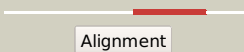



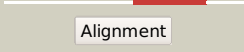

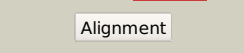
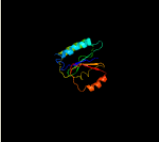


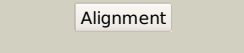

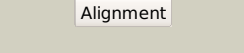


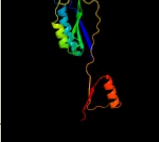
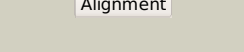
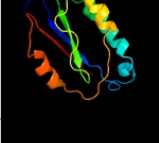
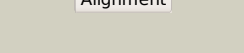
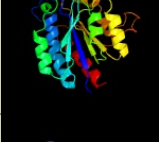
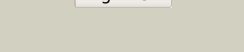
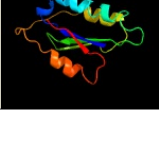


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3163c_(-)_3531639_3532910
Date	Thu Aug 8 16:20:35 BST 2019
Unique Job ID	d9e7d1c983e28df1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6nmiE_	 Alignment		97.9	12	PDB header: transcription Chain: E: PDB Molecule: general transcription factor iih subunit 2, p44; PDBTitle: cryo-em structure of the human tfiih core complex
2	c4fx5A_	 Alignment		97.8	13	PDB header: blood clotting Chain: A: PDB Molecule: von willebrand factor type a; PDBTitle: von willebrand factor type a from catenulispora acidiphila
3	c5oqj6_	 Alignment		97.7	12	PDB header: transcription Chain: 6: PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
4	c6o9l6_	 Alignment		97.7	14	PDB header: transcription/dna Chain: 6: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
5	d1jeyb2	 Alignment		97.6	14	Fold: vWA-like Superfamily: vWA-like Family: Ku80 subunit N-terminal domain
6	c4b4tW_	 Alignment		97.6	18	PDB header: hydrolase Chain: W: PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
7	d1yvra2	 Alignment		97.4	10	Fold: vWA-like Superfamily: vWA-like Family: RoRNP C-terminal domain-like
8	c4rckB_	 Alignment		97.3	17	PDB header: membrane protein Chain: B: PDB Molecule: hypothetical membrane spanning protein; PDBTitle: crystal structure of uncharacterized membrane spanning protein from2 vibrio fischeri
9	c2x31F_	 Alignment		97.3	13	PDB header: ligase Chain: F: PDB Molecule: magnesium-chelatase 60 kda subunit; PDBTitle: modelling of the complex between subunits bchi and bchd of magnesium2 chelatase based on single-particle cryo-em reconstruction at 7.5 ang
10	c3ibsA_	 Alignment		97.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein batb; PDBTitle: crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron
11	c2iueA_	 Alignment		96.8	14	PDB header: membrane protein Chain: A: PDB Molecule: pactolus i-domain; PDBTitle: pactolus i-domain: functional switching of the rossmann2 fold

