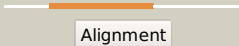

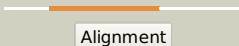

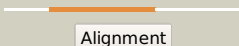

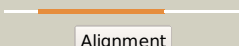

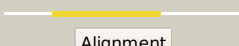

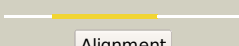

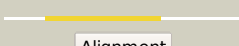

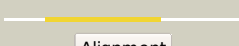

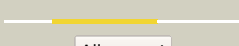

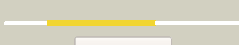






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0430 (-) _518736_519044
Date	Tue Jul 23 14:50:50 BST 2019
Unique Job ID	afcd674ca09e725a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3jsoA_	 Alignment		89.1	22	PDB header: hydrolase/dna Chain: A: PDB Molecule: lexa repressor; PDBTitle: classic protein with a new twist: crystal structure of a lexa2 repressor dna complex
2	d1jhfa1	 Alignment		89.0	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
3	c3k2zA_	 Alignment		85.6	24	PDB header: hydrolase Chain: A: PDB Molecule: lexa repressor; PDBTitle: crystal structure of a lexa protein from thermotoga maritima
4	c2l4aA_	 Alignment		83.7	13	PDB header: dna binding protein Chain: A: PDB Molecule: leucine responsive regulatory protein; PDBTitle: nmr structure of the dna-binding domain of e.coli lrp
5	d2cfxa1	 Alignment		77.3	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
6	d2cg4a1	 Alignment		74.7	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
7	c1dpuA_	 Alignment		73.3	22	PDB header: dna binding protein Chain: A: PDB Molecule: replication protein a (rpa32) c-terminal domain; PDBTitle: solution structure of the c-terminal domain of human rpa322 complexed with ung2(73-88)
8	d1dpuA_	 Alignment		73.3	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal domain of RPA32
9	d1l1ga1	 Alignment		73.2	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
10	d1ku7a_	 Alignment		72.7	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
11	c1z1jE_	 Alignment		71.3	17	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis hypoxic2 response regulator dosr c-terminal domain

12	d1a04a1	Alignment		65.1	23	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)
13	c3sztB	Alignment		63.6	17	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
14	c2q0aA	Alignment		62.1	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
15	c4czdA	Alignment		60.8	6	PDB header: lyase Chain: A: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: 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.
16	c4lfuA	Alignment		56.3	14	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
17	d1ku3a	Alignment		56.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
18	c4czdD	Alignment		55.4	13	PDB header: lyase Chain: D: PDB Molecule: putative transcriptional regulator, asnc family; PDBTitle: 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.
19	d1l3la1	Alignment		55.1	19	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)
20	c6jqsA	Alignment		54.0	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
21	c2krfB	Alignment	not modelled	53.8	26	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
22	d2cvya1	Alignment	not modelled	52.7	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
23	c1i1gA	Alignment	not modelled	52.6	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpa; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
24	c2cg4B	Alignment	not modelled	52.4	9	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc
25	c1h0mD	Alignment	not modelled	51.7	25	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
26	c4pcqC	Alignment	not modelled	50.7	16	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
27	c2dbbA	Alignment	not modelled	49.0	9	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
28	c2ia0A	Alignment	not modelled	48.5	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative hth-type transcriptional regulator pf0864; PDBTitle: transcriptional regulatory protein pf0864 from pyrococcus furiosus a2 member of the asnc family (pf0864)

