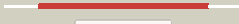



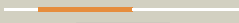
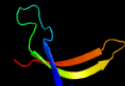





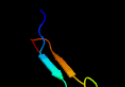
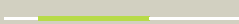






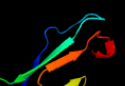

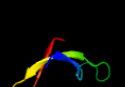


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0569_(-)_661006_661272
Date	Fri Jul 26 01:50:12 BST 2019
Unique Job ID	da365df7839f1adc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2a7yA_	 Alignment		100.0	62	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rv2302/mt2359; PDBTitle: solution structure of the conserved hypothetical protein2 rv2302 from the bacterium mycobacterium tuberculosis
2	d2a7ya1	 Alignment		100.0	62	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Rv2302-like
3	c2ekoA_	 Alignment		82.4	18	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase htatip; PDBTitle: solution structure of ruh-073, a pseudo chromo domain from2 human cdna
4	d2huga1	 Alignment		76.7	30	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
5	c5znpB_	 Alignment		71.4	21	PDB header: gene regulation Chain: B: PDB Molecule: short life family protein; PDBTitle: crystal structure of ptshl in complex with an h3k4me3 peptide
6	c6d7yA_	 Alignment		70.6	29	PDB header: toxin Chain: A: PDB Molecule: hemagglutinin; PDBTitle: 1.75 angstrom resolution crystal structure of the toxic c-terminal tip2 of cdia from pseudomonas aeruginosa in complex with immune protein
7	c3qiiA_	 Alignment		67.4	17	PDB header: transcription regulator Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 2 of human phd finger protein 20
8	d2ix0a1	 Alignment		67.2	17	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
9	c1w4sA_	 Alignment		65.7	24	PDB header: nuclear protein Chain: A: PDB Molecule: polybromo 1 protein; PDBTitle: crystal structure of the proximal bah domain of polybromo
10	d1fcga2	 Alignment		61.8	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
11	c4bb7A_	 Alignment		57.1	26	PDB header: transcription Chain: A: PDB Molecule: chromatin structure-remodeling complex subunit rsc2; PDBTitle: crystal structure of the yeast rsc2 bah domain

12	c3qz9D_	Alignment		54.4	21	PDB header: lyase Chain: D: PDB Molecule: co-type nitrile hydratase beta subunit; PDBTitle: crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
13	d2f5ka1	Alignment		48.5	11	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
14	d1f2qa2	Alignment		46.7	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
15	d1ugpb_	Alignment		44.6	21	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
16	c1u9pA_	Alignment		44.6	31	PDB header: unknown function Chain: A: PDB Molecule: parc; PDBTitle: permuted single-chain arc
17	d1v6za1	Alignment		44.6	22	Fold: PUA domain-like Superfamily: PUA domain-like Family: Yggj N-terminal domain-like
18	c1xnll_	Alignment		44.3	21	PDB header: cell cycle Chain: I: PDB Molecule: tumor suppressor p53-binding protein 1; PDBTitle: tandem tudor domain of 53bp1
19	c2ro0A_	Alignment		43.3	8	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase esa1; PDBTitle: solution structure of the knotted tudor domain of the yeast2 histone acetyltransferase, esa1
20	c5in1A_	Alignment		41.6	14	PDB header: transcription Chain: A: PDB Molecule: mrg701; PDBTitle: crystal structure of the mrg701 chromodomain
21	c2rnzA_	Alignment	not modelled	38.5	13	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase esa1; PDBTitle: solution structure of the presumed chromodomain of the2 yeast histone acetyltransferase, esa1
22	c4fsxB_	Alignment	not modelled	38.5	26	PDB header: transferase Chain: B: PDB Molecule: dna (cytosine-5)-methyltransferase 1; PDBTitle: crystal structure of se-substituted zea mays zmet2 in complex with sah
23	d1wgsa_	Alignment	not modelled	37.1	18	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
24	c2qqSB_	Alignment	not modelled	36.8	11	PDB header: oxidoreductase Chain: B: PDB Molecule: jmjc domain-containing histone demethylation PDBTitle: jmjd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide
25	c4uc4A_	Alignment	not modelled	35.8	18	PDB header: replication Chain: A: PDB Molecule: lysine-specific demethylase 4b; PDBTitle: crystal structure of hybrid tudor domain of human lysine demethylase2 kdm4b
26	c2lrqA_	Alignment	not modelled	35.5	5	PDB header: transcription Chain: A: PDB Molecule: nua4 complex subunit eaf3 homolog; PDBTitle: chemical shift assignment and solution structure of fr822a from2 drosophila melanogaster. northeast structural genomics consortium3 target fr822a
27	d2fcba2	Alignment	not modelled	34.1	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
28	c2xdpA_	Alignment	not modelled	33.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 4c; PDBTitle: crystal structure of the tudor domain of human jmjd2c

