



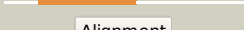

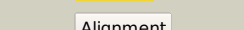

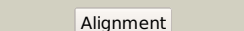
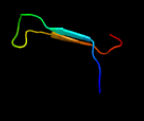



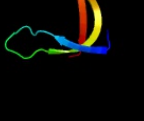
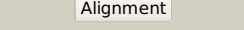

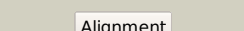

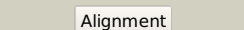
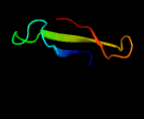


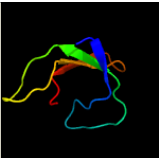

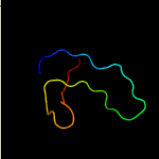
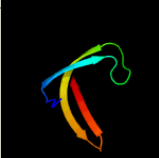
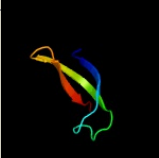
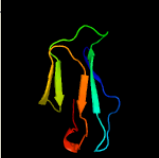

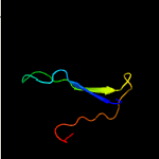
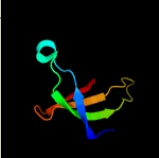


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2302_(-)_2573823_2574065
Date	Mon Aug 5 13:25:44 BST 2019
Unique Job ID	bd27ee881b857f29

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2a7yA_	 Alignment		100.0	100	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	100	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Rv2302-like
3	c2ekoA_	 Alignment		82.2	24	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		77.6	37	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
5	c6d7yA_	 Alignment		77.6	33	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
6	c3qiiA_	 Alignment		77.5	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
7	c5znpB_	 Alignment		72.4	21	PDB header: gene regulation Chain: B: PDB Molecule: short life family protein; PDBTitle: crystal structure of ptshl in complex with an h3k4me3 peptide
8	d1fcga2	 Alignment		69.7	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
9	d2ix0a1	 Alignment		68.5	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
10	c1w4sA_	 Alignment		65.7	21	PDB header: nuclear protein Chain: A: PDB Molecule: polybromo 1 protein; PDBTitle: crystal structure of the proximal bah domain of polybromo
11	c3qz9D_	 Alignment		59.6	26	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.

