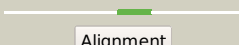

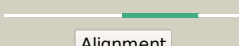
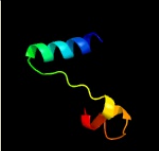
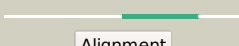
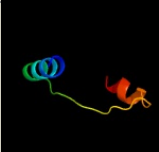
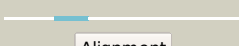

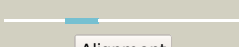
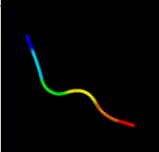

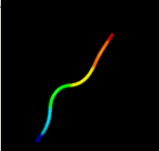




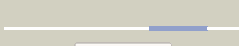
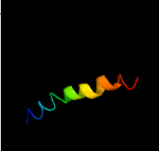

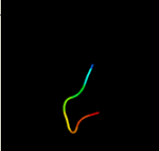




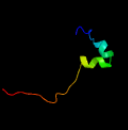
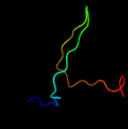
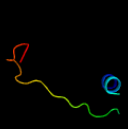


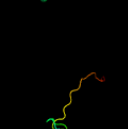



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2274c (-)_2546498_2546815
Date	Mon Aug 5 13:25:41 BST 2019
Unique Job ID	78d9a27be31fa8c4

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f8xM_	 Alignment		53.2	82	PDB header: transcription/dna Chain: M: PDB Molecule: mastermind-like protein 1; PDBTitle: crystal structure of activated notch, csl and mam1 on hes-12 promoter dna sequence
2	d2p10a1	 Alignment		42.0	39	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: MII9387-like
3	c2p10D_	 Alignment		41.9	39	PDB header: hydrolase Chain: D: PDB Molecule: mll9387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
4	d1wgea1	 Alignment		33.2	38	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
5	c2nudD_	 Alignment		31.5	100	PDB header: toxin/protein binding Chain: D: PDB Molecule: rpm1-interacting protein 4; PDBTitle: the structure of the type iii effector avrb complexed with2 a high-affinity rin4 peptide
6	c2nudC_	 Alignment		31.5	100	PDB header: toxin/protein binding Chain: C: PDB Molecule: rpm1-interacting protein 4; PDBTitle: the structure of the type iii effector avrb complexed with2 a high-affinity rin4 peptide
7	c2jr7A_	 Alignment		29.0	43	PDB header: metal binding protein Chain: A: PDB Molecule: dph3 homolog; PDBTitle: solution structure of human desr1
8	d1ywsa1	 Alignment		28.5	38	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
9	c1xnlA_	 Alignment		24.9	44	PDB header: viral protein Chain: A: PDB Molecule: membrane protein gp37; PDBTitle: aslv fusion peptide
10	c5wb8B_	 Alignment		24.5	78	PDB header: signaling protein Chain: B: PDB Molecule: epigen; PDBTitle: crystal structure of the epidermal growth factor receptor2 extracellular region in complex with epigen
11	d1h4ua2	 Alignment		23.0	67	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-like domain of nidogen-1

