3k7_27; <b>PDBTitle:</b> crystal structure of the n-terminal domain of caseinolytic protease2 associated chaperone clpd from arabidopsis thaliana
10	<a href="#">c4uqwA_</a>	 Alignment		100.0	15	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> protein clpv1; <b>PDBTitle:</b> coevolution of the atpase clpv, the tssb-tssc sheath and2 the accessory hsie protein distinguishes two type vi3 secretion classes
11	<a href="#">c3fesB_</a>	 Alignment		100.0	31	<b>PDB header:</b> atp binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent clp endopeptidase; <b>PDBTitle:</b> crystal structure of the atp-dependent clp protease clpc from2 clostridium difficile

12	<a href="#">d1khya_</a>	Alignment		100.0	27	<b>Fold:</b> Double Clp-N motif <b>Superfamily:</b> Double Clp-N motif <b>Family:</b> Double Clp-N motif
13	<a href="#">d1qvr1</a>	Alignment		100.0	27	<b>Fold:</b> Double Clp-N motif <b>Superfamily:</b> Double Clp-N motif <b>Family:</b> Double Clp-N motif
14	<a href="#">c4irfA_</a>	Alignment		100.0	19	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> malarial clpb2 atpase/hsp101 protein; <b>PDBTitle:</b> preliminary structural investigations of a malarial protein secretion2 system
15	<a href="#">c4hh5A_</a>	Alignment		100.0	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> putative type vi secretion protein; <b>PDBTitle:</b> n-terminal domain (1-163) of clpV1 atpase from e.coli eaec sci1 t6ss.
16	<a href="#">c6emwX_</a>	Alignment		99.9	29	<b>PDB header:</b> chaperone <b>Chain:</b> X: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> structure of s.aureus clpc in complex with meca
17	<a href="#">d1k6ka_</a>	Alignment		99.9	19	<b>Fold:</b> Double Clp-N motif <b>Superfamily:</b> Double Clp-N motif <b>Family:</b> Double Clp-N motif
18	<a href="#">c3pxqA_</a>	Alignment		99.9	32	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mecb; <b>PDBTitle:</b> structure of meca121 and clpc1-485 complex
19	<a href="#">c3pxiB_</a>	Alignment		99.9	33	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mecb; <b>PDBTitle:</b> structure of meca108:clpc
20	<a href="#">c1qvrB_</a>	Alignment		99.9	24	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
21	<a href="#">c6azyA_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein hsp104; <b>PDBTitle:</b> crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
22	<a href="#">c4d2qC_</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> clpb; <b>PDBTitle:</b> negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpp)
23	<a href="#">c5kneD_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> cryoem reconstruction of hsp104 hexamer
24	<a href="#">c5vy9C_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> heat shock protein 104; <b>PDBTitle:</b> s. cerevisiae hsp104:casein complex, middle domain conformation
25	<a href="#">c6em8F_</a>	Alignment	not modelled	99.7	32	<b>PDB header:</b> chaperone <b>Chain:</b> F: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> s.aureus clpc resting state, c2 symmetrised
26	<a href="#">c6em8E_</a>	Alignment	not modelled	99.6	33	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpc; <b>PDBTitle:</b> s.aureus clpc resting state, c2 symmetrised
27	<a href="#">c1r6bX_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
28	<a href="#">d1q9ca_</a>	Alignment	not modelled	86.0	18	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
						<b>Fold:</b> Histone-fold

29	<a href="#">d1id3c_</a>	Alignment	not modelled	83.3	32	<b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
30	<a href="#">d1kx5c_</a>	Alignment	not modelled	82.4	32	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
31	<a href="#">c2e7xA_</a>	Alignment	not modelled	81.7	19	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> 150aa long hypothetical transcriptional regulator; <b>PDBTitle:</b> structure of the lrp/asnc like transcriptional regulator from <i>Sulfolobus tokodaii</i> 7 complexed with its cognate ligand
32	<a href="#">d1eqza_</a>	Alignment	not modelled	80.7	29	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
33	<a href="#">c4pcqC_</a>	Alignment	not modelled	80.3	19	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> possible transcriptional regulatory protein (probably <b>PDBTitle:</b> crystal structure of mtbaldR (rv2779c)
