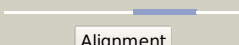
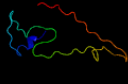
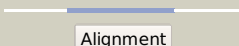

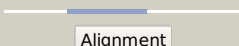

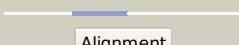

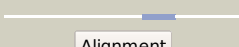
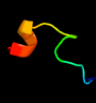
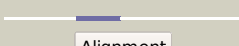

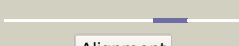











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3349c_(-)_3754464_3755204
Date	Thu Aug 8 16:20:56 BST 2019
Unique Job ID	c8ce6958f02edec8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4r4zD_	 Alignment		28.9	24	PDB header: hydrolase Chain: D; PDB Molecule: pngf-ii; PDBTitle: structure of pngf-ii in p21 space group
2	c1yt3A_	 Alignment		25.9	18	PDB header: hydrolase,translation Chain: A; PDB Molecule: ribonuclease d; PDBTitle: crystal structure of escherichia coli rnase d, an2 exoribonuclease involved in structured rna processing
3	d1yt3a1	 Alignment		23.3	18	Fold: SAM domain-like Superfamily: HRDC-like Family: RNase D C-terminal domains
4	c3u0kA_	 Alignment		22.9	14	PDB header: fluorescent protein Chain: A; PDB Molecule: rcamp; PDBTitle: crystal structure of the genetically encoded calcium indicator rcamp
5	d3deoa1	 Alignment		21.6	53	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
6	c3sztB_	 Alignment		19.8	6	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
7	c5twaD_	 Alignment		19.4	48	PDB header: apoptosis Chain: D; PDB Molecule: bak-2 protein; PDBTitle: crystal structure of geodia cydonium bhp2 in complex with lubomirskia2 baicalensis bak-2
8	d1f54a_	 Alignment		19.2	13	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
9	c5twaC_	 Alignment		18.4	48	PDB header: apoptosis Chain: C; PDB Molecule: bak-2 protein; PDBTitle: crystal structure of geodia cydonium bhp2 in complex with lubomirskia2 baicalensis bak-2
10	c5jffD_	 Alignment		18.4	21	PDB header: transferase Chain: D; PDB Molecule: uncharacterized protein yhfg; PDBTitle: e. coli ecfct mutant g55r in complex with ecfca
11	c4wwaB_	 Alignment		16.2	17	PDB header: transferase Chain: B; PDB Molecule: rekc/keops complex subunit cgj121; PDBTitle: crystal structure of binary complex bud32-cgj121