12	d3pmga4	Alignment		22.8	37	Fold: TBP-like Superfamily: Phosphoglucosyltransferase, C-terminal domain Family: Phosphoglucosyltransferase, C-terminal domain
13	d1kfia4	Alignment		21.9	37	Fold: TBP-like Superfamily: Phosphoglucosyltransferase, C-terminal domain Family: Phosphoglucosyltransferase, C-terminal domain
14	c4i3rG	Alignment		19.2	46	PDB header: viral protein/immune system Chain: G: PDB Molecule: outer domain of hiv-1 gp120 (ker2018 od4.2.2); PDBTitle: crystal structure of the outer domain of hiv-1 gp120 in complex with2 vrc-pg04 space group p3221
15	c3j3iA	Alignment		18.9	56	PDB header: virus Chain: A: PDB Molecule: capsid protein; PDBTitle: penicillium chrysogenum virus (pcv) capsid structure
16	d5ruba1	Alignment		15.7	21	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
17	c9rubB	Alignment		14.8	25	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase; PDBTitle: crystal structure of activated ribulose-1,5-bisphosphate carboxylase2 complexed with its substrate, ribulose-1,5-bisphosphate
18	c3ctrA	Alignment		14.6	23	PDB header: hydrolase Chain: A: PDB Molecule: poly(a)-specific ribonuclease parn; PDBTitle: crystal structure of the rrm-domain of the poly(a)-specific2 ribonuclease parn bound to m7gtp
19	c3dnoC	Alignment		13.5	50	PDB header: viral protein Chain: C: PDB Molecule: hiv-1 envelope glycoprotein gp120; PDBTitle: molecular structure for the hiv-1 gp120 trimer in the cd4-bound state
20	d1ixsa	Alignment		13.1	50	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
21	d2gp4a1	Alignment	not modelled	12.9	25	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: IlvD/EDD C-terminal domain-like
22	c6m8rL	Alignment	not modelled	12.6	35	PDB header: protein binding Chain: L: PDB Molecule: gamma-aminobutyric acid type b receptor subunit 2; PDBTitle: crystal structure of the kctd16 btb domain in complex with gabab22 peptide
23	c6m8rK	Alignment	not modelled	12.4	35	PDB header: protein binding Chain: K: PDB Molecule: gamma-aminobutyric acid type b receptor subunit 2; PDBTitle: crystal structure of the kctd16 btb domain in complex with gabab22 peptide
24	c2crcA	Alignment	not modelled	12.3	50	PDB header: ligase Chain: A: PDB Molecule: ubiquitin conjugating enzyme 7 interacting PDBTitle: solution structure of the zf-ranbp domain of the protein2 hbv associated factor
25	c1h4uA	Alignment	not modelled	12.0	43	PDB header: extracellular matrix protein Chain: A: PDB Molecule: nidogen-1; PDBTitle: domain g2 of mouse nidogen-1
26	c5v8wG	Alignment	not modelled	11.7	57	PDB header: hydrolase Chain: G: PDB Molecule: integrator complex subunit 9; PDBTitle: crystal structure of human integrator ints9-ints11 ctd complex
27	c2rusB	Alignment	not modelled	11.3	21	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribisco (ribulose-1,5-bisphosphate carboxylase(/slash) PDBTitle: crystal structure of the ternary complex of ribulose-1,5-bisphosphate2 carboxylase, mg(ii), and activator co2 at 2.3-angstroms resolution PDB header: gtp-binding protein

