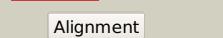
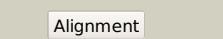
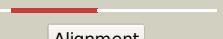
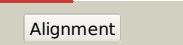
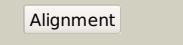
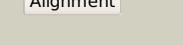
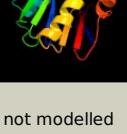
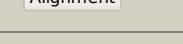


Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD0060_(-)_63906_64964
Date	Tue Jul 23 14:50:09 BST 2019
Unique Job ID	7f33f496484f97f9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5m3iB_			100.0	100	PDB header: antitoxin Chain: B; PDB Molecule: rnase iii inhibitor; PDBTitle: macrodomain of mycobacterium tuberculosis darg
2	c5m3iA_			100.0	56	PDB header: antitoxin Chain: A; PDB Molecule: appr-1-p processing domain protein; PDBTitle: macrodomain of thermus aquaticus darg
3	c5e3bA_			100.0	25	PDB header: hydrolase Chain: A; PDB Molecule: macrodomain protein; PDBTitle: structure of macrodomain protein from streptomyces coelicolor
4	c2eeeA_			100.0	24	PDB header: gene regulation Chain: A; PDB Molecule: uncharacterized protein c6orf130; PDBTitle: solution structure of the a1pp domain from human protein2 c6orf130
5	d2fg1a1			100.0	22	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
6	c5iitC_			100.0	18	PDB header: inositol phosphate binding protein Chain: C; PDB Molecule: vacuolar transporter chaperone 4,core histone macro-h2a.1; PDBTitle: structure of spx domain of the yeast inorganic polyphosphate polymerase2 vtc4 crystallized by carrier-driven crystallization in fusion with3 the macro domain of human histone macroh2a.1
7	c2dx6B_			100.0	23	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: hypothetical protein ttha0132; PDBTitle: crystal structure of conserved hypothetical protein, ttha0132 from2 thermus thermophilus hb8
8	c3q71A_			100.0	17	PDB header: transferase Chain: A; PDB Molecule: poly [adp-ribose] polymerase 14; PDBTitle: human parp14 (artd8) - macro domain 2 in complex with adenosine-5'-2' diphosphoribose
9	c3vfqA_			100.0	19	PDB header: transferase Chain: A; PDB Molecule: poly [adp-ribose] polymerase 14; PDBTitle: human parp14 (artd8, bal2) - macro domains 1 and 2 in complex with2 adenosine-5'-diphosphoribose
10	d1zr5a1			100.0	16	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
11	c1zr5B_			100.0	16	PDB header: gene regulation Chain: B; PDB Molecule: h2afy protein; PDBTitle: crystal structure of the macro-domain of human core histone variant2 macroh2a1.2

12	d1spva			100.0	17	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
13	d1yd9a1			100.0	17	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
14	c2xd7B			100.0	16	PDB header: dna binding protein Chain: B: PDB Molecule: core histone macro-h2a.2; PDBTitle: crystal structure of the macro domain of human core histone h2a
15	c5l9kB			100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: macrod-type macrodomain; PDBTitle: oceanobacillus iheyensis macrodomain with adpr
16	c3q6zA			99.9	20	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 14; PDBTitle: human parp14 (artd8)-macro domain 1 in complex with adenosine-5-2 diphosphoribose
17	c5iq5A			99.9	24	PDB header: viral protein Chain: A: PDB Molecule: macro domain; PDBTitle: nmr solution structure of mayaro virus macro domain
18	c4iqyB			99.9	17	PDB header: hydrolase Chain: B: PDB Molecule: o-acetyl-adp-ribose deacetylase macrod2; PDBTitle: crystal structure of the human protein-proximal adp-ribosyl-hydrolase2 macrod2
19	d1vhua			99.9	21	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
20	c5ailA			99.9	19	PDB header: transcription Chain: A: PDB Molecule: poly [adp-ribose] polymerase 9; PDBTitle: human parp9 2nd macrodomain
21	c2x47A		not modelled	99.9	18	PDB header: signaling protein Chain: A: PDB Molecule: macro domain-containing protein 1; PDBTitle: crystal structure of human macrod1
22	c3kh6A		not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 15; PDBTitle: human poly(adp-ribose) polymerase 15, macro domain 2 in complex with2 adenosine-5-diphosphoribose PDB header: signaling protein Chain: A: PDB Molecule: ganglioside-induced differentiation-associated protein 2; PDBTitle: crystal structure of ganglioside induced differentiation2 associated protein 2 (gdap2) macro domain
23	c4um1A		not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 14; PDBTitle: human parp14 (artd8, bal2) - macro domain 3