12	c5jw9A_	Alignment		14.8	53	PDB header: protein binding Chain: A: PDB Molecule: af4/fmr2 family member 4; PDBTitle: the crystal structure of ell2 ocludin domain and aff4 peptide
13	c3cymA_	Alignment		13.0	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bad_0989; PDBTitle: crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
14	d1yioa1	Alignment		12.6	10	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)
15	c2kukA_	Alignment		12.5	80	PDB header: antiviral protein Chain: A: PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
16	c5ly5A_	Alignment		12.1	60	PDB header: unknown function Chain: A: PDB Molecule: arcadin-1; PDBTitle: arcadin-1 from pyrobaculum calidifontis
17	c6irtA_	Alignment		12.0	33	PDB header: membrane protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: human lat1-4f2hc complex bound with bch
18	c4ct0B_	Alignment		11.9	40	PDB header: circadian clock protein Chain: B: PDB Molecule: period circadian protein homolog 2; PDBTitle: crystal structure of mouse cryptochrome1 in complex with period2
19	c2amiA_	Alignment		11.6	13	PDB header: cell cycle Chain: A: PDB Molecule: caltractin; PDBTitle: solution structure of the calcium-loaded n-terminal sensor domain of2 centrin
20	c3enpA_	Alignment		11.1	33	PDB header: hydrolase Chain: A: PDB Molecule: tp53rk-binding protein; PDBTitle: crystal structure of human cgi121
21	c2zpnB_	Alignment	not modelled	11.1	26	PDB header: protein transport Chain: B: PDB Molecule: autophagy-related protein 8; PDBTitle: the crystal structure of saccharomyces cerevisiae atg8-2 atg19(412-415) complex
22	c3k1qE_	Alignment	not modelled	11.1	35	PDB header: PDB COMPND:
23	c6cfwK_	Alignment	not modelled	11.0	32	PDB header: membrane protein Chain: K: PDB Molecule: membrane-bound hydrogenase subunit beta; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
24	c4i2yB_	Alignment	not modelled	10.7	14	PDB header: fluorescent protein Chain: B: PDB Molecule: rgeco1; PDBTitle: crystal structure of the genetically encoded calcium indicator rgeco1
25	c2ipcB_	Alignment	not modelled	10.7	41	PDB header: transport protein Chain: B: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
26	c3w1yA_	Alignment	not modelled	10.4	26	PDB header: transport protein/ribosomal protein Chain: A: PDB Molecule: microtubule-associated protein 1a/1b, light chain 3; PDBTitle: crystal structure of t brucei atg8.2 in complex with e coli s10
27	c1nl3B_	Alignment	not modelled	10.4	41	PDB header: protein transport Chain: B: PDB Molecule: preprotein translocase seca 1 subunit; PDBTitle: crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
28	c1zljE_	Alignment	not modelled	10.1	16	PDB header: transcription Chain: E: PDB Molecule: dormancy survival regulator; PDBTitle: crystal structure of the mycobacterium tuberculosis