29	c2vbzA_	Alignment	not modelled	47.4	11	PDB header: dna-binding protein Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: feast or famine regulatory protein (rv3291c)from m.2 tuberculosis complexed with l-tryptophan
30	d2p7vb1	Alignment	not modelled	44.8	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
31	d2oyoa1	Alignment	not modelled	42.7	15	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
32	c6c05F_	Alignment	not modelled	40.4	15	PDB header: transcription Chain: F: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: mycobacterium tuberculosis rnap holo/rbpa in relaxed state
33	c3qp5C_	Alignment	not modelled	39.4	22	PDB header: transcription Chain: C: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir bound to antagonist chlorolactone (cl)
34	c2cfxD_	Alignment	not modelled	39.0	9	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
35	c2e7xA_	Alignment	not modelled	38.3	11	PDB header: transcription regulator Chain: A: PDB Molecule: 150aa long hypothetical transcriptional regulator; PDBTitle: structure of the lrp/asnc like transcriptional regulator from2 sulfobolus tokodaii 7 complexed with its cognate ligand
36	d3proc1	Alignment	not modelled	38.2	22	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
37	c2e1cA_	Alignment	not modelled	38.1	11	PDB header: transcription/dna Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph1519; PDBTitle: structure of putative hth-type transcriptional regulator ph1519/dna2 complex
38	d1fsea_	Alignment	not modelled	36.4	17	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)
39	c2p6tH_	Alignment	not modelled	35.1	19	PDB header: transcription Chain: H: PDB Molecule: transcriptional regulator, lrp/asnc family; PDBTitle: crystal structure of transcriptional regulator nmb0573 and l-leucine2 complex from neisseria meningitidis
40	d1ttya_	Alignment	not modelled	34.2	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
41	c2rniA_	Alignment	not modelled	32.4	21	PDB header: transcription Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
42	c1rp3G_	Alignment	not modelled	32.1	15	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
43	c2vn2B_	Alignment	not modelled	31.2	17	PDB header: replication Chain: B: PDB Molecule: chromosome replication initiation protein; PDBTitle: crystal structure of the n-terminal domain of dnad protein2 from geobacillus kaustophilus hta426
44	d2fm8c1	Alignment	not modelled	29.6	44	Fold: SipA N-terminal domain-like Superfamily: SipA N-terminal domain-like Family: SipA N-terminal domain-like
45	c1l9uH_	Alignment	not modelled	29.2	19	PDB header: transcription Chain: H: PDB Molecule: sigma factor siga; PDBTitle: thermus aquaticus rna polymerase holoenzyme at 4 a2 resolution
46	c3t72o_	Alignment	not modelled	28.1	20	PDB header: transcription/dna Chain: O: PDB Molecule: pho box dna (strand 1); PDBTitle: phob(e)-sigma70(4)-(rnap-beta-flap-tip-helix)-dna transcription2 activation sub-complex
47	d2v9va2	Alignment	not modelled	27.7	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: C-terminal fragment of elongation factor SelB
48	d2fm9a1	Alignment	not modelled	27.5	44	Fold: SipA N-terminal domain-like Superfamily: SipA N-terminal domain-like Family: SipA N-terminal domain-like
49	d1bl0a2	Alignment	not modelled	27.4	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
50	d1smyf2	Alignment	not modelled	26.9	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
51	c2dg6A_	Alignment	not modelled	25.6	24	PDB header: gene regulation Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of the putative transcriptional regulator sco55502 from streptomyces coelicolor a3(2)
52	d1p4wa_	Alignment	not modelled	24.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: GerE-like (LuxR/UhpA family of transcriptional regulators)
53	c3wodF_	Alignment	not modelled	23.5	23	PDB header: transferase/transcription Chain: F: PDB Molecule: rna polymerase sigma factor; PDBTitle: rna polymerase-gp39 complex
54	c5ipmF_	Alignment	not modelled	23.0	13	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
55	d2pfxa1	Alignment	not modelled	22.4	17	Fold: AhpD-like Superfamily: AhpD-like Family: Atu0492-like
56	c2v79B	Alignment	not modelled	22.3	17	PDB header: dna binding protein Chain: B: PDB Molecule: dna replication protein dnad; PDBTitle: crystal structure of the n-terminal domain of dnad from bacillus2 subtilis
57	d1u5ta2	Alignment	not modelled	22.3	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
58	c5tw1F	Alignment	not modelled	22.0	13	PDB header: transcription activator/transferase/dna Chain: F: PDB Molecule: rna polymerase sigma factor siga; PDBTitle: crystal structure of a mycobacterium smegmatis transcription2 initiation complex with rbpA
59	c2v9vA	Alignment	not modelled	21.4	17	PDB header: transcription Chain: A: PDB Molecule: selenocysteine-specific elongation factor; PDBTitle: crystal structure of moorella thermoacetica selb(377-511)
60	c2zmeA	Alignment	not modelled	21.2	25	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
61	d1gjsa	Alignment	not modelled	20.9	32	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Bacterial immunoglobulin/albumin-binding domains Family: GA module, an albumin-binding domain
62	d1yioa1	Alignment	not modelled	20.7	17	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)
63	c3cuqA	Alignment	not modelled	20.5	26	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
64	c1x3uA	Alignment	not modelled	20.0	20	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
65	d2d1ha1	Alignment	not modelled	20.0	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: TrmB-like
66	c2mulA	Alignment	not modelled	19.8	8	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase huwe1; PDBTitle: solution structure of the ubm1 domain of human huwe1/arf-bp1
67	c3u07A	Alignment	not modelled	18.5	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vpa0106; PDBTitle: crystal structure of the vpa0106 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr106.
68	c6cmvA	Alignment	not modelled	17.3	22	PDB header: gene regulation Chain: A: PDB Molecule: transcriptional regulator lrs14-like protein; PDBTitle: crystal structure of archaeal biofilm regulator (abfr2) from2 sulfolobus acidocaldarius
69	d2p3ya1	Alignment	not modelled	17.1	13	Fold: VPA0735-like Superfamily: VPA0735-like Family: VPA0735-like
70	c2p3yA	Alignment	not modelled	17.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein vpa0735; PDBTitle: crystal structure of vpa0735 from vibrio parahaemolyticus. northeast2 structural genomics target vpr109
71	c4yifE	Alignment	not modelled	16.3	13	PDB header: dna binding protein Chain: E: PDB Molecule: marr family protein rv0880; PDBTitle: crystal structure of rv0880
72	d1myla	Alignment	not modelled	15.5	25	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
73	c3mkIB	Alignment	not modelled	14.8	14	PDB header: transcription regulator Chain: B: PDB Molecule: hth-type transcriptional regulator gadx; PDBTitle: crystal structure of dna-binding transcriptional dual regulator from2 escherichia coli k-12
74	c2gqqB	Alignment	not modelled	14.7	19	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (lrp)
75	d1b28a	Alignment	not modelled	14.2	25	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
76	c3iydF	Alignment	not modelled	14.1	20	PDB header: transcription/dna Chain: F: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: three-dimensional em structure of an intact activator-dependent2 transcription initiation complex
77	d1d5ya2	Alignment	not modelled	12.0	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
78	d2i15a1	Alignment	not modelled	12.0	28	Fold: MG296-like Superfamily: MG296-like Family: MG296-like
79	c5bqtC	Alignment	not modelled	11.8	20	PDB header: dna binding protein Chain: C: PDB Molecule: putative hth-type transcriptional regulator trmbI2; PDBTitle: structure of trmbI2, an archaeal chromatin protein, shows a novel mode2 of dna binding.
80	c3klnC	Alignment	not modelled	11.2	22	PDB header: transcription Chain: C: PDB Molecule: transcriptional regulator, luxr family; PDBTitle: vibrio cholerae vpst