24	c4ablA		not modelled	99.9	18	PDB header: viral protein/rna Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of macro domain of chikungunya virus in complex with2 rna
25	c3gpqA		not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: macrodomain; PDBTitle: crystal structure of trypanosoma cruzi macrodomain
26	c5fszA		not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: macrodomain; PDBTitle: crystal structure of trypanosoma brucei macrodomain2 (crystal form 1)
27	c3ewqA		not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: hcov-229e nsf3 adrp domain
28	c5fsuA		not modelled	99.9	12	PDB header: hydrolase Chain: A: PDB Molecule: macrodomain; PDBTitle: crystal structure of trypanosoma brucei macrodomain2 (crystal form 1)

29	c3ejfA		Alignment	not modelled	99.9	17	PDB header: hydrolase Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of ibv x-domain at ph 8.5
30	c5kivA		Alignment	not modelled	99.9	15	PDB header: hydrolase Chain: A: PDB Molecule: protein-adp-ribose hydrolase; PDBTitle: crystal structure of saumacro (sav0325)
31	c5dusA		Alignment	not modelled	99.9	19	PDB header: viral protein Chain: A: PDB Molecule: orf1a; PDBTitle: crystal structure of mers-cov macro domain in complex with adp-ribose
32	c3ejgA		Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of hcov-229e x-domain
33	c3gqeA		Alignment	not modelled	99.9	20	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of macro domain of venezuelan equine encephalitis2 virus
34	c3ew5B		Alignment	not modelled	99.9	15	PDB header: rna binding protein Chain: B: PDB Molecule: macro domain of non-structural protein 3; PDBTitle: structure of the tetragonal crystal form of x (adrp) domain2 from fcov
35	d2acfa1		Alignment	not modelled	99.9	16	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
36	c2vriA		Alignment	not modelled	99.9	16	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: structure of the nsp3 x-domain of human coronavirus n163
37	c4guaB		Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: B: PDB Molecule: non-structural polyprotein; PDBTitle: alphavirus p23pro-zbd
38	d1nira		Alignment	not modelled	99.7	21	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
39	c5lw0A		Alignment	not modelled	99.4	17	PDB header: adp-ribose-binding protein Chain: A: PDB Molecule: basic helix-loop-helix, putative, expressed; PDBTitle: oryza sativa apl macromain in complex with adp-ribose
40	c3siiA		Alignment	not modelled	96.4	12	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: poly(adp-ribose) glycohydrolase; PDBTitle: the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from thermomonospora curvata
41	c5zdcL		Alignment	not modelled	96.3	10	PDB header: hydrolase Chain: L: PDB Molecule: poly adp-ribose glycohydrolase; PDBTitle: crystal structure of poly(adp-ribose) glycohydrolase (parg) from2 deinococcus radiodurans in complex with adp-ribose (p32)
42	d1gyta1		Alignment	not modelled	91.3	11	Fold: Macro domain-like Superfamily: Macro domain-like Family: Leucine aminopeptidase (Aminopeptidase A), N-terminal domain
43	c1gytG		Alignment	not modelled	73.5	11	PDB header: hydrolase Chain: G: PDB Molecule: cytosol aminopeptidase; PDBTitle: e. coli aminopeptidase a (pepa)
44	c3l7wA		Alignment	not modelled	71.5	16	PDB header: transcription Chain: A: PDB Molecule: putative uncharacterized protein smu.1704; PDBTitle: the crystal structure of smu.1704 from streptococcus mutans ua159
45	c6omeA		Alignment	not modelled	63.1	11	PDB header: hydrolase Chain: A: PDB Molecule: probable cytosol aminopeptidase; PDBTitle: crystal structure of a probable cytosol aminopeptidase (leucine2 aminopeptidase, lap) from chlamydia trachomatis d/uw-3/cx
46	c3r0aB		Alignment	not modelled	62.3	10	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator; PDBTitle: possible transcriptional regulator from methanosaicina maezi go1 (gi 21227196)
47	c1vqwB		Alignment	not modelled	60.6	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein with similarity to flavin-containing PDBTitle: crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine monooxygenases
48	c5jlsA		Alignment	not modelled	54.7	11	PDB header: transcription Chain: A: PDB Molecule: adhesin competence repressor; PDBTitle: crystal structure of adhesin competence repressor (adcr) from2 streptococcus pyogenes (c-terminally his tagged)
49	d2esha1		Alignment	not modelled	54.0	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like
