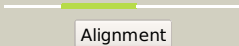

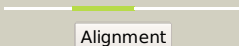

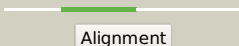

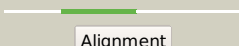

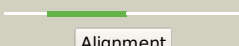

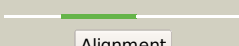

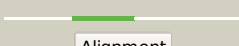

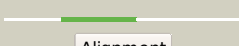







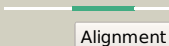

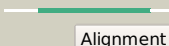

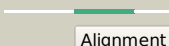



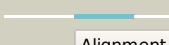




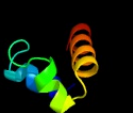



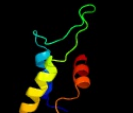
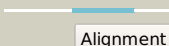

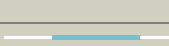
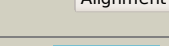
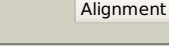

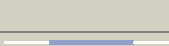
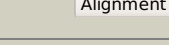


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1042c_(-)_1165096_1165503
Date	Wed Jul 31 22:05:11 BST 2019
Unique Job ID	a83c593c46985520

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2l4aA_	 Alignment		67.3	22	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
2	d2cg4a1	 Alignment		61.2	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
3	dlilga1	 Alignment		56.8	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
4	c4czdA_	 Alignment		56.8	23	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.
5	d2coba1	 Alignment		56.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
6	d2cyya1	 Alignment		53.8	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
7	c6paxA_	 Alignment		53.5	19	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
8	d2cfxa1	 Alignment		51.9	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Lrp/AsnC-like transcriptional regulator N-terminal domain
9	c2ia0A_	 Alignment		45.9	22	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)
10	c2dbbA_	 Alignment		43.9	15	PDB header: transcriptional regulator Chain: A: PDB Molecule: putative hth-type transcriptional regulator ph0061; PDBTitle: crystal structure of ph0061
11	c2cg4B_	 Alignment		42.6	27	PDB header: transcription Chain: B: PDB Molecule: regulatory protein asnc; PDBTitle: structure of e.coli asnc