34	<a href="#">c3i4pA_</a>	Alignment	not modelled	79.4	20	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, asnc family; <b>PDBTitle:</b> crystal structure of asnc family transcriptional regulator from <i>Agrobacterium tumefaciens</i>
35	<a href="#">c2f8nK_</a>	Alignment	not modelled	78.6	29	<b>PDB header:</b> structural protein/dna <b>Chain:</b> K: <b>PDB Molecule:</b> histone h2a type 1; <b>PDBTitle:</b> 2.9 angstrom x-ray structure of hybrid macroH2a nucleosomes
36	<a href="#">d1s7oa_</a>	Alignment	not modelled	78.5	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
37	<a href="#">c1i1gA_</a>	Alignment	not modelled	78.2	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator lrpA; <b>PDBTitle:</b> crystal structure of the lrp-like transcriptional regulator from the archaeon <i>Pyrococcus furiosus</i>
38	<a href="#">c2ia0A_</a>	Alignment	not modelled	78.1	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator pf0864; <b>PDBTitle:</b> transcriptional regulatory protein pf0864 from <i>Pyrococcus furiosus</i> a2 member of the asnc family (pf0864)
39	<a href="#">c2cfxD_</a>	Alignment	not modelled	78.1	15	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> hth-type transcriptional regulator lrpC; <b>PDBTitle:</b> structure of b.subtilis lrpC
40	<a href="#">c1u78A_</a>	Alignment	not modelled	76.9	7	<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
41	<a href="#">c2vbzA_</a>	Alignment	not modelled	76.7	27	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulatory protein; <b>PDBTitle:</b> feast or famine regulatory protein (rv3291c) from <i>M. tuberculosis</i> complexed with l-tryptophan
42	<a href="#">c2dbbA_</a>	Alignment	not modelled	76.7	16	<b>PDB header:</b> transcriptional regulator <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph0061; <b>PDBTitle:</b> crystal structure of ph0061
43	<a href="#">d1u35c1</a>	Alignment	not modelled	76.2	26	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
44	<a href="#">d1vkea_</a>	Alignment	not modelled	76.0	14	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> CMD-like
45	<a href="#">c2e1cA_</a>	Alignment	not modelled	76.0	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> putative hth-type transcriptional regulator ph1519; <b>PDBTitle:</b> structure of putative hth-type transcriptional regulator ph1519/dna2 complex
46	<a href="#">d1a0ic_</a>	Alignment	not modelled	75.8	29	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
47	<a href="#">d1kx3c_</a>	Alignment	not modelled	75.7	29	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
48	<a href="#">c2cg4B_</a>	Alignment	not modelled	75.2	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> regulatory protein asnc; <b>PDBTitle:</b> structure of e.coli asnc
49	<a href="#">c2p6tH_</a>	Alignment	not modelled	75.1	8	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> transcriptional regulator, lrp/asnc family; <b>PDBTitle:</b> crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from <i>Neisseria meningitidis</i>
50	<a href="#">d1tzya_</a>	Alignment	not modelled	73.1	29	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
51	<a href="#">c2qeuA_</a>	Alignment	not modelled	72.4	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative carboxymuconolactone decarboxylase; <b>PDBTitle:</b> crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from <i>Burkholderia xenovorans</i> lb400 at 1.65 Å resolution
52	<a href="#">c2gqqB_</a>	Alignment	not modelled	70.7	17	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> leucine-responsive regulatory protein; <b>PDBTitle:</b> crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
53	<a href="#">d2cwqa1</a>	Alignment	not modelled	70.4	19	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> TTHA0727-like
						<b>PDB header:</b> chaperone/nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> chimera of histone h2b.1 and histone

54	<a href="#">c2jssA_</a>	Alignment	not modelled	68.3	32	<b>h2a.z;</b> <b>PDBTitle:</b> nmr structure of chaperone chz1 complexed with histone2 h2a.z-h2b
55	<a href="#">d2jssa1</a>	Alignment	not modelled	68.1	32	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