12	c1xnii_	Alignment		56.4	26	PDB header: cell cycle Chain: I: PDB Molecule: tumor suppressor p53-binding protein 1; PDBTitle: tandem tudor domain of 53bp1
13	c4bb7A_	Alignment		55.1	18	PDB header: transcription Chain: A: PDB Molecule: chromatin structure-remodeling complex subunit rsc2; PDBTitle: crystal structure of the yeast rsc2 bah domain
14	d1ugpb_	Alignment		49.6	18	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
15	d1v6za1	Alignment		48.2	31	Fold: PUA domain-like Superfamily: PUA domain-like Family: Yggj N-terminal domain-like
16	d2f5ka1	Alignment		47.6	14	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
17	d2fcba2	Alignment		47.1	14	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
18	c2ro0A_	Alignment		46.4	17	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase esa1; PDBTitle: solution structure of the knotted tudor domain of the yeast2 histone acetyltransferase, esa1
19	d1f2qa2	Alignment		46.1	12	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
20	c2equA_	Alignment		43.7	20	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
21	c2qqsB_	Alignment	not modelled	43.1	16	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
22	c5in1A_	Alignment	not modelled	43.1	14	PDB header: transcription Chain: A: PDB Molecule: mrg701; PDBTitle: crystal structure of the mrg701 chromodomain
23	c4fsxB_	Alignment	not modelled	41.7	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
24	c4uc4A_	Alignment	not modelled	40.5	18	PDB header: replication Chain: A: PDB Molecule: lysine-specific demethylase 4b; PDBTitle: crystal structure of hybrid tudor domain of human lysine demethylase2 kdm4b
25	c2dxcG_	Alignment	not modelled	40.1	18	PDB header: hydrolase Chain: G: PDB Molecule: thiocyanate hydrolase subunit alpha; PDBTitle: recombinant thiocyanate hydrolase, fully-matured form
26	d1wgsa_	Alignment	not modelled	38.3	18	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
27	c2lrqA_	Alignment	not modelled	37.9	9	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
28	c2ldmA_	Alignment	not modelled	35.0	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
29	c2rnzA_	Alignment	not modelled	34.3	22	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase esa1; PDBTitle: solution structure of the presumed chromodomain of the2 yeast histone acetyltransferase, esa1
30	c4fm4D_	Alignment	not modelled	34.0	21	PDB header: lyase Chain: D: PDB Molecule: nitrile hydratase beta subunit; PDBTitle: wild type fe-type nitrile hydratase from comamonas testosteroni ni1
31	c4pl6A_	Alignment	not modelled	33.4	16	PDB header: transcription Chain: A: PDB Molecule: at1g02740; PDBTitle: structure of the chromodomain of mrg2 in complex with h3k4me3
32	c2e5qA_	Alignment	not modelled	33.4	19	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]
33	c3dlmA_	Alignment	not modelled	33.4	15	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
34	c1u9pA_	Alignment	not modelled	31.7	36	PDB header: unknown function Chain: A: PDB Molecule: parc; PDBTitle: permuted single-chain arc
35	c3luuA_	Alignment	not modelled	31.3	20	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
36	c3p8dB_	Alignment	not modelled	30.4	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)
37	c2e5pA_	Alignment	not modelled	29.2	23	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)
38	c5n1tM_	Alignment	not modelled	27.3	60	PDB header: oxidoreductase Chain: M: PDB Molecule: copc; PDBTitle: crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
39	c2d9uA_	Alignment	not modelled	27.0	33	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
40	c2lccA_	Alignment	not modelled	25.6	24	PDB header: transcription Chain: A: PDB Molecule: at-rich interactive domain-containing protein 4a; PDBTitle: solution structure of rbbp1 chromobarrel domain
41	d2z1ca1	Alignment	not modelled	23.5	40	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
42	d2qdyb1	Alignment	not modelled	23.2	23	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
43	c4a4fA_	Alignment	not modelled	23.2	21	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
44	c2xdpA_	Alignment	not modelled	23.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: lysine-specific demethylase 4c; PDBTitle: crystal structure of the tudor domain of human jmjd2c
45	d2ot2a1	Alignment	not modelled	21.8	30	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
46	d1v29b_	Alignment	not modelled	21.8	25	Fold: SH3-like barrel Superfamily: Electron transport accessory proteins Family: Nitrile hydratase beta chain
47	d1vk3a3	Alignment	not modelled	21.6	29	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
48	c5icuA_	Alignment	not modelled	21.4	42	PDB header: chaperone Chain: A: PDB Molecule: copc; PDBTitle: the crystal structure of copc from methylosinus trichosporium ob3b
49	d2c9qa1	Alignment	not modelled	21.0	40	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Copper resistance protein C (CopC, PcoC)
50	c3j4uA_	Alignment	not modelled	20.7	27	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
51	d1pfba_	Alignment	not modelled	20.1	35	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
52	c2v3mF_	Alignment	not modelled	19.5	21	PDB header: ribosomal protein Chain: F: PDB Molecule: naf1; PDBTitle: structure of the gar1 domain of naf1
53	c1q3lA_	Alignment	not modelled	19.0	33	PDB header: structural protein Chain: A: PDB Molecule: heterochromatin protein 1; PDBTitle: chromodomain of hp1 complexed with histone h3 tail2 containing monomethyllysine 9.
						Fold: SH3-like barrel

54	d1q3la_	Alignment	not modelled	19.0	33	Superfamily: Chromo domain-like Family: Chromo domain
55	c1g5vA_	Alignment	not modelled	18.7	20	PDB header: translation Chain: A: PDB Molecule: survival motor neuron protein 1; PDBTitle: solution structure of the tudor domain of the human smn2 protein
56	c2k1bA_	Alignment	not modelled	18.4	33	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
57	d2dnva1	Alignment	not modelled	18.4	29	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
58	d1guwa_	Alignment	not modelled	17.9	22	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
59	c3pt9A_	Alignment	not modelled	17.3	22	PDB header: transferase Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 1; PDBTitle: crystal structure of mouse dnmt1(731-1602) in the free state
60	d3d3ra1	Alignment	not modelled	16.9	27	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
61	c2l6pA_	Alignment	not modelled	16.9	15	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
62	c5e4wD_	Alignment	not modelled	16.8	37	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
63	c4bxsV_	Alignment	not modelled	16.8	33	PDB header: blood clotting Chain: V: PDB Molecule: venom prothrombin activator pseutarin-c non-catalytic PDBTitle: crystal structure of the prothrombinase complex from the2 venom of pseudonaja textilis
64	d2ix0a2	Alignment	not modelled	16.7	15	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
65	c3fdtA_	Alignment	not modelled	16.7	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
66	c3d3rA_	Alignment	not modelled	16.6	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
67	d2j5wa1	Alignment	not modelled	16.4	33	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
68	d2j5wa4	Alignment	not modelled	15.9	42	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
69	c2eqjA_	Alignment	not modelled	15.8	8	PDB header: transcription Chain: A: PDB Molecule: metal-response element-binding transcription PDBTitle: solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
70	c1ssfA_	Alignment	not modelled	15.7	23	PDB header: cell cycle Chain: A: PDB Molecule: transformation related protein 53 binding PDBTitle: solution structure of the mouse 53bp1 fragment (residues2 1463-1617)
71	c2l12A_	Alignment	not modelled	15.7	33	PDB header: transcription regulator Chain: A: PDB Molecule: chromobox homolog 7; PDBTitle: solution nmr structure of the chromobox protein 7 with h3k9me3
72	c1pdqA_	Alignment	not modelled	15.5	39	PDB header: structural protein Chain: A: PDB Molecule: polycomb protein; PDBTitle: polycomb chromodomain complexed with the histone h3 tail2 containing trimethyllysine 27.
73	c3mtsA_	Alignment	not modelled	15.4	17	PDB header: transferase Chain: A: PDB Molecule: histone-lysine n-methyltransferase suv39h1; PDBTitle: chromo domain of human histone-lysine n-methyltransferase suv39h1
74	c2kvmA_	Alignment	not modelled	15.4	33	PDB header: transcription Chain: A: PDB Molecule: chromobox protein homolog 7; PDBTitle: solution structure of the cbx7 chromodomain in complex with a h3k27me22 peptide
75	d1nxza1	Alignment	not modelled	15.1	25	Fold: PUA domain-like Superfamily: PUA domain-like Family: Yggj N-terminal domain-like
76	c3uaiC_	Alignment	not modelled	14.8	13	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
77	c2dnvA_	Alignment	not modelled	14.3	29	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
78	d2j5wa3	Alignment	not modelled	14.2	42	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
						Fold: Sm-like fold