12	d1jey2	Alignment		96.8	14	Fold: vWA-like Superfamily: vWA-like Family: Ku70 subunit N-terminal domain
13	c5a8jA	Alignment		96.7	13	PDB header: transcription Chain: A; PDB Molecule: vwa2; PDBTitle: crystal structure of the arnb paralog vwa2 from2 sulfobolbus acidocaldarius
14	c4okuA	Alignment		96.6	15	PDB header: cell adhesion Chain: A; PDB Molecule: micronemal protein mic2; PDBTitle: structure of toxoplasma gondii promic2
15	c5gjqW	Alignment		96.5	15	PDB header: hydrolase Chain: W; PDB Molecule: 26s proteasome non-atpase regulatory subunit 4; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
16	c2b2xB	Alignment		96.3	15	PDB header: immune system Chain: B; PDB Molecule: integrin alpha-1; PDBTitle: vla1 rdelta1 i-domain complexed with a quadruple mutant of the aqc22 fab
17	c2i6sA	Alignment		96.3	10	PDB header: hydrolase Chain: A; PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
18	c4cnbA	Alignment		96.2	15	PDB header: structural protein Chain: A; PDB Molecule: proximal thread matrix protein 1; PDBTitle: structure of proximal thread matrix protein 1 (ptmp1) from the2 mussel byssus - crystal form 2
19	c2nvoA	Alignment		96.2	12	PDB header: rna binding protein Chain: A; PDB Molecule: ro sixty-related protein, rsr; PDBTitle: crystal structure of deinococcus radiodurans ro (rsr) protein
20	c6fpzA	Alignment		96.1	13	PDB header: structural protein Chain: A; PDB Molecule: inter-alpha-trypsin inhibitor heavy chain h1; PDBTitle: inter-alpha-inhibitor heavy chain 1, d298a
21	c2ok5A	Alignment	not modelled	95.9	12	PDB header: hydrolase Chain: A; PDB Molecule: complement factor b; PDBTitle: human complement factor b
22	c1jeyB	Alignment	not modelled	95.8	14	PDB header: dna binding protein/dna Chain: B; PDB Molecule: ku80; PDBTitle: crystal structure of the ku heterodimer bound to dna
23	c3n2nC	Alignment	not modelled	95.7	15	PDB header: toxin receptor Chain: C; PDB Molecule: anthrax toxin receptor 1; PDBTitle: the crystal structure of tumor endothelial marker 8 (tem8)2 extracellular domain
24	c4wfqA	Alignment	not modelled	95.4	15	PDB header: transcription Chain: A; PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: crystal structure of tfiih subunit
25	c2x5nA	Alignment	not modelled	95.4	15	PDB header: nuclear protein Chain: A; PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: crystal structure of the sprpn10 vwa domain
26	c1rs0A	Alignment	not modelled	94.8	12	PDB header: hydrolase Chain: A; PDB Molecule: complement factor b; PDBTitle: crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)
27	c4hqkB	Alignment	not modelled	94.7	13	PDB header: cell adhesion Chain: B; PDB Molecule: sporozoite surface protein 2; PDBTitle: crystal structure of manganese-loaded plasmodium vivax trap protein
28	c2xgqB	Alignment	not modelled	94.1	15	PDB header: hydrolase Chain: B; PDB Molecule: microneme protein 2; PDBTitle: structure of toxoplasma gondii micronemal protein 2 a_i2 domain
						PDB header: cell adhesion

29	c5e6rA_	Alignment	not modelled	94.0	13	Chain: A: PDB Molecule: integrin alpha-I; PDBTitle: structures of leukocyte integrin alb2: the ai domain, the headpiece,2 and the pocket for the internal ligand
30	d2ok5a1	Alignment	not modelled	93.5	12	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
31	d1shux_	Alignment	not modelled	93.0	16	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
32	c5gjfF_	Alignment	not modelled	91.9	15	PDB header: membrane protein Chain: F: PDB Molecule: voltage-dependent calcium channel subunit alpha-2/delta-1; PDBTitle: structure of the mammalian voltage-gated calcium channel cav1.12 complex at near atomic resolution
33	c5iy70_	Alignment	not modelled	91.8	11	PDB header: transcription, transferase/dna Chain: 0: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the open state
34	c3txaA_	Alignment	not modelled	90.1	18	PDB header: cell adhesion Chain: A: PDB Molecule: cell wall surface anchor family protein; PDBTitle: structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae
35	c5y58E_	Alignment	not modelled	90.0	10	PDB header: rna binding protein Chain: E: PDB Molecule: atp-dependent dna helicase ii subunit 1; PDBTitle: crystal structure of ku70/80 and tic1
36	c3jbrF_	Alignment	not modelled	89.1	10	PDB header: membrane protein Chain: F: PDB Molecule: voltage-dependent calcium channel subunit alpha-2/delta-1; PDBTitle: cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
37	d1v7pc_	Alignment	not modelled	88.7	16	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
38	d1ck4a_	Alignment	not modelled	88.1	12	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
39	d1pd0a3	Alignment	not modelled	87.1	15	Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
40	c4hqfA_	Alignment	not modelled	86.5	15	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin-related anonymous protein, trap; PDBTitle: crystal structure of plasmodium falciparum trap, i4 form
41	d1u0oc1	Alignment	not modelled	83.7	12	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
42	d1pt6a_	Alignment	not modelled	82.5	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
43	c5y59B_	Alignment	not modelled	81.7	10	PDB header: protein binding Chain: B: PDB Molecule: atp-dependent dna helicase ii subunit 2; PDBTitle: crystal structure of ku80 and sir4
44	c3tw0D_	Alignment	not modelled	81.2	20	PDB header: cell adhesion Chain: D: PDB Molecule: cell wall surface anchor family protein; PDBTitle: structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae
45	d1n3ya_	Alignment	not modelled	81.1	12	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
46	c1jeqA_	Alignment	not modelled	80.9	13	PDB header: dna binding protein Chain: A: PDB Molecule: ku70; PDBTitle: crystal structure of the ku heterodimer
47	c2kl6A_	Alignment	not modelled	80.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
48	d1q0pa_	Alignment	not modelled	78.3	9	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
49	c6djpB_	Alignment	not modelled	76.1	14	PDB header: membrane protein Chain: B: PDB Molecule: integrin beta-8; PDBTitle: integrin alpha-v beta-8 in complex with the fabs 8b8 and 68
50	c1yvrA_	Alignment	not modelled	75.5	11	PDB header: rna binding protein Chain: A: PDB Molecule: 60-kda ss-a/ro ribonucleoprotein; PDBTitle: ro autoantigen
51	d1w8oa1	Alignment	not modelled	75.3	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
52	d1atza_	Alignment	not modelled	72.9	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
53	c3we7A_	Alignment	not modelled	71.1	16	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph0499; PDBTitle: crystal structure of diacetylchitobiose deacetylase from pyrococcus2 horikoshii
54	c3dfmA_	Alignment	not modelled	71.1	15	PDB header: hydrolase Chain: A: PDB Molecule: teicoplanin pseudoaglycone deacetylase orf2; PDBTitle: the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2 PDB header: cell adhesion/immune system

