

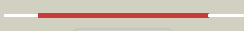






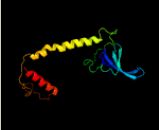

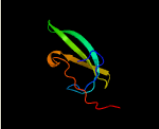





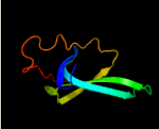






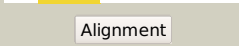


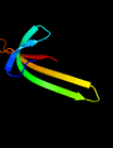
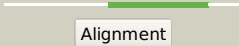
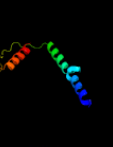






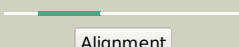
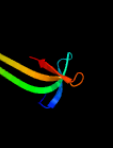
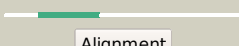
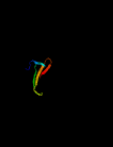
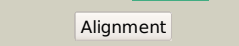

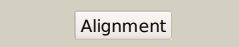
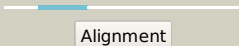



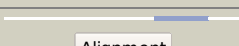



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3583c_(-)_4025235_4025723
Date	Fri Aug 9 18:20:26 BST 2019
Unique Job ID	57ccda42585a512d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2lwjA_	 Alignment		100.0	32	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, card family; PDBTitle: nmr solution structure myxococcus xanthus cdnl
2	c4l5gA_	 Alignment		100.0	25	PDB header: transcription Chain: A: PDB Molecule: card; PDBTitle: crystal structure of thermus thermophilus card
3	c4kmbB_	 Alignment		100.0	99	PDB header: transferase/transcription Chain: B: PDB Molecule: rna polymerase-binding transcription factor card; PDBTitle: structure of the mtb card/rnap beta subunit b1-b2 domains complex
4	c2lt3A_	 Alignment		99.9	33	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, card family; PDBTitle: solution nmr structure of the c-terminal domain of cdnl from2 myxococcus xanthus
5	c2eyqA_	 Alignment		99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of escherichia coli transcription-repair2 coupling factor
6	c2lt4A_	 Alignment		99.8	29	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, card family; PDBTitle: cdnlnt from myxococcus xanthus
7	c2lt1A_	 Alignment		99.8	31	PDB header: transcription Chain: A: PDB Molecule: card protein; PDBTitle: solution nmr structure of the 72-residue n-terminal domain of2 myxococcus xanthus card
8	c2lqkA_	 Alignment		99.8	29	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator; PDBTitle: nmr solution structure of the n-terminal domain of the cdnl protein2 from thermus thermophilus
9	d2eyqa1	 Alignment		99.6	23	Fold: SH3-like barrel Superfamily: CarD-like Family: CarD-like
10	c3mlqE_	 Alignment		98.1	27	PDB header: transferase/transcription Chain: E: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain
11	c3mlqH_	 Alignment		98.0	24	PDB header: transferase/transcription Chain: H: PDB Molecule: transcription-repair coupling factor; PDBTitle: crystal structure of the thermus thermophilus transcription-repair2 coupling factor rna polymerase interacting domain with the thermus3 aquaticus rna polymerase beta1 domain