12	c2p6tH_	 Alignment		42.5	14	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
13	d1p6ra_	 Alignment		42.3	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
14	c1u78A_	 Alignment		41.2	3	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
15	c4ch7A_	 Alignment		39.6	21	PDB header: transcription Chain: A: PDB Molecule: nird-like protein; PDBTitle: crystal structure of the siroheme decarboxylase nirdl
16	c2e7xA_	 Alignment		38.8	19	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
17	d1pdnc_	 Alignment		38.8	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
18	c1ilgA_	 Alignment		37.4	27	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lrpA; PDBTitle: crystal structure of the lrp-like transcriptional regulator from the2 archaeon pyrococcus furiosus
19	c4pcaC_	 Alignment		36.4	27	PDB header: transcription Chain: C: PDB Molecule: possible transcriptional regulatory protein (probably PDBTitle: crystal structure of mtbaldr (rv2779c)
20	d2ezha_	 Alignment		35.7	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
21	c2vbzA_	 Alignment	not modelled	35.7	19	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
22	c3r1fO_	 Alignment	not modelled	34.7	15	PDB header: transcription Chain: O: PDB Molecule: esx-1 secretion-associated regulator espr; PDBTitle: crystal structure of a key regulator of virulence in mycobacterium2 tuberculosis
23	c2m8eA_	 Alignment	not modelled	33.4	16	PDB header: dna binding protein Chain: A: PDB Molecule: sleeping beauty transposase; PDBTitle: nmr structure of the pai subdomain of sleeping beauty transposase
24	d2g7la1	 Alignment	not modelled	32.7	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
25	c4czdD_	 Alignment	not modelled	30.8	26	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.
26	d1k78a1	 Alignment	not modelled	28.0	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
27	c2hwkA_	 Alignment	not modelled	27.8	19	PDB header: hydrolase Chain: A: PDB Molecule: helicase nsp2; PDBTitle: crystal structure of venezuelan equine encephalitis alphavirus nsp22 protease domain
28	c2e1cA_	 Alignment	not modelled	26.4	17	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
29	d2ezia_	Alignment	not modelled	25.4	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
30	c2gqqB_	Alignment	not modelled	24.6	19	PDB header: transcription Chain: B: PDB Molecule: leucine-responsive regulatory protein; PDBTitle: crystal structure of e. coli leucine-responsive regulatory protein2 (Irp)
31	c3g7rB_	Alignment	not modelled	23.8	13	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of sco4454, a tetr-family transcriptional regulator2 from streptomyces coelicolor
32	c2yxhB_	Alignment	not modelled	23.1	36	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: mazg-related protein; PDBTitle: crystal structure of mazg-related protein from thermotoga maritima
33	c4e5vA_	Alignment	not modelled	22.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative thua-like protein; PDBTitle: crystal structure of a putative thua-like protein (parmer_02418) from2 parabacteroides merdae atcc 43184 at 1.75 a resolution
34	c2jg6A_	Alignment	not modelled	22.4	15	PDB header: hydrolase Chain: A: PDB Molecule: dna-3-methyladenine glycosidase; PDBTitle: crystal structure of a 3-methyladenine dna glycosylase i from2 staphylococcus aureus
35	c2p73A_	Alignment	not modelled	21.8	37	PDB header: transferase Chain: A: PDB Molecule: putative glycosyltransferase (mannosyltransferase) involved PDBTitle: crystal structure of a glycosyltransferase involved in the2 glycosylation of the major capsid of pbcv-1
36	c2g7gA_	Alignment	not modelled	21.4	15	PDB header: transcription Chain: A: PDB Molecule: rha04620, putative transcriptional regulator; PDBTitle: the crystal structure of the putative transcriptional regulator2 rha04620 from rhodococcus sp. rha1
37	c6j05B_	Alignment	not modelled	20.9	16	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulator arsr; PDBTitle: structures of two arsr as(iii)-responsive repressors: implications for2 the mechanism of derepression
38	c3trkA_	Alignment	not modelled	20.7	15	PDB header: hydrolase Chain: A: PDB Molecule: nonstructural polyprotein; PDBTitle: structure of the chikungunya virus nsp2 protease
39	c4pdyA_	Alignment	not modelled	19.3	24	PDB header: transferase Chain: A: PDB Molecule: aminoglycoside phosphotransferase; PDBTitle: crystal structure of aminoglycoside phosphotransferase from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
40	d1nkua_	Alignment	not modelled	18.2	19	Fold: DNA-glycosylase Superfamily: DNA-glycosylase Family: 3-Methyladenine DNA glycosylase I (Tag)
41	c2a5wC_	Alignment	not modelled	18.0	12	PDB header: oxidoreductase Chain: C: PDB Molecule: sulfite reductase, desulfoviridin-type subunit gamma PDBTitle: crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrC) from archaeoglobus fulgidus
42	d1ijwc_	Alignment	not modelled	17.3	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
43	d1hcra_	Alignment	not modelled	16.8	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
44	d2v4jc1	Alignment	not modelled	15.8	23	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase
45	d1ji8a_	Alignment	not modelled	15.3	31	Fold: DsrC, the gamma subunit of dissimilatory sulfite reductase Superfamily: DsrC, the gamma subunit of dissimilatory sulfite reductase Family: DsrC, the gamma subunit of dissimilatory sulfite reductase
46	c2cfxD_	Alignment	not modelled	15.0	16	PDB header: transcription Chain: D: PDB Molecule: hth-type transcriptional regulator lrpc; PDBTitle: structure of b.subtilis lrpc
47	c3hefB_	Alignment	not modelled	15.0	11	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small subunit
48	d1okra_	Alignment	not modelled	14.9	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
49	d1pbya1	Alignment	not modelled	14.5	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
50	c2zb9A_	Alignment	not modelled	14.5	13	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of tetr family transcription regulator2 sco0332
51	d1sd4a_	Alignment	not modelled	13.7	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
52	c1yx3A_	Alignment	not modelled	13.6	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dsrC; PDBTitle: nmr structure of allochromatium vinosum dsrC: northeast2 structural genomics consortium target op4
53	c2g7IA_	Alignment	not modelled	12.2	11	PDB header: transcription Chain: A: PDB Molecule: tetr-family transcriptional regulator; PDBTitle: crystal structure of putative transcription regulator