55	c3vi3D_	Alignment	not modelled	71.1	17	Chain: D: PDB Molecule: integrin beta-1; PDBTitle: crystal structure of alpha5beta1 integrin headpiece (ligand-free form)
56	c4ihkA_	Alignment	not modelled	68.7	16	PDB header: cell adhesion Chain: A: PDB Molecule: collagen alpha3(vi); PDBTitle: crystal structure of the collagen vi alpha3 n5 domain r1061q
57	c6bxjA_	Alignment	not modelled	66.9	12	PDB header: cell adhesion Chain: A: PDB Molecule: chimera protein of integrin beta-3 and integrin alpha-l; PDBTitle: structure of a single-chain beta3 integrin
58	c5y58D_	Alignment	not modelled	66.9	9	PDB header: rna binding protein Chain: D: PDB Molecule: atp-dependent dna helicase ii subunit 2; PDBTitle: crystal structure of ku70/80 and tic1
59	c3ragA_	Alignment	not modelled	65.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
60	c3v4pB_	Alignment	not modelled	65.3	21	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-7; PDBTitle: crystal structure of a4b7 headpiece complexed with fab act-1
61	d1mjna_	Alignment	not modelled	64.6	12	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
62	d1mf7a_	Alignment	not modelled	62.8	11	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
63	c5bmoB_	Alignment	not modelled	62.1	16	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein lnmx; PDBTitle: lnmx protein, a putative glcnac-pi de-n-acetylase from streptomyces2 atroolivaceus
64	c5cgzA_	Alignment	not modelled	61.0	9	PDB header: lyase Chain: A: PDB Molecule: 4-oxalmesaconate hydratase; PDBTitle: crystal structure of galb, the 4-carboxy-2-hydroxyumuconate hydratase,2 from pseudomonas putida kt2440
65	d1cfla2	Alignment	not modelled	60.7	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
66	c2kutA_	Alignment	not modelled	59.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of gmr58a from geobacter metallireducens.2 northeast structural genomics consortium target gmr58a
67	d1layra2	Alignment	not modelled	59.1	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
68	d1tyeb2	Alignment	not modelled	58.4	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
69	d1uana_	Alignment	not modelled	57.9	10	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
70	c4um9D_	Alignment	not modelled	53.2	17	PDB header: immune system Chain: D: PDB Molecule: integrin beta-6; PDBTitle: crystal structure of alpha v beta 6 with peptide
71	d1g4ma2	Alignment	not modelled	53.2	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arrestin/Vps26-like
72	c6adqP_	Alignment	not modelled	51.1	25	PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
73	c3gxzbB_	Alignment	not modelled	50.3	13	PDB header: cell adhesion Chain: B: PDB Molecule: von willebrand factor; PDBTitle: crystal structure of vwf a2 domain
74	c3dfiA_	Alignment	not modelled	49.6	15	PDB header: hydrolase Chain: A: PDB Molecule: pseudoaglycone deacetylase dbv21; PDBTitle: the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
75	c2l0dA_	Alignment	not modelled	48.2	16	PDB header: cell adhesion Chain: A: PDB Molecule: cell surface protein; PDBTitle: solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
76	c2ixdB_	Alignment	not modelled	46.8	18	PDB header: hydrolase Chain: B: PDB Molecule: lmbE-related protein; PDBTitle: crystal structure of the putative deacetylase bc1534 from bacillus2 cereus
77	d1ijba_	Alignment	not modelled	46.1	12	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
78	c6bxfA_	Alignment	not modelled	44.8	12	PDB header: cell adhesion Chain: A: PDB Molecule: chimera protein of integrin beta-3 and integrin alpha-l; PDBTitle: crystal structure of an extended b3 integrin l33
79	d1q74a_	Alignment	not modelled	43.8	13	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
80	c1u8cB_	Alignment	not modelled	41.3	15	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: a novel adaptation of the integrin psi domain revealed from its2 crystal structure