56	<a href="#">c2l4aA_</a>	Alignment	not modelled	66.8	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> leucine responsive regulatory protein; <b>PDBTitle:</b> nmr structure of the dna-binding domain of e.coli lrp
57	<a href="#">d2cg4a1</a>	Alignment	not modelled	66.6	17	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
58	<a href="#">c1p8cD_</a>	Alignment	not modelled	66.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of tm1620 (apc4843) from thermotoga2 maritima
59	<a href="#">d1rp3a2</a>	Alignment	not modelled	65.8	5	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
60	<a href="#">c4czdA_</a>	Alignment	not modelled	64.8	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
61	<a href="#">d1f66c_</a>	Alignment	not modelled	63.8	32	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
62	<a href="#">c1f66C_</a>	Alignment	not modelled	63.8	32	<b>PDB header:</b> structural protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> histone h2a.z; <b>PDBTitle:</b> 2.6 a crystal structure of a nucleosome core particle2 containing the variant histone h2a.z
63	<a href="#">d2huec1</a>	Alignment	not modelled	63.2	18	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
64	<a href="#">d1xsva_</a>	Alignment	not modelled	63.0	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> YlxM/p13-like
65	<a href="#">c4czdD_</a>	Alignment	not modelled	62.1	10	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> putative transcriptional regulator, asnc family; <b>PDBTitle:</b> sirohaem decarboxylase ahba/b - an enzyme with structural homology2 to the lrp/asnc transcription factor family that is part of the3 alternative haem biosynthesis pathway.
66	<a href="#">d1hiod_</a>	Alignment	not modelled	60.9	17	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
67	<a href="#">c3t72o_</a>	Alignment	not modelled	59.3	20	<b>PDB header:</b> transcription/dna <b>Chain:</b> O: <b>PDB Molecule:</b> pho box dna (strand 1); <b>PDBTitle:</b> phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
68	<a href="#">d1ku3a_</a>	Alignment	not modelled	58.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
69	<a href="#">d2p7vb1</a>	Alignment	not modelled	57.6	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
70	<a href="#">c1or7A_</a>	Alignment	not modelled	55.4	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma-e factor; <b>PDBTitle:</b> crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
71	<a href="#">c6c05F_</a>	Alignment	not modelled	54.8	25	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> rna polymerase sigma factor siga; <b>PDBTitle:</b> mycobacterium tuberculosis rnap holo/rbpa in relaxed state
72	<a href="#">d1ku7a_</a>	Alignment	not modelled	54.8	19	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
73	<a href="#">d1ttya_</a>	Alignment	not modelled	53.7	14	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
74	<a href="#">c6in7B_</a>	Alignment	not modelled	53.7	29	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> rna polymerase sigma-h factor; <b>PDBTitle:</b> crystal structure of alga in complex with muca(cyto)
75	<a href="#">c3vepA_</a>	Alignment	not modelled	52.2	24	<b>PDB header:</b> membrane protein/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> probable rna polymerase sigma-d factor; <b>PDBTitle:</b> crystal structure of sigd4 in complex with its negative regulator rsda
76	<a href="#">c5zx3F_</a>	Alignment	not modelled	51.8	19	<b>PDB header:</b> transcription <b>Chain:</b> F: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigh; <b>PDBTitle:</b> mycobacterium tuberculosis rna polymerase holoenzyme with ecf sigma2 factor sigma h
77	<a href="#">d2gena1</a>	Alignment	not modelled	51.3	10	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
78	<a href="#">c1vz0B_</a>	Alignment	not modelled	51.1	13	<b>PDB header:</b> nuclear protein <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome-partitioning protein spo0j; <b>PDBTitle:</b> chromosome segregation protein spo0j from thermus thermophilus
79	<a href="#">d1id3b_</a>	Alignment	not modelled	51.0	6	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold

						<b>Family:</b> Nucleosome core histones
80	<a href="#">d2cfxa1</a>	Alignment	not modelled	50.1	15	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