12	c5dmaA	 Alignment		94.2	29	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pcra; PDBTitle: crystal structure of c-terminal tudor domain in pcra/uvrd helicase
13	c3t9nG	 Alignment		70.0	24	PDB header: membrane protein Chain: G: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: crystal structure of a membrane protein
14	d2vv5a1	 Alignment		52.5	24	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
15	d2eyqa3	 Alignment		52.1	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
16	d1in4a1	 Alignment		49.5	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain
17	c2lrqA	 Alignment		49.5	22	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
18	c6au8A	 Alignment		48.9	16	PDB header: chaperone Chain: A: PDB Molecule: golgi to er traffic protein 4 homolog; PDBTitle: 1.8 angstrom crystal structure of the human bag6-nls & trc35 complex
19	c2vv5D	 Alignment		44.0	24	PDB header: membrane protein Chain: D: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: the open structure of mscs
20	c4hw9E	 Alignment		42.7	27	PDB header: membrane protein Chain: E: PDB Molecule: mechanosensitive channel mscs; PDBTitle: crystal structure of helicobacter pylori mscs (closed state)
21	c6ghbB	 Alignment	not modelled	40.1	14	PDB header: protein binding Chain: B: PDB Molecule: upf0413 protein gk0824; PDBTitle: crystal structure of spx in complex with yjbh (oxidized)
22	c5y4oA	 Alignment	not modelled	40.1	27	PDB header: membrane protein Chain: A: PDB Molecule: low conductance mechanosensitive channel ynai; PDBTitle: cryo-em structure of mscs channel, ynai
23	d1aono	 Alignment	not modelled	36.4	29	Fold: GroES-like Superfamily: GroES-like Family: GroES
24	c3nx6A	 Alignment	not modelled	35.7	37	PDB header: chaperone Chain: A: PDB Molecule: 10kda chaperonin; PDBTitle: crystal structure of co-chaperonin, groes (xoo4289) from xanthomonas2 oryzae pv. oryzae kacc10331
25	d1vbva1	 Alignment	not modelled	34.9	14	Fold: SH3-like barrel Superfamily: YccV-like Family: YccV-like
26	d1p3ha	 Alignment	not modelled	31.0	30	Fold: GroES-like Superfamily: GroES-like Family: GroES
27	d1lepa	 Alignment	not modelled	29.2	33	Fold: GroES-like Superfamily: GroES-like Family: GroES
28	d1ixrc1	 Alignment	not modelled	29.1	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain
29	c5in1A	 Alignment	not modelled	27.9	24	PDB header: transcription Chain: A: PDB Molecule: mrg701;

						PDBTitle: crystal structure of the mrg701 chromodomain
30	c1w4sA	Alignment	not modelled	27.1	24	PDB header: nuclear protein Chain: A: PDB Molecule: polybromo 1 protein; PDBTitle: crystal structure of the proximal bah domain of polybromo
31	c4pl6A	Alignment	not modelled	26.1	21	PDB header: transcription Chain: A: PDB Molecule: at1g02740; PDBTitle: structure of the chromodomain of mrg2 in complex with h3k4me3
32	c2wvpG	Alignment	not modelled	25.5	15	PDB header: protein binding Chain: G: PDB Molecule: upf0363 protein yor164c; PDBTitle: crystal structure of s. cerevisiae get4-get5 complex
33	d1j20a2	Alignment	not modelled	25.3	23	Fold: Argininosuccinate synthetase, C-terminal domain Superfamily: Argininosuccinate synthetase, C-terminal domain Family: Argininosuccinate synthetase, C-terminal domain
34	d1vl2a2	Alignment	not modelled	24.1	18	Fold: Argininosuccinate synthetase, C-terminal domain Superfamily: Argininosuccinate synthetase, C-terminal domain Family: Argininosuccinate synthetase, C-terminal domain
35	d1we3o	Alignment	not modelled	22.8	35	Fold: GroES-like Superfamily: GroES-like Family: GroES
36	c4pj1V	Alignment	not modelled	22.3	33	PDB header: chaperone Chain: V: PDB Molecule: 10 kda heat shock protein, mitochondrial; PDBTitle: crystal structure of the human mitochondrial chaperonin symmetrical2 'football' complex
37	d1k92a2	Alignment	not modelled	21.6	25	Fold: Argininosuccinate synthetase, C-terminal domain Superfamily: Argininosuccinate synthetase, C-terminal domain Family: Argininosuccinate synthetase, C-terminal domain
38	d2i5nh1	Alignment	not modelled	21.6	18	Fold: PRC-barrel domain Superfamily: PRC-barrel domain Family: Photosynthetic reaction centre, H-chain, cytoplasmic domain
39	d1iz6a1	Alignment	not modelled	21.4	16	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
40	c5xonW	Alignment	not modelled	21.1	17	PDB header: transcription/rna Chain: W: PDB Molecule: protein that forms a complex with spt4p; PDBTitle: rna polymerase ii elongation complex bound with spt4/5 and tfiis
41	c3e20C	Alignment	not modelled	20.9	8	PDB header: translation Chain: C: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
42	d2f5ka1	Alignment	not modelled	20.0	24	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo barrel domain
43	c3pnwX	Alignment	not modelled	18.6	15	PDB header: protein binding/immune system Chain: X: PDB Molecule: tudor domain-containing protein 3; PDBTitle: crystal structure of the tudor domain of human tdrd3 in complex with2 an anti-tdrd3 fab
44	d2eifa1	Alignment	not modelled	18.2	20	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
45	c4ytiB	Alignment	not modelled	17.7	20	PDB header: transcription Chain: B: PDB Molecule: transcription elongation factor spt5; PDBTitle: structure of the kow2-kow3 domain of transcription elongation factor2 spt5.
46	c3qtmB	Alignment	not modelled	17.6	19	PDB header: translation Chain: B: PDB Molecule: uncharacterized protein c4b3.07; PDBTitle: structure of s. pombe nuclear import adaptor nro1 (space group p21)
47	d2cwya1	Alignment	not modelled	17.1	22	Fold: Hyaluronidase domain-like Superfamily: TTHA0068-like Family: TTHA0068-like
48	c2ymyB	Alignment	not modelled	16.7	17	PDB header: apoptosis Chain: B: PDB Molecule: ras association domain-containing protein 5; PDBTitle: structure of the murine nore1-sarah domain
49	c2lcIA	Alignment	not modelled	16.4	21	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator rfah; PDBTitle: solution structure of rfah carboxyterminal domain
50	c3nojA	Alignment	not modelled	15.2	32	PDB header: lyase Chain: A: PDB Molecule: 4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate PDBTitle: the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
51	c2ko4A	Alignment	not modelled	15.2	12	PDB header: transcription Chain: A: PDB Molecule: mediator of rna polymerase ii transcription subunit 15; PDBTitle: complex structure of the activation domain of gcn4 bound to the2 mediator co-activator domain of gal11/med15
52	d1dt9a3	Alignment	not modelled	14.7	11	Fold: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Superfamily: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 Family: N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1
53	d2ijqa1	Alignment	not modelled	14.7	14	Fold: Hyaluronidase domain-like Superfamily: TTHA0068-like Family: TTHA0068-like
54	d1ku3a	Alignment	not modelled	14.4	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
						Fold: SH3-like barrel