79	d2vv5a1	Alignment	not modelled	13.6	22	Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
80	c2r7eB	Alignment	not modelled	13.6	33	PDB header: blood clotting Chain: B; PDB Molecule: coagulation factor viii; PDBTitle: crystal structure analysis of coagulation factor viii
81	c2l6nA	Alignment	not modelled	13.4	18	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
82	c2lcdA	Alignment	not modelled	13.2	33	PDB header: transcription Chain: A; PDB Molecule: at-rich interactive domain-containing protein 4a; PDBTitle: solution structure of rbbp1 tudor domain
83	c4haeA	Alignment	not modelled	13.2	33	PDB header: protein binding Chain: A; PDB Molecule: chromodomain y-like protein 2; PDBTitle: crystal structure of the cdy12-chromodomain
84	d1x3pa1	Alignment	not modelled	13.0	36	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
85	c4dowA	Alignment	not modelled	13.0	24	PDB header: replication Chain: A; PDB Molecule: origin recognition complex subunit 1; PDBTitle: structure of mouse orc1 bah domain bound to h4k20me2
86	c3lweA	Alignment	not modelled	12.6	33	PDB header: cell cycle Chain: A; PDB Molecule: m-phase phosphoprotein 8; PDBTitle: the crystal structure of mpp8
87	c3dkmA	Alignment	not modelled	11.8	11	PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase hectd1; PDBTitle: crystal structure of the hectd1 cph domain
88	c6bs8C	Alignment	not modelled	11.7	27	PDB header: hydrolase Chain: C; PDB Molecule: replicative dna helicase; PDBTitle: the class 3 dnaB intein from mycobacterium smegmatis
89	c2eqnA	Alignment	not modelled	11.0	32	PDB header: transcription Chain: A; PDB Molecule: hypothetical protein loc92345; PDBTitle: solution structure of the naf1 domain of hypothetical2 protein bc008207 [homo sapiens]
90	c3fpnB	Alignment	not modelled	10.9	11	PDB header: dna binding protein Chain: B; PDB Molecule: geobacillus stearothermophilus uvrb interaction domain; PDBTitle: crystal structure of uvra-uvrb interaction domains
91	d1d7ya3	Alignment	not modelled	10.7	15	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
92	c4qucA	Alignment	not modelled	10.7	30	PDB header: protein binding Chain: A; PDB Molecule: re36324p; PDBTitle: crystal structure of chromodomain of rhino
93	d1ix2a	Alignment	not modelled	10.7	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Copper resistance protein C (CopC, PcoC)
94	c2m2IA	Alignment	not modelled	10.5	29	PDB header: nuclear protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of entamoeba histolytica hp1 chromodomain
95	c3pifD	Alignment	not modelled	10.4	13	PDB header: hydrolase Chain: D; PDB Molecule: 5'->3' exoribonuclease (xrn1); PDBTitle: crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
96	c4y9vA	Alignment	not modelled	10.3	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
97	d1mhna	Alignment	not modelled	10.3	20	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
98	c6npcB	Alignment	not modelled	10.3	24	PDB header: oxidoreductase Chain: B; PDB Molecule: tmpa, 2-trimethylaminoethylphosphonate hydroxylase; PDBTitle: x-ray crystal structure of tmpa, 2-trimethylaminoethylphosphonate2 hydroxylase, with fe, 2og, and 2-trimethylaminoethylphosphonate
99	c3h91B	Alignment	not modelled	10.2	33	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