81	<a href="#">c3rkxA</a>	Alignment	not modelled	49.0	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> biotin-[acetyl-coa-carboxylase] ligase; <b>PDBTitle:</b> structural characterisation of staphylococcus aureus biotin protein2 ligase
82	<a href="#">d1iiga1</a>	Alignment	not modelled	47.9	27	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
83	<a href="#">c5g49A</a>	Alignment	not modelled	47.5	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear transcription factor y subunit b-6; <b>PDBTitle:</b> crystal structure of the arabidopsis thaliana histone-fold dimer I1I2 nf-yc3
84	<a href="#">c2qvWA</a>	Alignment	not modelled	44.8	60	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glp_546_48378_50642; <b>PDBTitle:</b> structure of giardia dicer refined against twinned data
85	<a href="#">d1or7a1</a>	Alignment	not modelled	44.7	24	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
86	<a href="#">c4wzsB</a>	Alignment	not modelled	44.5	16	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> tata-binding protein-associated phosphoprotein; <b>PDBTitle:</b> crystal structure of the mot1 n-terminal domain in complex with tbp2 and nc2 bound to a promoter dna fragment
87	<a href="#">d1hioa</a>	Alignment	not modelled	44.2	29	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
88	<a href="#">c1l9uH</a>	Alignment	not modelled	42.4	20	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> sigma factor siga; <b>PDBTitle:</b> thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
89	<a href="#">c3hugA</a>	Alignment	not modelled	42.3	24	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigI
90	<a href="#">c5ij5O</a>	Alignment	not modelled	42.2	28	<b>PDB header:</b> splicing <b>Chain:</b> O: <b>PDB Molecule:</b> pre-mrna-splicing factor cef1; <b>PDBTitle:</b> overall structure of the yeast spliceosome immediately after2 branching.
91	<a href="#">c6a7uA</a>	Alignment	not modelled	41.8	17	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> histone h2b type 2-e,histone h2a-bbd type 2/3; <b>PDBTitle:</b> crystal structure of histone h2a.bbd-h2b dimer
92	<a href="#">c2llkA</a>	Alignment	not modelled	41.8	16	<b>PDB header:</b> cell cycle, transcription <b>Chain:</b> A: <b>PDB Molecule:</b> cyclin-d-binding myb-like transcription factor 1; <b>PDBTitle:</b> solution nmr structure of the n-terminal myb-like 1 domain of the2 human cyclin-d-binding transcription factor 1 (hdmp1), northeast3 structural genomics consortium (nesg) target id hr8011a
93	<a href="#">d1n1jb</a>	Alignment	not modelled	41.6	3	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
94	<a href="#">c2w7nA</a>	Alignment	not modelled	41.4	25	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> trfb transcriptional repressor protein; <b>PDBTitle:</b> crystal structure of kora bound to operator dna: insight into2 repressor cooperation in rp4 gene regulation
95	<a href="#">d1v7ba1</a>	Alignment	not modelled	39.9	11	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
96	<a href="#">d2cyya1</a>	Alignment	not modelled	38.9	20	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Lrp/AsnC-like transcriptional regulator N-terminal domain
97	<a href="#">c5z7iC</a>	Alignment	not modelled	38.7	47	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> cell cycle regulatory protein gcra; <b>PDBTitle:</b> caulobacter crescentum gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna
98	<a href="#">d1kx5b</a>	Alignment	not modelled	38.5	17	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
99	<a href="#">d2vkea1</a>	Alignment	not modelled	38.5	9	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Tetracyclin repressor-like, N-terminal domain
100	<a href="#">c5djpB</a>	Alignment	not modelled	36.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkyl hydroperoxide reductase ahpd; <b>PDBTitle:</b> crystal structure of lpg0406 in reduced form from legionella2 pneumophila
101	<a href="#">c1zx4B</a>	Alignment	not modelled	36.1	21	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> plasmid partition par b protein; <b>PDBTitle:</b> structure of parb bound to dna