29	c2dxcG_	Alignment	not modelled	33.0	25	PDB header: hydrolase Chain: G: PDB Molecule: thiocyanate hydrolase subunit alpha; PDBTitle: recombinant thiocyanate hydrolase, fully-matured form
30	c4in3C_	Alignment	not modelled	32.5	19	PDB header: protein transport Chain: C: PDB Molecule: chitin biosynthesis protein chs5; PDBTitle: crystal structure of the chs5-bch1 exomer cargo adaptor complex
31	c4pl6A_	Alignment	not modelled	32.4	16	PDB header: transcription Chain: A: PDB Molecule: at1g02740; PDBTitle: structure of the chromodomain of mrg2 in complex with h3k4me3
32	c3luuA_	Alignment	not modelled	32.3	7	PDB header: biosynthetic protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with unknown function which belongs to2 pfam duf971 family (afe_2189) from acidithiobacillus ferrooxidans3 atcc 23270 at 1.93 a resolution
33	c2d9uA_	Alignment	not modelled	28.9	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: chromobox protein homolog 2 (isoform 2); PDBTitle: solution structure of the chromo domain of chromobox2 homolog 2 from human
34	c2equA_	Alignment	not modelled	28.6	15	PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1
35	c4fm4D_	Alignment	not modelled	28.1	14	PDB header: lyase Chain: D: PDB Molecule: nitrile hydratase beta subunit; PDBTitle: wild type fe-type nitrile hydratase from comamonas testosteroni ni1
36	d2z1ca1	Alignment	not modelled	26.4	40	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
37	c3dlmA_	Alignment	not modelled	25.5	11	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase setdb1; PDBTitle: crystal structure of tudor domain of human histone-lysine n-2 methyltransferase setdb1
38	d2ot2a1	Alignment	not modelled	24.5	30	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
39	c4m6tA_	Alignment	not modelled	22.9	15	PDB header: transcription regulator Chain: A: PDB Molecule: rna polymerase ii-associated factor 1 homolog, linker, rna PDBTitle: structure of human paf1 and leo1 complex
40	c2e5qA_	Alignment	not modelled	22.8	30	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 19; PDBTitle: solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]
41	d1pfa_	Alignment	not modelled	22.8	35	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
42	c2v3mF_	Alignment	not modelled	22.5	21	PDB header: ribosomal protein Chain: F: PDB Molecule: naf1; PDBTitle: structure of the gar1 domain of naf1
43	d1gkpa1	Alignment	not modelled	21.9	22	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase)
44	c4a4fA_	Alignment	not modelled	21.6	17	PDB header: rna binding protein Chain: A: PDB Molecule: survival of motor neuron-related-splicing factor 30; PDBTitle: solution structure of spf30 tudor domain in complex with symmetrically2 dimethylated arginine
45	d1q3la_	Alignment	not modelled	21.3	30	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
46	c1q3lA_	Alignment	not modelled	21.3	30	PDB header: structural protein Chain: A: PDB Molecule: heterochromatin protein 1; PDBTitle: chromodomain of hp1 complexed with histone h3 tail2 containing monomethyllysine 9.
47	d1vk3a3	Alignment	not modelled	21.3	25	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
48	d2dnva1	Alignment	not modelled	20.8	26	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
49	c2k1bA_	Alignment	not modelled	20.8	30	PDB header: transcription regulator Chain: A: PDB Molecule: chromobox protein homolog 7; PDBTitle: solution nmr structure of the chromo domain of the2 chromobox protein homolog 7
50	c2ldmA_	Alignment	not modelled	20.6	17	PDB header: transcription/protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of human phf20 tudor2 domain bound to a p53 segment2 containing a dimethyllysine analog p53k370me2
51	c4q66J_	Alignment	not modelled	20.4	19	PDB header: protein transport Chain: J: PDB Molecule: chs5p; PDBTitle: structure of exomer bound to arf1.
52	c1g5vA_	Alignment	not modelled	20.4	17	PDB header: translation Chain: A: PDB Molecule: survival motor neuron protein 1; PDBTitle: solution structure of the tudor domain of the human smn2 protein
53	d1guwa_	Alignment	not modelled	19.8	20	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
54	c3j4uA_	Alignment	not modelled	18.9	20	PDB header: virus Chain: A: PDB Molecule: major capsid protein; PDBTitle: a new topology of the hk97-like fold revealed in bordetella2 bacteriophage: non-covalent chainmail secured by