						sco7704 from2 streptomyces coelicor
54	d1musa_	Alignment	not modelled	10.9	8	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Transposase inhibitor (Tn5 transposase)
55	c2npiD_	Alignment	not modelled	10.7	40	PDB header: transcription Chain: D: PDB Molecule: protein pcf11; PDBTitle: clp1-atp-pcf11 complex
56	d2id3a1	Alignment	not modelled	10.1	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
57	c5ojyA_	Alignment	not modelled	10.1	10	PDB header: transcription Chain: A: PDB Molecule: tetr family transcription regulator; PDBTitle: co-complex structure of regulator protein 2 (pamr2) with pamamycin 6072 from streptomyces alboniger
58	d1stza1	Alignment	not modelled	9.7	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Heat-inducible transcription repressor HrcA, N-terminal domain
59	c2npiC_	Alignment	not modelled	9.6	40	PDB header: transcription Chain: C: PDB Molecule: protein pcf11; PDBTitle: clp1-atp-pcf11 complex
60	c1bjzA_	Alignment	not modelled	9.5	14	PDB header: transcription regulation Chain: A: PDB Molecule: tetracycline repressor; PDBTitle: tetracycline chelated mg2+-ion initiates helix unwinding for tet2 repressor induction
61	c2i0kA_	Alignment	not modelled	9.4	26	PDB header: transcription Chain: A: PDB Molecule: stage iii sporulation protein d; PDBTitle: nmr solution structure of a transcription factor spoiiiid in complex2 with dna
62	c3e66B_	Alignment	not modelled	9.3	38	PDB header: splicing Chain: B: PDB Molecule: prp8; PDBTitle: crystal structure of the beta-finger domain of yeast prp8
63	c2uutA_	Alignment	not modelled	9.3	10	PDB header: hydrolase Chain: A: PDB Molecule: rna-directed rna polymerase; PDBTitle: the 2.4 angstrom resolution structure of the d346g mutant of the2 sapporo virus rdrp polymerase
64	c4oi4B_	Alignment	not modelled	9.0	40	PDB header: transcription Chain: B: PDB Molecule: protein pcf11; PDBTitle: protein complex of clp1 bound to atp and mg2+ with2 pcf11deltan454deltac563 of s. cerevisiae
65	c4c0bC_	Alignment	not modelled	8.9	40	PDB header: transcription Chain: C: PDB Molecule: pcf11p; PDBTitle: structure of wild-type clp1p-pcf11p (454 -563) complex
66	d2g7ga1	Alignment	not modelled	8.5	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
67	c4c0hD_	Alignment	not modelled	8.5	40	PDB header: transcription Chain: D: PDB Molecule: pcf11p; PDBTitle: extended interface between pcf11p and clp1p and structural basis for2 atp loss in gly135arg point mutant
68	c3bjbE_	Alignment	not modelled	8.3	13	PDB header: transcription regulator Chain: E: PDB Molecule: probable transcriptional regulator, tetr family protein; PDBTitle: crystal structure of a tetr transcriptional regulator from rhodococcus2 sp. rha1
69	c1apfA_	Alignment	not modelled	8.2	46	PDB header: cardiac stimulant Chain: A: PDB Molecule: anthopleurin-b; PDBTitle: anthopleurin-b, nmr, 20 structures
70	d1z0xa1	Alignment	not modelled	8.0	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
71	c2g7sA_	Alignment	not modelled	7.9	12	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, tetr family; PDBTitle: the crystal structure of transcriptional regulator, tetr family, from2 agrobacterium tumefaciens
72	c6o4mA_	Alignment	not modelled	7.6	23	PDB header: toxin Chain: A: PDB Molecule: melittin; PDBTitle: racemic melittin
73	c3i4pA_	Alignment	not modelled	7.3	22	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, asnc family; PDBTitle: crystal structure of asnc family transcriptional regulator from2 agrobacterium tumefaciens
74	c2mw6A_	Alignment	not modelled	7.3	23	PDB header: toxin Chain: A: PDB Molecule: melittin; PDBTitle: structure of the bee venom toxin melittin with [(c5h5)ru]+ fragment2 attached to the tryptophan residue
75	c4oi4D_	Alignment	not modelled	7.3	57	PDB header: transcription Chain: D: PDB Molecule: protein pcf11; PDBTitle: protein complex of clp1 bound to atp and mg2+ with2 pcf11deltan454deltac563 of s. cerevisiae
76	d2np5a1	Alignment	not modelled	7.2	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
77	d2fd5a1	Alignment	not modelled	7.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
78	c4cgrA_	Alignment	not modelled	7.1	13	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structure of regulator protein sco3201 from streptomyces coelicolor
79	c4fcyA_	Alignment	not modelled	6.9	9	PDB header: dna binding protein/dna Chain: A: PDB Molecule: transposase; PDBTitle: crystal structure of the bacteriophage mu transpososome