50	c3jruB		Alignment	not modelled	51.8	9	PDB header: hydrolase Chain: B: PDB Molecule: probable cytosol aminopeptidase; PDBTitle: crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331
51	c3h8gC		Alignment	not modelled	48.9	13	PDB header: hydrolase Chain: C: PDB Molecule: cytosol aminopeptidase; PDBTitle: bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
52	c5zhcA		Alignment	not modelled	48.2	15	PDB header: dna binding protein Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of the padr-family transcriptional regulator rv34882 of mycobacterium tuberculosis h37rv
53	c5lw6A		Alignment	not modelled	47.3	10	PDB header: adp-ribose binding protein Chain: A: PDB Molecule: ddb_g0293866; PDBTitle: crystal structure of a se-met substituted dictyostelium discoideum 2 adp-ribose binding macrodomain (residues 342-563) of ddb_g0293866
							PDB header: dna binding protein

54	c4hw0B	Alignment	not modelled	46.6	13	Chain: B: PDB Molecule: dna-binding protein sso10a-2; PDBTitle: crystal structure of sso10a-2, a dna-binding protein from sulfolobus2 solfataricus
55	d1r7ja	Alignment	not modelled	45.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Archaeal DNA-binding protein
56	c5nmwA	Alignment	not modelled	44.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of the pyrrolizidine alkaloid n-oxygenase from2 zonocerus variegatus in complex with fad
57	c5x11G	Alignment	not modelled	44.7	14	PDB header: transcription/dna Chain: G: PDB Molecule: transcriptional regulator; PDBTitle: crystal structure of bacillus subtilis padr in complex with operator2 dna
58	c1fx7C	Alignment	not modelled	43.1	15	PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis
59	c5zqhA	Alignment	not modelled	42.2	12	PDB header: dna binding protein Chain: A: PDB Molecule: padr family transcriptional regulator; PDBTitle: crystal structure of streptococcus transcriptional regulator
60	c5cvbB	Alignment	not modelled	41.8	15	PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor
61	c2qvoA	Alignment	not modelled	39.9	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein af_1382; PDBTitle: crystal structure of af1382 from archaeoglobus fulgidus
62	c1xmaA	Alignment	not modelled	39.8	7	PDB header: transcription Chain: A: PDB Molecule: predicted transcriptional regulator; PDBTitle: structure of a transcriptional regulator from clostridium thermocellum2 cth-833
63	d1xmaa	Alignment	not modelled	39.8	7	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: PadR-like
64	c3krbB	Alignment	not modelled	39.5	22	PDB header: oxidoreductase Chain: B: PDB Molecule: aldose reductase; PDBTitle: structure of aldose reductase from giardia lamblia at 1.75a resolution
65	c5dymA	Alignment	not modelled	39.3	10	PDB header: dna binding protein Chain: A: PDB Molecule: padr-family transcriptional regulator; PDBTitle: crystal structure of a padr family transcription regulator from2 hypervirulent clostridium difficile r20291 - cdpadr_0991 to 1.893 angstrom resolution
66	d1vp5a	Alignment	not modelled	39.1	23	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
67	c5h20A	Alignment	not modelled	35.0	12	PDB header: transcription regulator Chain: A: PDB Molecule: putative padr-family transcriptional regulatory protein; PDBTitle: x-ray structure of padr-like transcription factor from bacteroid2 fragilis
68	d1ixra2	Alignment	not modelled	34.8	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
69	d1cuka3	Alignment	not modelled	34.1	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
70	c2e1nA	Alignment	not modelled	33.3	16	PDB header: circadian clock protein Chain: A: PDB Molecule: pex; PDBTitle: crystal structure of the cyanobacterium circadian clock modifier pex
71	c2x4hA	Alignment	not modelled	33.3	10	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
72	c4q3mF	Alignment	not modelled	32.6	16	PDB header: hydrolase Chain: F: PDB Molecule: mgs-m4; PDBTitle: crystal structure of mgs-m4, an aldo-keto reductase enzyme from a2 medee basin deep-sea metagenome library
73	c4esbA	Alignment	not modelled	31.9	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, padr family; PDBTitle: crystal structure of padr-like transcriptional regulator (bc4206) from2 bacillus cereus strain atcc 14579
74	c4otkA	Alignment	not modelled	31.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterial enzyme rv2971; PDBTitle: a structural characterization of the isoniazid mycobacterium2 tuberculosis drug target, rv2971, in its unliganded form