81	c1q7tA_	Alignment	not modelled	37.2	14	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein rv1170; PDBTitle: rv1170 (mshb) from mycobacterium tuberculosis
82	c1cf1B_	Alignment	not modelled	34.0	16	PDB header: structural protein Chain: B: PDB Molecule: protein (arrestin); PDBTitle: arrestin from bovine rod outer segments
83	c5z87B_	Alignment	not modelled	33.4	14	PDB header: hydrolase Chain: B: PDB Molecule: emgh1; PDBTitle: structural of a novel b-glucosidase emgh1 at 2.3 angstrom from2 erythrobacter marinus
84	c1jsyA_	Alignment	not modelled	32.2	16	PDB header: signaling protein Chain: A: PDB Molecule: bovine arrestin-2 (full length); PDBTitle: crystal structure of bovine arrestin-2
85	d1h70a_	Alignment	not modelled	31.9	22	Fold: Pentein, beta/alpha-propeller Superfamily: Pentein Family: Dimethylarginine dimethylaminohydrolase DDAH
86	c1ayrA_	Alignment	not modelled	29.3	16	PDB header: sensory transduction Chain: A: PDB Molecule: arrestin; PDBTitle: arrestin from bovine rod outer segments
87	c1g4mA_	Alignment	not modelled	29.0	16	PDB header: signaling protein Chain: A: PDB Molecule: beta-arrestin1; PDBTitle: crystal structure of bovine beta-arrestin 1
88	c2wfbA_	Alignment	not modelled	27.6	9	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative uncharacterized protein orp; PDBTitle: high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
89	c1sujA_	Alignment	not modelled	27.6	10	PDB header: signaling protein Chain: A: PDB Molecule: cone arrestin; PDBTitle: x-ray crystal structure of ambystoma tigrinum cone arrestin
90	c4zlpB_	Alignment	not modelled	24.1	12	PDB header: transcription Chain: B: PDB Molecule: neurogenic locus notch homolog protein 3; PDBTitle: crystal structure of notch3 negative regulatory region
91	d2iea1_	Alignment	not modelled	22.7	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
92	c5jp0A_	Alignment	not modelled	22.0	13	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase bogh3b; PDBTitle: bacteroides ovatus xyloglucan pul gh3b with bound glucose
93	d1uc8a1_	Alignment	not modelled	21.6	10	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Lysine biosynthesis enzyme LysX, N-terminal domain
94	d1im5a_	Alignment	not modelled	21.4	15	Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
95	c5z9sB_	Alignment	not modelled	21.0	12	PDB header: hydrolase Chain: B: PDB Molecule: glycosyl hydrolase family 3 protein; PDBTitle: functional and structural characterization of a beta-glucosidase2 involved in saponin metabolism from intestinal bacteria
96	c1i9mB_	Alignment	not modelled	20.7	13	PDB header: transferase Chain: B: PDB Molecule: protein-glutamine glutamyltransferase e3; PDBTitle: three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
97	c4i3gB_	Alignment	not modelled	20.4	16	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of desr, a beta-glucosidase from streptomyces2 venezuelae in complex with d-glucose.
98	c5k2mG_	Alignment	not modelled	19.7	16	PDB header: biosynthetic protein Chain: G: PDB Molecule: rimk-related lysine biosynthesis protein; PDBTitle: bifunctional lysx/argx from thermococcus kodakarensis with lysw-gamma-2 aaa
99	d1rl2a2_	Alignment	not modelled	19.3	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like