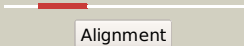

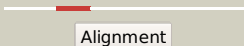

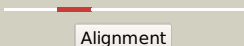

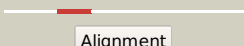

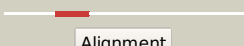

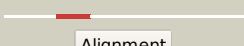

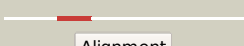















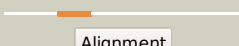

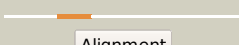

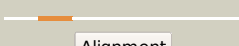

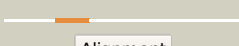





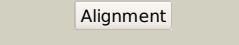
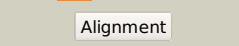

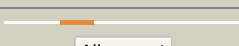

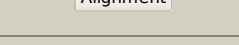


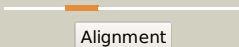


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3798 (-)_4253171_4254505
Date	Fri Aug 9 18:20:50 BST 2019
Unique Job ID	6903aad8c3865fb

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gn5B_	 Alignment		95.9	9	PDB header: dna binding protein Chain: B; PDB Molecule: hth-type transcriptional regulator mqsa (ygit/b3021); PDBTitle: structure of the e. coli protein mqsa (ygit/b3021)
2	d2jn6a1	 Alignment		93.1	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cgl2762-like
3	d1k78a1	 Alignment		92.9	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
4	d6paxa1	 Alignment		92.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
5	c2rn7A_	 Alignment		91.9	4	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
6	d1pdnc_	 Alignment		91.7	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
7	c1zljE_	 Alignment		91.6	18	PDB header: transcription Chain: E; PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain
8	c2krfB_	 Alignment		91.0	4	PDB header: transcription Chain: B; PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
9	c6paxA_	 Alignment		91.0	13	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
10	c2qkdA_	 Alignment		90.5	18	PDB header: signaling protein, cell cycle Chain: A; PDB Molecule: zinc finger protein zpr1; PDBTitle: crystal structure of tandem zpr1 domains
11	d1p4wa_	 Alignment		90.4	6	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)

12	c3sztB	 Alignment		90.2	15	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
13	c4lfuA	 Alignment		90.0	9	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
14	d1a04a1	 Alignment		89.7	16	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)
15	c6jqsA	 Alignment		89.6	12	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
16	d1l3la1	 Alignment		89.5	13	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)
17	d2fiya1	 Alignment		89.5	17	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
18	c2q0oA	 Alignment		88.7	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
19	c1h0mD	 Alignment		88.2	15	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
20	d1yioa1	 Alignment		87.6	13	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	d1fsea	 Alignment	not modelled	87.5	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)
22	c2rnjA	 Alignment	not modelled	87.0	16	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
23	c1u78A	 Alignment	not modelled	86.4	2	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
24	c3qp5C	 Alignment	not modelled	85.7	20	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
25	c6cnbR	 Alignment	not modelled	85.4	19	PDB header: transcription/dna Chain: R: PDB Molecule: transcription factor iibb 70 kda subunit,tata-box-binding PDBTitle: yeast rna polymerase iii initial transcribing complex
26	c1x3uA	 Alignment	not modelled	85.4	15	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
27	c5u1cA	 Alignment	not modelled	85.0	12	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 integrase, sso7d chimera; PDBTitle: structure of tetrameric hiv-1 strand transfer complex intasome
28	d2hsga1	 Alignment	not modelled	84.5	18	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
		 Alignment				PDB header: viral protein