102	<a href="#">c2jvA</a>	Alignment	not modelled	35.9	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> trmbf1; <b>PDBTitle:</b> nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
103	<a href="#">c5xe7A</a>	Alignment	not modelled	35.8	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigj; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis extracytoplasmic2 function sigma factor sigj
104	<a href="#">c3vwbA</a>	Alignment	not modelled	35.6	24	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> virulence regulon transcriptional activator virb; <b>PDBTitle:</b> crystal structure of virb core domain (se-met derivative)

						complexed2 with the cis-acting site (5-bru modifications) upstream icsb promoter
105	<a href="#">c2yusA_</a>	Alignment	not modelled	34.6	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> swi/snf-related matrix-associated actin- <b>PDBTitle:</b> solution structure of the sant domain of human swi/snf-2 related matrix-associated actin-dependent regulator of3 chromatin subfamily c member 1
106	<a href="#">d1gv2a2</a>	Alignment	not modelled	34.5	32	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Homeodomain-like <b>Family:</b> Myb/SANT domain
107	<a href="#">c2ewnA_</a>	Alignment	not modelled	34.4	20	<b>PDB header:</b> ligase, transcription <b>Chain:</b> A: <b>PDB Molecule:</b> bira bifunctional protein; <b>PDBTitle:</b> ecoli biotin repressor with co-repressor analog
108	<a href="#">c2kfsA_</a>	Alignment	not modelled	34.3	11	<b>PDB header:</b> dna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical regulatory protein; <b>PDBTitle:</b> nmr structure of rv2175c
109	<a href="#">d1smyf2</a>	Alignment	not modelled	33.6	21	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> Sigma3 and sigma4 domains of RNA polymerase sigma factors <b>Family:</b> Sigma4 domain
110	<a href="#">c5eybB_</a>	Alignment	not modelled	33.2	22	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna-binding protein reb1; <b>PDBTitle:</b> x-ray structure of reb1-ter complex
111	<a href="#">c5y26B_</a>	Alignment	not modelled	32.9	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative transcription factor c16c4.22; <b>PDBTitle:</b> crystal structure of native dpb4-dpb3
112	<a href="#">d1vi0a1</a>	Alignment	not modelled	31.2	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="#">c4ch7A_</a>	Alignment	not modelled	31.1	16	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nird-like protein; <b>PDBTitle:</b> crystal structure of the siroheme decarboxylase nirdl
114	<a href="#">c2lf3A_</a>	Alignment	not modelled	30.6	29	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> effector protein hopab3; <b>PDBTitle:</b> solution nmr structure of hoppmal_281_385 from pseudomonas syringae2 pv. maculicola str. es4326, midwest center for structural genomics3 target apc40104.5 and northeast structural genomics consortium target4 pst2a
115	<a href="#">d1vkeb_</a>	Alignment	not modelled	30.1	17	<b>Fold:</b> AhpD-like <b>Superfamily:</b> AhpD-like <b>Family:</b> CMD-like
116	<a href="#">c5uxxC_</a>	Alignment	not modelled	30.1	23	<b>PDB header:</b> dna binding protein/unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> rna polymerase sigma factor; <b>PDBTitle:</b> co-crystal structure of the sigma factor rpoE in complex with the2 anti-sigma factor nepr from bartonella quintana
117	<a href="#">c2lf6A_</a>	Alignment	not modelled	27.9	26	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> effector protein hopab1; <b>PDBTitle:</b> solution nmr structure of hopabpph1448_220_320 from pseudomonas2 syringae pv. phaseolicola str. 1448a, midwest center for structural3 genomics target apc40132.4 and northeast structural genomics4 consortium target pst3a
118	<a href="#">c5y26A_</a>	Alignment	not modelled	26.4	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase epsilon subunit d; <b>PDBTitle:</b> crystal structure of native dpb4-dpb3
119	<a href="#">c5wurB_</a>	Alignment	not modelled	26.3	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> ecf rna polymerase sigma factor sigw; <b>PDBTitle:</b> crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
120	<a href="#">c6mzIM_</a>	Alignment	not modelled	25.6	24	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 9, taf9; <b>PDBTitle:</b> human tfiid canonical state