55	d1nppa2	Alignment	not modelled	13.8	13	Superfamily: Translation proteins SH3-like domain Family: N-utilization substance G protein NusG, C-terminal domain
56	c1k97A	Alignment	not modelled	13.4	25	PDB header: ligase Chain: A: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
57	d1bkba1	Alignment	not modelled	13.3	25	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
58	c2fq0B	Alignment	not modelled	12.8	35	PDB header: hydrolase Chain: B: PDB Molecule: cog0791: cell wall-associated hydrolases (invasion- PDBTitle: crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
59	c3j21R	Alignment	not modelled	12.7	57	PDB header: ribosome Chain: R: PDB Molecule: 50s ribosomal protein l21e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
60	c4d10C	Alignment	not modelled	12.6	8	PDB header: signaling protein Chain: C: PDB Molecule: cop9 signalosome complex subunit 3; PDBTitle: crystal structure of the cop9 signalosome
61	d1ttya	Alignment	not modelled	12.5	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
62	d2do3a1	Alignment	not modelled	12.4	71	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: SPT5 KOW domain-like
63	d1ixsb1	Alignment	not modelled	12.2	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Helicase DNA-binding domain
64	d1vqoq1	Alignment	not modelled	12.1	43	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
65	c5znpB	Alignment	not modelled	12.1	26	PDB header: gene regulation Chain: B: PDB Molecule: short life family protein; PDBTitle: crystal structure of ptshl in complex with an h3k4me3 peptide
66	d1ku7a	Alignment	not modelled	12.1	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
67	d7odca1	Alignment	not modelled	11.7	21	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Alanine racemase C-terminal domain-like Family: Eukaryotic ODC-like
68	c1zljE	Alignment	not modelled	11.5	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
69	c3sztB	Alignment	not modelled	11.3	26	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
70	c2e6zA	Alignment	not modelled	11.1	57	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt5; PDBTitle: solution structure of the second kow motif of human2 transcription elongation factor spt5
71	d2p7vb1	Alignment	not modelled	11.0	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma4 domain
72	c4u7jB	Alignment	not modelled	10.9	18	PDB header: ligase Chain: B: PDB Molecule: argininosuccinate synthase; PDBTitle: crystal structure of argininosuccinate synthase from mycobacterium2 thermoresistibile
73	d1a04a1	Alignment	not modelled	10.9	14	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)
74	d1x6oa1	Alignment	not modelled	10.6	18	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
75	c6n1fD	Alignment	not modelled	10.5	50	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, 2og-fe(ii) oxygenase family; PDBTitle: crystal structure of oxidoreductase, 2og-fe(ii) oxygenase family, from2 burkholderia pseudomallei
76	c2zkrq	Alignment	not modelled	10.4	57	PDB header: ribosomal protein/rna Chain: Q: PDB Molecule: rna expansion segment es31 part ii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
77	c5gjqS	Alignment	not modelled	10.3	17	PDB header: hydrolase Chain: S: PDB Molecule: 26s proteasome non-atpase regulatory subunit 3; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
78	c4a4fA	Alignment	not modelled	10.2	20	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
79	c5a5tM	Alignment	not modelled	9.9	4	PDB header: hydrolase Chain: M: PDB Molecule: eukaryotic translation initiation factor 3 subunit m; PDBTitle: structure of mammalian eif3 in the context of the 43s