29	c3jcaE	Alignment	not modelled	84.3	13	Chain: E: PDB Molecule: integrase; PDBTitle: core model of the mouse mammary tumor virus intasome
30	c2elhA	Alignment	not modelled	83.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: cg11849-pa; PDBTitle: solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
31	d1luxca	Alignment	not modelled	83.6	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
32	d1x3za1	Alignment	not modelled	83.1	19	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
33	d1luxda	Alignment	not modelled	82.7	9	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
34	d2bjca1	Alignment	not modelled	82.7	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
35	c3eswA	Alignment	not modelled	82.6	17	PDB header: hydrolase Chain: A: PDB Molecule: peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine PDBTitle: complex of yeast pngase with glcnac2-iac.
36	d1bw6a	Alignment	not modelled	82.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
37	d1lcda	Alignment	not modelled	82.5	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
38	c5m0rF	Alignment	not modelled	82.2	11	PDB header: hydrolase Chain: F: PDB Molecule: integrase; PDBTitle: cryo-em reconstruction of the maedi-visna virus (mvv) strand transfer2 complex
39	d1qpza1	Alignment	not modelled	82.2	14	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
40	c3c3wB	Alignment	not modelled	81.9	20	PDB header: transcription Chain: B: PDB Molecule: two component transcriptional regulatory protein devr; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic response2 regulator dosr
41	c2m8eA	Alignment	not modelled	81.3	13	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase
42	d2cg4a1	Alignment	not modelled	81.2	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
43	c1efaA	Alignment	not modelled	81.1	22	PDB header: transcription/dna Chain: A: PDB Molecule: lac repressor; PDBTitle: crystal structure of the lac repressor dimer bound to operator and the2 anti-inducer onpf
44	c5o8yG	Alignment	not modelled	81.0	6	PDB header: transcription Chain: G: PDB Molecule: transcriptional regulatory protein rcsb; PDBTitle: conformational dynamism for dna interaction in salmonella typhimurium2 rcsb response regulator.
45	c5yszA	Alignment	not modelled	80.6	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: transcriptional regulator celr-cellobiose complex
46	d1efaa1	Alignment	not modelled	80.5	22	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: GalR/LacI-like bacterial regulator
47	c1bdhA	Alignment	not modelled	80.2	14	PDB header: transcription/dna Chain: A: PDB Molecule: protein (purine repressor); PDBTitle: purine repressor mutant-hypoxanthine-palindromic operator2 complex
48	c2jpcA	Alignment	not modelled	80.0	9	PDB header: dna binding protein Chain: A: PDB Molecule: :ssrb; PDBTitle: ssrb dna binding protein
49	c1k6yB	Alignment	not modelled	79.8	13	PDB header: transferase Chain: B: PDB Molecule: integrase; PDBTitle: crystal structure of a two-domain fragment of hiv-1 integrase
50	d2cfxa1	Alignment	not modelled	79.5	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
51	d1l1ga1	Alignment	not modelled	79.4	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
52	c6ideA	Alignment	not modelled	79.1	13	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
53	c5ejkG	Alignment	not modelled	78.8	10	PDB header: transferase/dna Chain: G: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: crystal structure of the rous sarcoma virus intasome
54	c1zvva	Alignment	not modelled	78.0	17	PDB header: transcription/dna Chain: A: PDB Molecule: glucose-resistance amylase regulator; PDBTitle: crystal structure of a ccpa-crh-dna complex
55	c1rn1A	Alignment	not modelled	78.0	15	PDB header: signal transduction protein Chain: A: PDB Molecule: nitrate/nitrite response regulator protein narI; PDBTitle: the nitrate/nitrite response regulator protein narI from