						jellyrolls
55	c5e4wD_	Alignment	not modelled	18.9	30	PDB header: transport protein Chain: D: PDB Molecule: signal recognition particle 43 kda protein, chloroplastic; PDBTitle: crystal structure of cpsrp43 chromodomains 2 and 3 in complex with the2 alb3 tail
56	c3fdtA_	Alignment	not modelled	18.8	20	PDB header: protein binding Chain: A: PDB Molecule: chromobox protein homolog 5; PDBTitle: crystal structure of the complex of human chromobox homolog 5 (cbx5)2 with h3k9(me)3 peptide
57	d3d3ra1	Alignment	not modelled	18.8	27	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
58	c3d3rA_	Alignment	not modelled	18.6	27	PDB header: chaperone Chain: A: PDB Molecule: hydrogenase assembly chaperone hupc/hupf; PDBTitle: crystal structure of the hydrogenase assembly chaperone hupc/hupf2 family protein from shewanella oneidensis mr-1
59	d2qdyb1	Alignment	not modelled	18.3	21	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
60	c1pdqA_	Alignment	not modelled	18.1	35	PDB header: structural protein Chain: A: PDB Molecule: polycomb protein; PDBTitle: polycomb chromodomain complexed with the histone h3 tail2 containing trimethyllysine 27.
61	c2e5pA_	Alignment	not modelled	18.0	31	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 1 (phf1 protein)
62	c2kvmA_	Alignment	not modelled	18.0	30	PDB header: transcription Chain: A: PDB Molecule: chromobox protein homolog 7; PDBTitle: solution structure of the cbx7 chromodomain in complex with a h3k27me22 peptide
63	c2l6pA_	Alignment	not modelled	17.8	12	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: phac1, phac2 and phad genes; PDBTitle: nmr solution structure of the protein np_253742.1
64	d1v29b_	Alignment	not modelled	17.1	21	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
65	c3fnpB_	Alignment	not modelled	16.8	11	PDB header: dna binding protein Chain: B: PDB Molecule: geobacillus stearothermophilus uvrb interaction domain; PDBTitle: crystal structure of uvra-uvrb interaction domains
66	c2l12A_	Alignment	not modelled	16.7	30	PDB header: transcription regulator Chain: A: PDB Molecule: chromobox homolog 7; PDBTitle: solution nmr structure of the chromobox protein 7 with h3k9me3
67	c3p8dB_	Alignment	not modelled	16.6	17	PDB header: protein binding Chain: B: PDB Molecule: medulloblastoma antigen mu-mb-50.72; PDBTitle: crystal structure of the second tudor domain of human phf20 (homodimer2 form)
68	d1x3pa1	Alignment	not modelled	15.9	36	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
69	c4bxsV_	Alignment	not modelled	15.5	42	PDB header: blood clotting Chain: V: PDB Molecule: venom prothrombin activator psetuarin-c non-catalytic PDBTitle: crystal structure of the prothrombinase complex from the2 venom of pseudonaja textilis
70	c2l6nA_	Alignment	not modelled	15.4	12	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yp_001092504.1; PDBTitle: nmr solution structure of the protein yp_001092504.1
71	c2lccA_	Alignment	not modelled	14.8	18	PDB header: transcription Chain: A: PDB Molecule: at-rich interactive domain-containing protein 4a; PDBTitle: solution structure of rbbp1 chromobarrel domain
72	c4haeA_	Alignment	not modelled	14.7	30	PDB header: protein binding Chain: A: PDB Molecule: chromodomain y-like protein 2; PDBTitle: crystal structure of the cdy12-chromodomain
73	c3pt9A_	Alignment	not modelled	14.6	20	PDB header: transferase Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 1; PDBTitle: crystal structure of mouse dnmt1(731-1602) in the free state
74	c2dnvA_	Alignment	not modelled	14.6	26	PDB header: transcription Chain: A: PDB Molecule: chromobox protein homolog 8; PDBTitle: solution structure of rsgi ruh-055, a chromo domain from2 mus musculus cdna
75	c4dowA_	Alignment	not modelled	14.0	27	PDB header: replication Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: structure of mouse orc1 bah domain bound to h4k20me2
76	c3lweA_	Alignment	not modelled	13.9	30	PDB header: cell cycle Chain: A: PDB Molecule: m-phase phosphoprotein 8; PDBTitle: the crystal structure of mpp8
77	d2j5wa1	Alignment	not modelled	13.8	33	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
78	c3mtsA_	Alignment	not modelled	13.6	15	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase suv39h1; PDBTitle: chromo domain of human histone-lysine n-methyltransferase suv39h1
79	c4qucA_	Alignment	not modelled	13.5	30	PDB header: protein binding Chain: A: PDB Molecule: re36324p; PDBTitle: crystal structure of chromodomain of rhino
						Fold: Cupredoxin-like