						hypoxic2 response regulator dosr c-terminal domain
29	c5f5tD_	Alignment	not modelled	10.1	42	PDB header: splicing Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the prp38-mfap1 complex of chaetomium2 thermophilum
30	c2yskA_	Alignment	not modelled	10.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ttha1432; PDBTitle: crystal structure of a hypothetical protein ttha1432 from thermus2 thermophilus
31	c2w6bA_	Alignment	not modelled	9.8	25	PDB header: signaling protein Chain: A: PDB Molecule: rho guanine nucleotide exchange factor 7; PDBTitle: crystal structure of the trimeric beta-pix coiled-coil2 domain
32	c2krfB_	Alignment	not modelled	9.8	9	PDB header: transcription Chain: B: PDB Molecule: transcriptional regulatory protein coma; PDBTitle: nmr solution structure of the dna binding domain of competence protein2 a
33	c5camC_	Alignment	not modelled	9.7	18	PDB header: transcription Chain: C: PDB Molecule: pupr protein; PDBTitle: crystal structure of the cytoplasmic domain of the pseudomonas putida2 anti-sigma factor pupr (semet)
34	d1dvja_	Alignment	not modelled	9.7	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
35	d1nwwa_	Alignment	not modelled	9.5	25	Fold: Cystatin-like Superfamily: NTF2-like Family: Limonene-1,2-epoxide hydrolase-like
36	c6humJ_	Alignment	not modelled	9.3	27	PDB header: proton transport Chain: J: PDB Molecule: nad(p)h-quinone oxidoreductase subunit j; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
37	c5jxdA_	Alignment	not modelled	9.3	14	PDB header: immune system Chain: A: PDB Molecule: tumor necrosis factor alpha-induced protein 8; PDBTitle: crystal structure of murine tnfaip8 c165s mutant
38	c3me5A_	Alignment	not modelled	9.3	46	PDB header: transferase Chain: A: PDB Molecule: cytosine-specific methyltransferase; PDBTitle: crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 2457t
39	c4uz0B_	Alignment	not modelled	8.8	42	PDB header: apoptosis Chain: B: PDB Molecule: nucleolar protein 3; PDBTitle: crystal structure of apoptosis repressor with card (arc)
40	c5tz0B_	Alignment	not modelled	8.8	40	PDB header: protein binding Chain: B: PDB Molecule: fluorescence recovery protein; PDBTitle: structure of the fremyella diplosiphon fluorescence recovery protein
41	d1sw8a_	Alignment	not modelled	8.8	13	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
42	c2vdaA_	Alignment	not modelled	8.7	35	PDB header: protein transport Chain: A: PDB Molecule: translocase subunit seca; PDBTitle: solution structure of the seca-signal peptide complex
43	c3pt9A_	Alignment	not modelled	8.6	57	PDB header: transferase Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 1; PDBTitle: crystal structure of mouse dnmt1(731-1602) in the free state
44	c3r9jD_	Alignment	not modelled	8.6	26	PDB header: cell cycle,hydrolase/cell cycle Chain: D: PDB Molecule: cell division topological specificity factor; PDBTitle: 4.3a resolution structure of a mind-mine(i24n) protein complex
45	c2ynqD_	Alignment	not modelled	8.4	19	PDB header: membrane protein Chain: D: PDB Molecule: essb; PDBTitle: crystal structure of geobacillus thermodenitrificans essb2 extracellular fragment
46	d2fug51	Alignment	not modelled	8.3	23	Fold: Nqo5-like Superfamily: Nqo5-like Family: Nqo5-like
47	c3evrA_	Alignment	not modelled	8.3	14	PDB header: signaling protein Chain: A: PDB Molecule: myosin light chain kinase, green fluorescent protein, PDBTitle: crystal structure of calcium bound monomeric gcamp2
48	c6honB_	Alignment	not modelled	8.2	25	PDB header: gene regulation Chain: B: PDB Molecule: ccr4-not transcription complex subunit 4, isoform I; PDBTitle: drosophila not4 cbm peptide bound to human caf40
49	c6homB_	Alignment	not modelled	8.2	25	PDB header: gene regulation Chain: B: PDB Molecule: ccr4-not transcription complex subunit 4, isoform I; PDBTitle: drosophila not4 cbm peptide bound to human caf40
50	c6honD_	Alignment	not modelled	8.2	25	PDB header: gene regulation Chain: D: PDB Molecule: ccr4-not transcription complex subunit 4, isoform I; PDBTitle: drosophila not4 cbm peptide bound to human caf40
51	c2qrvA_	Alignment	not modelled	8.2	20	PDB header: transferase/transferase regulator Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 3a; PDBTitle: structure of dnmt3a-dnmt3l c-terminal domain complex
52	c5f5uB_	Alignment	not modelled	8.1	42	PDB header: splicing Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
53	c5f5uH_	Alignment	not modelled	8.1	42	PDB header: splicing Chain: H: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the snu23-prp38-mfap1(217-258) complex of2 chaetomium thermophilum
54	c3mcrA_	Alignment	not modelled	8.1	27	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase, subunit c; PDBTitle: crystal structure of nadh dehydrogenase subunit c (tfu_2693) from2 thermobifida fusca yx-er1 at 2.65 a resolution