81	c3lvyB_	Alignment	not modelled	11.2	10	PDB header: lyase Chain: B: PDB Molecule: carboxymuconolactone decarboxylase family; PDBTitle: crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
82	c3b73A_	Alignment	not modelled	10.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phih1 repressor-like protein; PDBTitle: crystal structure of the phih1 repressor-like protein from haloarcula2 marismortui
83	c3go5A_	Alignment	not modelled	10.9	27	PDB header: gene regulation Chain: A: PDB Molecule: multidomain protein with s1 rna-binding domains; PDBTitle: crystal structure of a multidomain protein with nucleic acid binding2 domains (sp_0946) from streptococcus pneumoniae tigr4 at 1.40 a3 resolution
84	c3h87D_	Alignment	not modelled	10.8	27	PDB header: toxin/antitoxin Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: rv0301 rv0300 toxin antitoxin complex from mycobacterium tuberculosis
85	c3zplE_	Alignment	not modelled	10.8	18	PDB header: transcription/dna Chain: E: PDB Molecule: putative marr-family transcriptional repressor; PDBTitle: crystal structure of sco3205, a marr family transcriptional regulator2 from streptomyces coelicolor, in complex with dna
86	d1heka_	Alignment	not modelled	10.6	62	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: EIAV matrix antigen
87	c2a6eF_	Alignment	not modelled	10.2	24	PDB header: transferase Chain: F: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: crystal structure of the t. thermophilus rna polymerase2 holoenzyme
88	d1rp3a1	Alignment	not modelled	9.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
89	c3mn2B_	Alignment	not modelled	9.4	11	PDB header: transcription regulator Chain: B: PDB Molecule: probable arac family transcriptional regulator; PDBTitle: the crystal structure of a probable arac family transcriptional2 regulator from rhodopseudomonas palustris cga009
90	c3rmrA_	Alignment	not modelled	9.4	29	PDB header: protein binding Chain: A: PDB Molecule: avirulence protein; PDBTitle: crystal structure of hyaloperonospora arabidopsidis atr1 effector2 domain
91	c4ch7A_	Alignment	not modelled	9.3	17	PDB header: transcription Chain: A: PDB Molecule: nird-like protein; PDBTitle: crystal structure of the siroheme decarboxylase nirdl
92	c2nyxB_	Alignment	not modelled	9.2	11	PDB header: transcription Chain: B: PDB Molecule: probable transcriptional regulatory protein, rv1404; PDBTitle: crystal structure of rv1404 from mycobacterium tuberculosis
93	c5wurB_	Alignment	not modelled	9.1	7	PDB header: metal binding protein Chain: B: PDB Molecule: ecf rna polymerase sigma factor sigw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, an2 oxidized form
94	c3r0aB_	Alignment	not modelled	9.1	9	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosarcina mazei go1 (gi2 21227196)
95	c3n41A_	Alignment	not modelled	9.0	50	PDB header: viral protein Chain: A: PDB Molecule: e3 envelope glycoprotein; PDBTitle: crystal structure of the mature envelope glycoprotein complex2 (spontaneous cleavage) of chikungunya virus.
96	d1sd4a_	Alignment	not modelled	8.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
97	d1d5ya1	Alignment	not modelled	8.5	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: AraC type transcriptional activator
98	c2k4bA_	Alignment	not modelled	8.4	16	PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: copr repressor structure
99	c4proD_	Alignment	not modelled	8.4	22	PDB header: serine protease Chain: D: PDB Molecule: alpha-lytic protease; PDBTitle: alpha-lytic protease complexed with pro region