						narI
56	c3kxD	Alignment	not modelled	77.8	17	PDB header: transcription regulator Chain: D: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from silicibacter pomeroyi
57	c4if4A	Alignment	not modelled	77.7	16	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vrar; PDBTitle: crystal structure of the magnesium and beryll fluoride-activated vrar2 from staphylococcus aureus
58	c2lcvA	Alignment	not modelled	77.6	15	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional repressor cytr; PDBTitle: structure of the cytidine repressor dna-binding domain; an alternate2 calculation
59	c1lbgB	Alignment	not modelled	77.4	21	PDB header: PDB COMPND:
60	c3h5tA	Alignment	not modelled	77.2	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family; PDBTitle: crystal structure of a transcriptional regulator, lacI2 family protein from corynebacterium glutamicum
61	d2p7vb1	Alignment	not modelled	77.2	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
62	c4yn8A	Alignment	not modelled	77.1	10	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
63	d1xsva	Alignment	not modelled	77.0	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
64	c2l8nA	Alignment	not modelled	76.5	15	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional repressor cytr; PDBTitle: nmr structure of the cytidine repressor dna binding domain in presence2 of operator half-site dna
65	c2k27A	Alignment	not modelled	75.4	12	PDB header: transcription regulator Chain: A: PDB Molecule: paired box protein pax-8; PDBTitle: solution structure of human pax8 paired box domain
66	d1hlva1	Alignment	not modelled	75.3	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
67	c5hevC	Alignment	not modelled	75.3	18	PDB header: transcription Chain: C: PDB Molecule: response regulator protein vrar; PDBTitle: crystal structure of the beryll fluoride-activated liar from2 enterococcus faecium
68	c3knC	Alignment	not modelled	73.9	14	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxR family; PDBTitle: vibrio cholerae vpst
69	c5f64C	Alignment	not modelled	73.8	16	PDB header: transcription regulator Chain: C: PDB Molecule: positive transcription regulator evga; PDBTitle: putative positive transcription regulator (sensor evgs) from shigella2 flexneri
70	c5fgmA	Alignment	not modelled	73.6	8	PDB header: hydrolase Chain: A: PDB Molecule: ecf rna polymerase sigma factor sigr; PDBTitle: streptomyces coelicolor sigr region 4
71	c2w48D	Alignment	not modelled	73.3	7	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
72	d1or7a1	Alignment	not modelled	73.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
73	d2oz6a1	Alignment	not modelled	72.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
74	c6gh5M	Alignment	not modelled	72.4	4	PDB header: transcription Chain: M: PDB Molecule: rna polymerase sigma-54 factor,rna polymerase sigma-54 PDBTitle: cryo-em structure of bacterial rna polymerase-sigma54 holoenzyme2 transcription open complex
75	d1b9ma1	Alignment	not modelled	72.3	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: N-terminal domain of molybdate-dependent transcriptional regulator ModE
76	c2vxzA	Alignment	not modelled	72.3	14	PDB header: viral protein Chain: A: PDB Molecule: pyrsv_gp04; PDBTitle: crystal structure of hypothetical protein pyrsv_gp04 from pyrobaculum2 spherical virus
77	c1ee8A	Alignment	not modelled	72.3	26	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermus thermophilus hb8
78	c2gm4B	Alignment	not modelled	72.2	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
79	c3ndjA	Alignment	not modelled	72.1	14	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
80	c2cg4B	Alignment	not modelled	72.1	9	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
81	c4go1A	Alignment	not modelled	72.1	9	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsrr; PDBTitle: crystal structure of full length transcription repressor lsrr