55	c6aagF_	Alignment	not modelled	8.1	26	PDB header: membrane protein Chain: F; PDB Molecule: transmembrane protein 184 homolog ykr051w,autophagy-related PDBTitle: crystal structure of budding yeast atg8 complexed with the helical aim2 of hfl1.
56	c6homD_	Alignment	not modelled	8.0	25	PDB header: gene regulation Chain: D; PDB Molecule: ccr4-not transcription complex subunit 4, isoform I; PDBTitle: drosophila not4 cbm peptide bound to human caf40
57	d3d32a1	Alignment	not modelled	7.9	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: GABARAP-like
58	d1n0ya_	Alignment	not modelled	7.9	15	Fold: EF Hand-like Superfamily: EF-hand Family: Calmodulin-like
59	c3n70F_	Alignment	not modelled	7.8	12	PDB header: transport protein Chain: F; PDB Molecule: transport activator; PDBTitle: the crystal structure of the p-loop ntpase domain of the sigma-542 transport activator from e. coli to 2.8a
60	c3f09B_	Alignment	not modelled	7.7	14	PDB header: transferase Chain: B; PDB Molecule: holo-[acyl-carrier-protein] synthase; PDBTitle: 1.82 angstrom resolution crystal structure of holo-(acyl-carrier-2 protein) synthase (acps) from staphylococcus aureus
61	d1klva_	Alignment	not modelled	7.7	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: GABARAP-like
62	c2mn1A_	Alignment	not modelled	7.6	80	PDB header: unknown function Chain: A; PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
63	c1h0mD_	Alignment	not modelled	7.5	16	PDB header: transcription/dna Chain: D; PDB Molecule: transcriptional activator protein trar; PDBTitle: three-dimensional structure of the quorum sensing protein trar bound2 to its autoinducer and to its target dna
64	c6gnxB_	Alignment	not modelled	7.5	55	PDB header: structural protein Chain: B; PDB Molecule: telomere repeats-binding bouquet formation protein 2; PDBTitle: crystal structure of the majin-terb2 heterotetrameric complex -2 selenomethionine derivative
65	c6gnyD_	Alignment	not modelled	7.4	55	PDB header: structural protein Chain: D; PDB Molecule: telomere repeats-binding bouquet formation protein 2; PDBTitle: crystal structure of the majin-terb2 heterotetrameric complex
66	c2kt5B_	Alignment	not modelled	7.1	71	PDB header: rna binding protein / viral protein Chain: B; PDB Molecule: icp27; PDBTitle: rrm domain of mrna export adaptor ref2-i bound to hsv-1 icp27 peptide
67	c1yybA_	Alignment	not modelled	7.1	28	PDB header: apoptosis Chain: A; PDB Molecule: programmed cell death protein 5; PDBTitle: solution structure of 1-26 fragment of human programmed2 cell death 5 protein
68	d1ykha1	Alignment	not modelled	7.0	47	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: MED7 hinge region
69	c6gboG_	Alignment	not modelled	7.0	54	PDB header: viral protein Chain: G; PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of the oligomerization domain of vp35 from ebola2 virus
70	c3vwwB_	Alignment	not modelled	7.0	21	PDB header: protein transport Chain: B; PDB Molecule: microtubule-associated proteins 1a/1b light chain 3c; PDBTitle: ndp52 in complex with lc3c
71	c4uecB_	Alignment	not modelled	6.9	57	PDB header: translation Chain: B; PDB Molecule: eukaryotic translation initiation factor 4g, isoform a; PDBTitle: complex of d. melanogaster eif4e with eif4g and cap analog
72	c4fsxB_	Alignment	not modelled	6.8	46	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
73	c1jhnA_	Alignment	not modelled	6.8	32	PDB header: chaperone Chain: A; PDB Molecule: calnexin; PDBTitle: crystal structure of the luminal domain of calnexin
74	c3dinB_	Alignment	not modelled	6.5	41	PDB header: membrane protein, protein transport Chain: B; PDB Molecule: protein translocase subunit seca; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
75	d2fd6u3	Alignment	not modelled	6.5	41	Fold: Snake toxin-like Superfamily: Snake toxin-like Family: Extracellular domain of cell surface receptors
76	c4jdxB_	Alignment	not modelled	6.5	40	PDB header: protein binding Chain: B; PDB Molecule: slr1964 protein; PDBTitle: structure of the fluorescence recovery protein from synechocystis sp2 pcc 6803
77	c2gj0A_	Alignment	not modelled	6.5	60	PDB header: plant protein Chain: A; PDB Molecule: cycloviolacin o14; PDBTitle: cycloviolacin o14
78	c1vw4c_	Alignment	not modelled	6.5	20	PDB header: ribosome Chain: C; PDB Molecule: PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
79	d2zjda1	Alignment	not modelled	6.5	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: GABARAP-like
						PDB header: transcription