75	c2bg5A	Alignment	not modelled	30.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: aldose reductase; PDBTitle: holo aldose reductase from barley
76	c1g3wA	Alignment	not modelled	30.3	15	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
77	c6bsvB	Alignment	not modelled	30.2	11	PDB header: transferase Chain: B: PDB Molecule: xyloglucan 6-xylosyltransferase 1; PDBTitle: crystal structure of xyloglucan xylosyltransferase binary form
78	c3f8fA	Alignment	not modelled	30.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, padr-like family; PDBTitle: crystal structure of multidrug binding transcriptional regulator lmrr2 complexed with daunomycin
79	d1bm9a	Alignment	not modelled	29.8	15	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Replication terminator protein (RTP)

80	c3wbwA		Alignment	not modelled	29.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2,5-diketo-d-gluconic acid reductase; PDBTitle: crystal structure of gox0644 in complex with nadph
81	c5yf1A		Alignment	not modelled	29.2	50	PDB header: transferase Chain: A: PDB Molecule: carnosine n-methyltransferase; PDBTitle: crystal structure of carnmt1 bound to carnosine and sfg
82	c3ri2B		Alignment	not modelled	28.3	13	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, padr-like family; PDBTitle: crystal structure of padr family transcriptional regulator from2 eggerthella lenta dsm 2243
83	d1mzra		Alignment	not modelled	26.7	21	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
84	c4ftbD		Alignment	not modelled	26.2	22	PDB header: virus Chain: D: PDB Molecule: capsid protein gamma; PDBTitle: crystal structure of the authentic flock house virus particle
85	c1ixrB		Alignment	not modelled	25.4	32	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
86	c1ixrA		Alignment	not modelled	25.3	32	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
87	c3df8A		Alignment	not modelled	25.0	19	PDB header: transcription Chain: A: PDB Molecule: possible hxlr family transcriptional factor; PDBTitle: the crystal structure of a possible hxlr family transcriptional factor2 from thermoplasma volcanium gss1
88	c2h5xA		Alignment	not modelled	24.3	28	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
89	d2ch5a2		Alignment	not modelled	23.8	17	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: BadF/BadG/BcrA/BcrD-like
90	d1uh6a		Alignment	not modelled	23.6	31	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
91	d1bvs3		Alignment	not modelled	23.6	24	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA helicase RuvA subunit, N-terminal domain
92	d1hsja1		Alignment	not modelled	23.1	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Mar-like transcriptional regulators
93	d1z7ua1		Alignment	not modelled	22.9	11	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hxlr-like
94	d1hw6a		Alignment	not modelled	22.8	19	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
95	c3elkA		Alignment	not modelled	22.8	12	PDB header: transcription regulator Chain: A: PDB Molecule: putative transcriptional regulator ta0346; PDBTitle: crystal structure of putative transcriptional regulator ta0346 from2 thermoplasma acidophilum
96	c1d8IA		Alignment	not modelled	22.6	24	PDB header: gene regulation Chain: A: PDB Molecule: protein (holliday junction dna helicase ruva); PDBTitle: e. coli holliday junction binding protein ruva nh2 region lacking2 domain iii
97	c1hjpA		Alignment	not modelled	22.4	24	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
98	c3hhhA		Alignment	not modelled	21.9	14	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, padr family; PDBTitle: crystal structure of transcriptional regulator, a member of padr2 family, from enterococcus faecalis v583
99	c3m0zD		Alignment	not modelled	21.4	15	PDB header: lyase Chain: D: PDB Molecule: putative aldolase; PDBTitle: crystal structure of putative aldolase from klebsiella pneumoniae.
100	c3muxB		Alignment	not modelled	20.7	10	PDB header: lyase Chain: B: PDB Molecule: putative 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
101	c3m6yA		Alignment	not modelled	20.6	10	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase; PDBTitle: structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
102	c4ijrA		Alignment	not modelled	20.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-arabinose dehydrogenase [nad(p+)] heavy chain; PDBTitle: crystal structure of saccharomyces cerevisiae arabinose dehydrogenase2 ara1 complexed with nadph