80	d2j5wa4	Alignment	not modelled	13.3	42	Superfamily: Cupredoxins Family: Multidomain cupredoxins
81	c4y9vA	Alignment	not modelled	13.1	35	PDB header: lyase Chain: A; PDB Molecule: particle-associated lyase; PDBTitle: gp54 tailspike of acinetobacter baumannii bacteriophage ap22 in2 complex with a. baumannii capsular saccharide
82	d2ix0a2	Alignment	not modelled	13.1	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
83	d2adza1	Alignment	not modelled	12.2	20	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
84	d1nxza1	Alignment	not modelled	12.2	18	Fold: PUA domain-like Superfamily: PUA domain-like Family: Yggj N-terminal domain-like
85	c2m2IA	Alignment	not modelled	12.2	26	PDB header: nuclear protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of entamoeba histolytica hp1 chromodomain
86	d1g6za	Alignment	not modelled	11.8	32	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
87	c4dfcC	Alignment	not modelled	11.8	12	PDB header: hydrolase/dna binding protein Chain: C; PDB Molecule: transcription-repair-coupling factor; PDBTitle: core uvra/trcf complex
88	d2j5wa3	Alignment	not modelled	11.8	33	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
89	c2r7eB	Alignment	not modelled	11.6	25	PDB header: blood clotting Chain: B; PDB Molecule: coagulation factor viii; PDBTitle: crystal structure analysis of coagulation factor viii
90	d2vv5a1	Alignment	not modelled	11.5	22	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
91	d2dnta1	Alignment	not modelled	11.4	37	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
92	c5tvzA	Alignment	not modelled	11.1	22	PDB header: transport protein Chain: A; PDB Molecule: nucleoporin pom152; PDBTitle: solution nmr structure of saccharomyces cerevisiae pom152 ig-like2 repeat, residues 718-820
93	c3h91B	Alignment	not modelled	11.1	30	PDB header: transcription Chain: B; PDB Molecule: chromobox protein homolog 2; PDBTitle: crystal structure of the complex of human chromobox homolog 2 (cbx2)2 and h3k27 peptide
94	d1mhna	Alignment	not modelled	11.1	17	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
95	c2rvmA	Alignment	not modelled	10.8	21	PDB header: transcription Chain: A; PDB Molecule: chromobox protein homolog 5; PDBTitle: solution structure of the chromodomain of hp1alpha with the2 phosphorylated n-terminal tail
96	c1ufiD	Alignment	not modelled	10.6	67	PDB header: dna binding protein Chain: D; PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of the dimerization domain of human cenp-b
97	c3uaiC	Alignment	not modelled	10.4	10	PDB header: isomerase/chaperone Chain: C; PDB Molecule: h/aca ribonucleoprotein complex subunit 1; PDBTitle: structure of the shq1-cbf5-nop10-gar1 complex from saccharomyces2 cerevisiae
98	c2xk0A	Alignment	not modelled	10.4	17	PDB header: transcription Chain: A; PDB Molecule: polycomb protein pcl; PDBTitle: solution structure of the tudor domain from drosophila2 polycomblake (pcl)
99	d1ufia	Alignment	not modelled	10.4	67	Fold: ROP-like Superfamily: Dimerisation domain of CENP-B Family: Dimerisation domain of CENP-B