80	d2vkea1	Alignment	not modelled	6.8	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracyclin repressor-like, N-terminal domain
81	c2raeA	Alignment	not modelled	6.7	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, acrr family protein; PDBTitle: crystal structure of a tetr/acrr family transcriptional regulator from2 rhodococcus sp. rha1
82	d2jn6a1	Alignment	not modelled	6.6	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Cg12762-like
83	c2mltA	Alignment	not modelled	6.6	23	PDB header: toxin (hemolytic polypeptide) Chain: A: PDB Molecule: melittin; PDBTitle: melittin
84	c1mbjA	Alignment	not modelled	6.5	14	PDB header: dna binding protein Chain: A: PDB Molecule: myb proto-oncogene protein; PDBTitle: mouse c-myb dna-binding domain repeat 3
85	d1mbja	Alignment	not modelled	6.5	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain
86	d1z84a2	Alignment	not modelled	6.4	11	Fold: HIT-like Superfamily: HIT-like Family: Hexose-1-phosphate uridylyltransferase
87	c3bqyA	Alignment	not modelled	6.4	7	PDB header: transcription regulator Chain: A: PDB Molecule: putative tetr family transcriptional regulator; PDBTitle: crystal structure of a possible tetr family transcriptional regulator2 from streptomyces coelicolor a3(2).
88	c4c0hC	Alignment	not modelled	6.3	57	PDB header: transcription Chain: C: PDB Molecule: pcf11p; PDBTitle: extended interface between pcf11p and clp1p and structural basis for2 atp loss in gly135arg point mutant
89	c2oerA	Alignment	not modelled	6.2	4	PDB header: transcription Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: probable transcriptional regulator from pseudomonas aeruginosa
90	c6o4mB	Alignment	not modelled	6.2	23	PDB header: toxin Chain: B: PDB Molecule: melittin; PDBTitle: racemic melittin
91	c2mltB	Alignment	not modelled	6.2	23	PDB header: toxin (hemolytic polypeptide) Chain: B: PDB Molecule: melittin; PDBTitle: melittin
92	d1jhfa1	Alignment	not modelled	6.1	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: LexA repressor, N-terminal DNA-binding domain
93	c2yvha	Alignment	not modelled	6.0	9	PDB header: transcription/dna Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of the operator-binding form of the multi-drug2 binding transcriptional repressor cgmr
94	c4omzG	Alignment	not modelled	5.9	8	PDB header: transcription Chain: G: PDB Molecule: nolr; PDBTitle: crystal structure of nolr from sinorhizobium fredii
95	d2g9wa1	Alignment	not modelled	5.7	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Penicillinase repressor
96	d1r1ua	Alignment	not modelled	5.6	5	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
97	c2qkoA	Alignment	not modelled	5.4	17	PDB header: transcription Chain: A: PDB Molecule: possible transcriptional regulator, tetr family protein; PDBTitle: crystal structure of transcriptional regulator rha06399 from2 rhodococcus sp. rha1
98	c4bqqB	Alignment	not modelled	5.4	15	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: protein crystal structure of the n-terminal and recombinase domains of2 the streptomyces temperate phage serine recombinase, fc31 integrase.
99	c4guaB	Alignment	not modelled	5.4	21	PDB header: hydrolase Chain: B: PDB Molecule: non-structural polyprotein; PDBTitle: alphavirus p23pro-zbd