						from e.2 coli.
82	c5xonU	Alignment	not modelled	72.0	26	PDB header: transcription/rna Chain: U: PDB Molecule: general transcription elongation factor tfiis; PDBTitle: rna polymerase ii elongation complex bound with spt4/5 and tfiis
83	c3t0yA	Alignment	not modelled	71.9	7	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
84	c3cngC	Alignment	not modelled	71.7	29	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
85	c2r0qF	Alignment	not modelled	71.4	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
86	d1rp3a2	Alignment	not modelled	71.4	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
87	c3iwfA	Alignment	not modelled	71.1	5	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
88	c3fzvC	Alignment	not modelled	71.0	12	PDB header: transcription regulator Chain: C: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of pa01 protein, putative lysr family2 transcriptional regulator from pseudomonas aeruginosa
89	c3mzyA	Alignment	not modelled	70.8	9	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
90	c3m1eA	Alignment	not modelled	70.7	8	PDB header: transcription regulator Chain: A: PDB Molecule: hth-type transcriptional regulator benm; PDBTitle: crystal structure of benm_dbd
91	c4rvqA	Alignment	not modelled	70.5	10	PDB header: transferase Chain: A: PDB Molecule: d-mycarose 3-c-methyltransferase; PDBTitle: crystal structure of mtmc in complex with sam and tdp
92	c6c03A	Alignment	not modelled	69.8	8	PDB header: transcription Chain: A: PDB Molecule: putative rna polymerase ecf-subfamily sigma factor; PDBTitle: the crystal structure streptomyces venezuelae rsbn-bldn complex
93	c2o8xA	Alignment	not modelled	69.8	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
94	c5fo5A	Alignment	not modelled	69.6	10	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional regulator metr; PDBTitle: structure of the dna-binding domain of escherichia coli methionine2 biosynthesis regulator metr
95	c5ijlA	Alignment	not modelled	69.5	19	PDB header: transferase Chain: A: PDB Molecule: dna polymerase ii large subunit; PDBTitle: d-family dna polymerase - dp2 subunit (catalytic subunit)
96	c3hpgC	Alignment	not modelled	68.7	12	PDB header: transferase Chain: C: PDB Molecule: integrase; PDBTitle: visna virus integrase (residues 1-219) in complex with ledgf2 ibd: examples of open integrase dimer-dimer interfaces
97	c2x5cB	Alignment	not modelled	68.6	34	PDB header: viral protein Chain: B: PDB Molecule: hypothetical protein orf131; PDBTitle: crystal structure of hypothetical protein orf131 from pyrobaculum2 spherical virus
98	c3hefB	Alignment	not modelled	68.3	20	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
99	c1k82D	Alignment	not modelled	67.8	16	PDB header: hydrolase/dna Chain: D: PDB Molecule: formamidopyrimidine-dna glycosylase; PDBTitle: crystal structure of e.coli formamidopyrimidine-dna2 glycosylase (fpg) covalently trapped with dna
100	c1hlvA	Alignment	not modelled	67.5	12	PDB header: dna binding protein/dna Chain: A: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of cenp-b(1-129) complexed with the cenp-2 b box dna
101	c4hyeB	Alignment	not modelled	67.5	10	PDB header: transcription activator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator spr1814 from streptococcus2 pneumoniae reveals unique interdomain contacts among narl family3 proteins
102	c5fz5M	Alignment	not modelled	67.1	14	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor iib; PDBTitle: transcription initiation complex structures elucidate dna opening (cc)
103	d1s7oa	Alignment	not modelled	67.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: YlxM/p13-like
104	c3vepA	Alignment	not modelled	67.0	10	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
105	c3hugA	Alignment	not modelled	66.9	13	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
106	d1ku2a	Alignment	not modelled	66.8	4	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase

106	u1ku3a_	Alignment	not modelled	66.8	4	sigma factors PDB header: signaling protein Family: Sigma4 domain
107	c2lfwA_	Alignment	not modelled	66.6	15	Chain: A: PDB Molecule: phyr sigma-like domain; PDBTitle: nmr structure of the phyrsl-nepr complex from sphingomonas sp. fr1
108	d1c0ma2	Alignment	not modelled	66.5	15	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
109	d2f4ma1	Alignment	not modelled	66.4	28	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
110	d1hyva_	Alignment	not modelled	66.2	14	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
111	c3nf9A_	Alignment	not modelled	65.7	14	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
112	c1zn2A_	Alignment	not modelled	65.6	13	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
113	c4j2nA_	Alignment	not modelled	65.4	17	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
114	c3twkB_	Alignment	not modelled	65.3	16	PDB header: hydrolase Chain: B: PDB Molecule: formamidopyrimidine-dna glycosylase 1; PDBTitle: crystal structure of arabidopsis thaliana fpg
115	c2gb5B_	Alignment	not modelled	65.1	35	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
116	c5y9sD_	Alignment	not modelled	64.7	4	PDB header: transcription Chain: D: PDB Molecule: vv2_1132; PDBTitle: crystal structure of vv2_1132, a lysr family transcriptional regulator
117	d1ft9a1	Alignment	not modelled	64.5	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
118	c4j2nB_	Alignment	not modelled	64.5	17	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
119	c5y2vA_	Alignment	not modelled	64.4	16	PDB header: transcription Chain: A: PDB Molecule: rubisco operon transcriptional regulator; PDBTitle: strcutrue of the full-length ccmr complexed with 2-og from2 synechocystis pcc6803
120	c4esjA_	Alignment	not modelled	64.1	19	PDB header: hydrolase/dna Chain: A: PDB Molecule: type-2 restriction enzyme dpni; PDBTitle: restriction endonuclease dpni in complex with target dna