28	c5dn8A_	Alignment	not modelled	10.6	13	Chain: A: PDB Molecule: gtpase der; PDBTitle: 1.76 angstrom crystal structure of gtp-binding protein der from 2 coxiella burnetii in complex with gdp.
29	c1kioA_	Alignment	not modelled	10.5	47	PDB header: hydrolase Chain: A: PDB Molecule: serine protease inhibitor i; PDBTitle: solution structure of the small serine protease inhibitor 2 sgci[130r, k31m]
30	c2l6lA_	Alignment	not modelled	10.5	75	PDB header: chaperone Chain: A: PDB Molecule: dna j homolog subfamily c member 24; PDBTitle: solution structure of human j-protein co-chaperone, dph4
31	d1fo8a_	Alignment	not modelled	10.5	71	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
32	c5e24D_	Alignment	not modelled	10.1	22	PDB header: transport/dna binding/dna Chain: D: PDB Molecule: protein hairless; PDBTitle: structure of the su(h)-hairless-dna repressor complex
33	c2mpjA_	Alignment	not modelled	10.0	55	PDB header: nucleotide binding protein Chain: A: PDB Molecule: recq4-helicase-like protein; PDBTitle: nmr structure of xenopus recq4 zinc knuckle
34	c4djzH_	Alignment	not modelled	9.8	39	PDB header: hydrolase/hydrolase inhibitor Chain: H: PDB Molecule: protease inhibitor sgpi-2; PDBTitle: catalytic fragment of masp-1 in complex with its specific inhibitor 2 developed by directed evolution on sgci scaffold
35	c5a48B_	Alignment	not modelled	9.4	30	PDB header: protein binding Chain: B: PDB Molecule: maternal effect protein oskar; PDBTitle: crystal structure of the lotus domain (aa 139-240) of drosophila 2 oskar in p65
36	d1mjsa_	Alignment	not modelled	9.3	53	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
37	c5c2gD_	Alignment	not modelled	9.3	31	PDB header: lyase Chain: D: PDB Molecule: form ii rubisco; PDBTitle: gws1b rubisco: form ii rubisco derived from uncultivated 2 gallionellacea species (cabp-bound).
38	c2zkgq_	Alignment	not modelled	9.2	50	PDB header: ribosomal protein/rna Chain: N: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex 2 obtained by docking homology models of the rna and proteins into an 3 8.7 a cryo-em map
39	c3ngbl_	Alignment	not modelled	9.1	50	PDB header: viral protein/immune system Chain: I: PDB Molecule: envelope glycoprotein gp160; PDBTitle: crystal structure of broadly and potentially neutralizing antibody vrc012 in complex with hiv-1 gp120
40	c5te4G_	Alignment	not modelled	8.9	50	PDB header: immune system Chain: G: PDB Molecule: hiv-1 clade g strain x2088 gp120; PDBTitle: crystal structure of broadly neutralizing vrc01-class antibody n6 in 2 complex with hiv-1 clade g strain x2088 gp120 core
41	c2yt2A_	Alignment	not modelled	8.6	43	PDB header: signaling protein Chain: A: PDB Molecule: fibroblast growth factor receptor substrate 3 and alk PDBTitle: solution structure of the chimera of the ptb domain of snt-2 and 19-2 residue peptide (aa 1571-1589) of halk
42	c5zwoW_	Alignment	not modelled	8.5	14	PDB header: splicing Chain: W: PDB Molecule: 23 kda u4/u6.u5 small nuclear ribonucleoprotein component; PDBTitle: cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
43	d1lm6a_	Alignment	not modelled	8.4	75	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
44	c3tbmA_	Alignment	not modelled	8.3	50	PDB header: metal binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a type 4 cdgsh iron-sulfur protein.
45	c4r9pA_	Alignment	not modelled	8.3	40	PDB header: transcription Chain: A: PDB Molecule: re28239p; PDBTitle: an expansion to the smad mh2-family: the structure of the n-mh22 expanded domain
46	c5a49l_	Alignment	not modelled	8.2	24	PDB header: protein binding Chain: I: PDB Molecule: maternal effect protein oskar; PDBTitle: crystal structure of the lotus domain (aa 139-222) of 2 drosophila oskar in c222
47	c3b08H_	Alignment	not modelled	8.2	71	PDB header: signaling protein/metal binding protein Chain: H: PDB Molecule: ranbp-type and c3hc4-type zinc finger-containing protein 1; PDBTitle: crystal structure of the mouse hoil1-l-nzf in complex with linear di-2 ubiquitin
48	c1kqiA_	Alignment	not modelled	8.1	50	PDB header: toxin Chain: A: PDB Molecule: actx-hi:ob4219; PDBTitle: nmr solution structure of the trans pro30 isomer of actx-2 hi:ob4219
49	c6ohyA_	Alignment	not modelled	8.1	50	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein gp160; PDBTitle: chimpanzee siv env trimeric ectodomain.
50	c3l87A_	Alignment	not modelled	8.0	78	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: the crystal structure of smu.143c from streptococcus mutans ua159
51	c2hjqA_	Alignment	not modelled	8.0	20	PDB header: hydrolase Chain: A: PDB Molecule: gtp-binding protein enga; PDBTitle: the crystal structure of the b. subtilis yphc gtpase in complex with 2 gdp
52	d1kqha_	Alignment	not modelled	7.8	50	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
53	c3j38P_	Alignment	not modelled	7.6	36	PDB header: ribosome Chain: P: PDB Molecule: 40s ribosomal protein s15, isoform a;

						PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
54	d1ykw1	Alignment	not modelled	7.6	34	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
55	c4kp2A	Alignment	not modelled	7.5	41	PDB header: lyase Chain: A: PDB Molecule: homoaconitase large subunit; PDBTitle: crystal structure of homoaconitase large subunit from methanococcus2 jannaschii (mj1003)
56	d2i9aa1	Alignment	not modelled	7.4	47	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
57	c5vbnB	Alignment	not modelled	7.2	27	PDB header: transferase Chain: B: PDB Molecule: dna polymerase epsilon catalytic subunit a; PDBTitle: crystal structure of human dna polymerase epsilon b-subunit in complex2 with c-terminal domain of catalytic subunit
58	d1yymg1	Alignment	not modelled	7.2	50	Fold: gp120 core Superfamily: gp120 core Family: gp120 core
59	c4nasD	Alignment	not modelled	7.2	28	PDB header: lyase Chain: D: PDB Molecule: ribulose-bisphosphate carboxylase; PDBTitle: the crystal structure of a rubisco-like protein (mtnw) from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
60	c3j8gX	Alignment	not modelled	7.2	30	PDB header: ribosome Chain: X: PDB Molecule: gtpase der; PDBTitle: electron cryo-microscopy structure of enga bound with the 50s2 ribosomal subunit
61	d1kiil	Alignment	not modelled	7.1	46	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
62	d1a8da2	Alignment	not modelled	7.1	30	Fold: beta-Trefoil Superfamily: STI-like Family: Clostridium neurotoxins, C-terminal domain
63	c2bf1A	Alignment	not modelled	7.0	42	PDB header: virus protein Chain: A: PDB Molecule: exterior membrane glycoprotein gp120; PDBTitle: structure of an unliganded and fully-glycosylated siv gp120 envelope2 glycoprotein
64	c3bvoA	Alignment	not modelled	6.9	29	PDB header: chaperone Chain: A: PDB Molecule: co-chaperone protein hscb, mitochondrial precursor; PDBTitle: crystal structure of human co-chaperone protein hscb
65	d1dd1a	Alignment	not modelled	6.8	39	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
66	c6iicD	Alignment	not modelled	6.7	63	PDB header: virus Chain: D: PDB Molecule: vp4 of mud crab dicistrovirus; PDBTitle: cryoem structure of mud crab dicistrovirus
67	c4nclB	Alignment	not modelled	6.7	18	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 5b-like protein; PDBTitle: crystal structure of eukaryotic translation initiation factor eif5b2 (517-970) from chaetomium thermophilum in complex with gdp
68	c3tvjl	Alignment	not modelled	6.6	33	PDB header: hydrolase Chain: I: PDB Molecule: protease inhibitor sgpi-2; PDBTitle: catalytic fragment of masp-2 in complex with its specific inhibitor2 developed by directed evolution on sgci scaffold
69	c3ocaB	Alignment	not modelled	6.6	63	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of peptide deformylase from ehrlichia chaffeensis
70	d1lm4a	Alignment	not modelled	6.6	78	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
71	d1ygsa	Alignment	not modelled	6.5	39	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
72	d1jhna4	Alignment	not modelled	6.4	44	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Calnexin/calreticulin
73	c4kp1A	Alignment	not modelled	6.4	46	PDB header: isomerase Chain: A: PDB Molecule: isopropylmalate/citramalate isomerase large subunit; PDBTitle: crystal structure of ipm isomerase large subunit from methanococcus2 jannaschii (mj0499)
74	c3g6nA	Alignment	not modelled	6.3	78	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of an efpdf complex with met-ala-ser
75	c4uzjB	Alignment	not modelled	6.2	25	PDB header: hydrolase Chain: B: PDB Molecule: notum; PDBTitle: structure of the wnt deacylase notum from drosophila -2 crystal form i - 2.4a
76	d1g7sa4	Alignment	not modelled	6.2	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
77	d1geha1	Alignment	not modelled	6.2	24	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
78	c5j84A	Alignment	not modelled	6.1	36	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form
						Fold: TIM beta/alpha-barrel