						preinitiation2 complex
80	c2krfB_	Alignment	not modelled	9.8	17	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
81	d1ed7a_	Alignment	not modelled	9.7	27	Fold: WW domain-like Superfamily: Carbohydrate binding domain Family: Carbohydrate binding domain
82	c1s1iO_	Alignment	not modelled	9.7	71	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l21-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
83	c3q1jA_	Alignment	not modelled	9.7	13	PDB header: transcription Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 1 of human phd finger protein 20
84	c2lxA_	Alignment	not modelled	9.4	50	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase i subunit e; PDBTitle: solution structure of hp1264 from helicobacter pylori
85	d1khca_	Alignment	not modelled	9.3	16	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
86	d1l3la1	Alignment	not modelled	9.2	21	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)
87	c3lpzA_	Alignment	not modelled	9.1	21	PDB header: protein transport Chain: A: PDB Molecule: get4 (yor164c homolog); PDBTitle: crystal structure of c. therm. get4
88	c3lrA_	Alignment	not modelled	9.0	13	PDB header: transferase Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: crystal structure of the pwwp domain of human dna (cytosine-5-)-2 methyltransferase 3 alpha
89	c3mb5A_	Alignment	not modelled	8.9	44	PDB header: transferase Chain: A: PDB Molecule: sam-dependent methyltransferase; PDBTitle: crystal structure of p. abyssi trna m1a58 methyltransferase in complex2 with s-adenosyl-l-methionine
90	c4v1ak_	Alignment	not modelled	8.6	38	PDB header: ribosome Chain: K: PDB Molecule: PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 22 of 2
91	d1eyba_	Alignment	not modelled	8.5	36	Fold: Double-stranded beta-helix Superfamily: RmC-like cupins Family: Homogentisate dioxygenase
92	c1ey2A_	Alignment	not modelled	8.5	36	PDB header: oxidoreductase Chain: A: PDB Molecule: homogentisate 1,2-dioxygenase; PDBTitle: human homogentisate dioxygenase with fe(ii)
93	c2dxcG_	Alignment	not modelled	8.5	63	PDB header: hydrolase Chain: G: PDB Molecule: thiocyanate hydrolase subunit alpha; PDBTitle: recombinant thiocyanate hydrolase, fully-matured form
94	d2nlua1	Alignment	not modelled	8.3	18	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: PWWP domain
95	c6jqSA_	Alignment	not modelled	8.1	7	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: structure of transcription factor, gere
96	d2cp5a1	Alignment	not modelled	8.1	15	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
97	c3cpfB_	Alignment	not modelled	7.9	9	PDB header: cell cycle Chain: B: PDB Molecule: eukaryotic translation initiation factor 5a-1; PDBTitle: crystal structure of human eukaryotic translation initiation factor2 eif5a
98	c2d49A_	Alignment	not modelled	7.9	33	PDB header: hydrolase Chain: A: PDB Molecule: chitinase c; PDBTitle: solution structure of the chitin-binding domain of2 streptomyces griseus chitinase c
99	c6nr84_	Alignment	not modelled	7.9	18	PDB header: chaperone Chain: 4: PDB Molecule: prefoldin subunit 4; PDBTitle: htric-hpfd class6