80	c2rniA	Alignment	not modelled	6.5	17	Chain: A: PDB Molecule: response regulator protein vvar; PDBTitle: nmr structure of the s. aureus vvar dna binding domain
81	c2k7bA	Alignment	not modelled	6.4	12	PDB header: metal binding protein Chain: A: PDB Molecule: calcium-binding protein 1; PDBTitle: nmr structure of mg2+-bound cabp1 n-domain
82	d1lyva	Alignment	not modelled	6.4	18	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Higher-molecular-weight phosphotyrosine protein phosphatases
83	c2xv9A	Alignment	not modelled	6.3	8	PDB header: lipid binding protein Chain: A: PDB Molecule: aba-1a1 repeat unit; PDBTitle: the solution structure of aba-1a saturated with oleic acid
84	c6a0cB	Alignment	not modelled	6.3	62	PDB header: structural protein Chain: B: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii
85	d1a04a1	Alignment	not modelled	6.2	13	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)
86	c3juxA	Alignment	not modelled	6.2	41	PDB header: protein transport Chain: A: PDB Molecule: protein translocase subunit seca; PDBTitle: structure of the translocation atpase seca from thermotoga2 maritima
87	d1ftha	Alignment	not modelled	6.1	13	Fold: 4'-phosphopantetheinyl transferase Superfamily: 4'-phosphopantetheinyl transferase Family: Holo-(acyl carrier protein) synthase ACPS
88	c5u0pG	Alignment	not modelled	6.1	41	PDB header: transcription Chain: G: PDB Molecule: mediator complex subunit 7; PDBTitle: cryo-em structure of the transcriptional mediator
89	c4z9vG	Alignment	not modelled	6.1	77	PDB header: apoptosis Chain: G: PDB Molecule: translationally-controlled tumor protein; PDBTitle: tctp contains a bh3-like domain, which instead of inhibiting,2 activates bcl-xl
90	d1l3la1	Alignment	not modelled	6.0	15	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)
91	c1x3uA	Alignment	not modelled	6.0	17	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein fixj; PDBTitle: solution structure of the c-terminal transcriptional2 activator domain of fixj from sinorhizobium melilot
92	c4ifuA	Alignment	not modelled	6.0	12	PDB header: dna binding protein Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: crystal structure of escherichia coli sdia in the space group c2
93	c3lx6B	Alignment	not modelled	5.9	43	PDB header: transferase Chain: B: PDB Molecule: cytosine-specific methyltransferase; PDBTitle: crystal structure of putative dna cytosine methylase from shigella2 flexneri 2a str. 2457t
94	c5xxuY	Alignment	not modelled	5.9	23	PDB header: ribosome Chain: Y: PDB Molecule: ribosomal protein es24; PDBTitle: small subunit of toxoplasma gondii ribosome
95	c1ej6D	Alignment	not modelled	5.9	22	PDB header: virus Chain: D: PDB Molecule: sigma2; PDBTitle: reovirus core
96	c6gbrA	Alignment	not modelled	5.7	46	PDB header: viral protein Chain: A: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of the oligomerization domain of vp35 from reston2 virus, mercury derivative
97	c5aj3k	Alignment	not modelled	5.7	50	PDB header: ribosome Chain: K: PDB Molecule: mitoribosomal protein us11m, mrps11; PDBTitle: structure of the small subunit of the mammalian mitoribosome
98	c2kgrA	Alignment	not modelled	5.7	20	PDB header: protein binding Chain: A: PDB Molecule: intersectin-1; PDBTitle: solution structure of protein itsn1 from homo sapiens.2 northeast structural genomics consortium target hr5524a
99	c6a0cA	Alignment	not modelled	5.7	62	PDB header: structural protein Chain: A: PDB Molecule: collagen type iii peptide; PDBTitle: structure of a triple-helix region of human collagen type iii