79	d1rbla1	Alignment	not modelled	6.1	34	Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
80	c3jwdA	Alignment	not modelled	6.1	50	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 gp120 envelope glycoprotein; PDBTitle: structure of hiv-1 gp120 with gp41-interactive region: layered2 architecture and basis of conformational mobility
81	d1khxa	Alignment	not modelled	6.1	44	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
82	c1kxA	Alignment	not modelled	6.1	44	PDB header: transcription Chain: A: PDB Molecule: smad2; PDBTitle: crystal structure of a phosphorylated smad2
83	d1lqya	Alignment	not modelled	6.1	78	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
84	d1wfla	Alignment	not modelled	6.0	50	Fold: AN1-like Zinc finger Superfamily: AN1-like Zinc finger Family: AN1-like Zinc finger
85	d1khua	Alignment	not modelled	6.0	47	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: SMAD domain
86	d1ju8a	Alignment	not modelled	5.9	60	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Albumin 1
87	c6gzuA	Alignment	not modelled	5.9	42	PDB header: transferase Chain: A: PDB Molecule: conserved membrane protein; PDBTitle: structure of chlamydia abortus effector protein chladub
88	c3g5pB	Alignment	not modelled	5.8	44	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase, mitochondrial; PDBTitle: structure and activity of human mitochondrial peptide deformylase, a2 novel cancer target
89	c3rg0A	Alignment	not modelled	5.7	67	PDB header: chaperone Chain: A: PDB Molecule: calreticulin; PDBTitle: structural and functional relationships between the lectin and arm2 domains of calreticulin
90	d1xeoa1	Alignment	not modelled	5.7	63	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
91	c3r0rA	Alignment	not modelled	5.7	36	PDB header: virus Chain: A: PDB Molecule: porcine circovirus 2 (pcv2) capsid protein; PDBTitle: the 2.3 a structure of porcine circovirus 2
92	c1zy1B	Alignment	not modelled	5.7	100	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase, mitochondrial; PDBTitle: x-ray structure of peptide deformylase from arabidopsis2 thaliana (atpdf1a) in complex with met-ala-ser
93	c5hcfF	Alignment	not modelled	5.6	56	PDB header: chaperone Chain: F: PDB Molecule: calreticulin, putative,calreticulin, putative; PDBTitle: t. cruzi calreticulin globular domain
94	c3fk4A	Alignment	not modelled	5.5	14	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
95	d1bwva1	Alignment	not modelled	5.5	34	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
96	c5tpjA	Alignment	not modelled	5.5	29	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
97	c3uwaA	Alignment	not modelled	5.4	63	PDB header: hydrolase Chain: A: PDB Molecule: riia-riib membrane-associated protein; PDBTitle: crystal structure of a probable peptide deformylase from synechococcus2 phage s-ssm7
98	c5hcaB	Alignment	not modelled	5.4	56	PDB header: sugar binding protein Chain: B: PDB Molecule: calreticulin,calreticulin; PDBTitle: globular domain of the entamoeba histolytica calreticulin in complex2 with glucose
99	d2b4cg1	Alignment	not modelled	5.4	50	Fold: gp120 core Superfamily: gp120 core Family: gp120 core