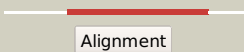

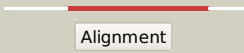

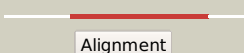

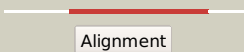

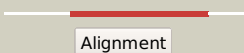
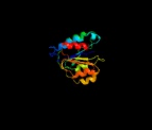
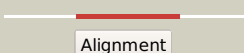

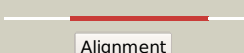
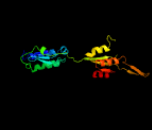




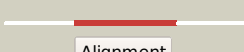
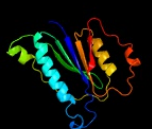
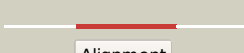












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1480_(-)_1670419_1671372
Date	Fri Aug 2 13:30:06 BST 2019
Unique Job ID	b690f627e68e99c3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ibsA_	 Alignment		99.2	14	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
2	c4fx5A_	 Alignment		99.1	13	PDB header: blood clotting Chain: A; PDB Molecule: von willebrand factor type a; PDBTitle: von willebrand factor type a from catenulispora acidiphila
3	c6nmIE_	 Alignment		98.9	13	PDB header: transcription Chain: E; PDB Molecule: general transcription factor iih subunit 2, p44; PDBTitle: cryo-em structure of the human tfiih core complex
4	c6fpzA_	 Alignment		98.9	10	PDB header: structural protein Chain: A; PDB Molecule: inter-alpha-trypsin inhibitor heavy chain h1; PDBTitle: inter-alpha-inhibitor heavy chain 1, d298a
5	c6o9l6_	 Alignment		98.8	14	PDB header: transcription/dna Chain: 6; PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
6	c5oqj6_	 Alignment		98.6	14	PDB header: transcription Chain: 6; PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
7	c4rckB_	 Alignment		98.6	16	PDB header: membrane protein Chain: B; PDB Molecule: hypothetical membrane spanning protein; PDBTitle: crystal structure of uncharacterized membrane spanning protein from2 vibrio fischeri
8	c2nvoA_	 Alignment		98.6	15	PDB header: rna binding protein Chain: A; PDB Molecule: ro sixty-related protein, rsr; PDBTitle: crystal structure of deinococcus radiodurans ro (rsr) protein
9	d1yvra2	 Alignment		98.5	13	Fold: vWA-like Superfamily: vWA-like Family: RoRNP C-terminal domain-like
10	c5a8jA_	 Alignment		98.4	16	PDB header: transcription Chain: A; PDB Molecule: vwa2; PDBTitle: crystal structure of the arnb paralog vwa2 from2 sulfobolus acidocaldarius
11	c4b4tW_	 Alignment		98.4	16	PDB header: hydrolase Chain: W; PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome

12	c4wfgA	Alignment		98.4	11	PDB header: transcription Chain: A: PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: crystal structure of tfiih subunit
13	c2x31F	Alignment		98.4	14	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
14	c5gjqW	Alignment		98.3	13	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
15	c5iy70	Alignment		98.3	16	PDB header: transcription, transferase/dna Chain: 0: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the open state
16	d1jeyb2	Alignment		98.3	9	Fold: vWA-like Superfamily: vWA-like Family: Ku80 subunit N-terminal domain
17	c2x5nA	Alignment		98.3	14	PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: crystal structure of the sprpn10 vwa domain
18	c1rs0A	Alignment		98.2	16	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)
19	d1jeya2	Alignment		98.2	9	Fold: vWA-like Superfamily: vWA-like Family: Ku70 subunit N-terminal domain
20	c2i6sA	Alignment		98.1	12	PDB header: hydrolase Chain: A: PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
21	c5gjfF	Alignment	not modelled	98.1	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
22	c3jbrF	Alignment	not modelled	98.0	11	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
23	c2iueA	Alignment	not modelled	98.0	10	PDB header: membrane protein Chain: A: PDB Molecule: pactolus i-domain; PDBTitle: pactolus i-domain: functional switching of the rossmann2 fold
24	c2ok5A	Alignment	not modelled	97.9	17	PDB header: hydrolase Chain: A: PDB Molecule: complement factor b; PDBTitle: human complement factor b
25	c4cnbA	Alignment	not modelled	97.7	16	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
26	c4hqnb	Alignment	not modelled	97.7	12	PDB header: cell adhesion Chain: B: PDB Molecule: sporozoite surface protein 2; PDBTitle: crystal structure of manganese-loaded plasmodium vivax trap protein
27	c4okuA	Alignment	not modelled	97.7	7	PDB header: cell adhesion Chain: A: PDB Molecule: micronemal protein mic2; PDBTitle: structure of toxoplasma gondii promic2
28	c3n2nC	Alignment	not modelled	97.6	12	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
29	d2ok5a1	Alignment	not modelled	97.6	14	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
30	d1pd0a3	Alignment	not modelled	97.3	14	Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
31	c1jeyB_	Alignment	not modelled	97.3	7	PDB header: dna binding protein/dna Chain: B: PDB Molecule: ku80; PDBTitle: crystal structure of the ku heterodimer bound to dna
32	c5e6rA_	Alignment	not modelled	97.3	12	PDB header: cell adhesion 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
33	c6bxjA_	Alignment	not modelled	97.3	14	PDB header: cell adhesion Chain: A: PDB Molecule: chimera protein of integrin beta-3 and integrin alpha-I; PDBTitle: structure of a single-chain beta3 integrin
34	c3txaA_	Alignment	not modelled	97.3	14	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	c1yvrA_	Alignment	not modelled	97.2	14	PDB header: rna binding protein Chain: A: PDB Molecule: 60-kda ss-a/ro ribonucleoprotein; PDBTitle: ro autoantigen
36	d1shux_	Alignment	not modelled	97.1	14	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
37	c6bxfA_	Alignment	not modelled	97.1	14	PDB header: cell adhesion Chain: A: PDB Molecule: chimera protein of integrin beta-3 and integrin alpha-I; PDBTitle: crystal structure of an extended b3 integrin I33
38	c2b2xB_	Alignment	not modelled	97.1	11	PDB header: immune system Chain: B: PDB Molecule: integrin alpha-1; PDBTitle: vla1 rdelta i-domain complexed with a quadruple mutant of the aqc22 fab
39	c2xggB_	Alignment	not modelled	97.0	12	PDB header: hydrolase Chain: B: PDB Molecule: microneme protein 2; PDBTitle: structure of toxoplasma gondii micronemal protein 2 a_i2 domain
40	d1q0pa_	Alignment	not modelled	96.8	19	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
41	c6djpB_	Alignment	not modelled	96.5	9	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
42	c3tw0D_	Alignment	not modelled	96.5	13	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
43	d1ck4a_	Alignment	not modelled	96.5	10	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
44	d1v7pc_	Alignment	not modelled	96.5	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
45	d1pt6a_	Alignment	not modelled	96.3	11	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
46	d1atza_	Alignment	not modelled	96.0	15	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
47	c4ihkA_	Alignment	not modelled	95.8	11	PDB header: cell adhesion Chain: A: PDB Molecule: collagen alpha3(vi); PDBTitle: crystal structure of the collagen vi alpha3 n5 domain r1061q
48	c1jeqA_	Alignment	not modelled	95.6	11	PDB header: dna binding protein Chain: A: PDB Molecule: ku70; PDBTitle: crystal structure of the ku heterodimer
49	c5y58E_	Alignment	not modelled	95.5	6	PDB header: rna binding protein Chain: E: PDB Molecule: atp-dependent dna helicase ii subunit 1; PDBTitle: crystal structure of ku70/80 and tlc1
50	c3vi3D_	Alignment	not modelled	95.3	13	PDB header: cell adhesion/immune system Chain: D: PDB Molecule: integrin beta-1; PDBTitle: crystal structure of alpha5beta1 integrin headpiece (ligand-free form)
51	d1tyeb2	Alignment	not modelled	94.7	11	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
52	d1mjna_	Alignment	not modelled	94.7	14	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
53	c4um9D_	Alignment	not modelled	94.7	15	PDB header: immune system Chain: D: PDB Molecule: integrin beta-6; PDBTitle: crystal structure of alpha v beta 6 with peptide
54	c3ragA_	Alignment	not modelled	94.5	16	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
55	c4hpfA_	Alignment	not modelled	94.5	17	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin-related anonymous

55	c4nq1A_	Alignment	not modelled	94.3	17	protein, trap; PDBTitle: crystal structure of plasmodium falciparum trap, i4 form
56	c3gxbB_	Alignment	not modelled	94.2	11	PDB header: cell adhesion Chain: B: PDB Molecule: von willebrand factor; PDBTitle: crystal structure of vwf a2 domain
57	c3fcuB_	Alignment	not modelled	93.8	11	PDB header: cell adhesion/blood clotting Chain: B: PDB Molecule: integrin beta-3; PDBTitle: structure of headpiece of integrin aiibb3 in open conformation
58	d1u0oc1	Alignment	not modelled	93.8	11	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
59	c3v4pB_	Alignment	not modelled	93.6	16	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-7; PDBTitle: crystal structure of a4b7 headpiece complexed with fab act-1
60	d1ijba_	Alignment	not modelled	92.8	11	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
61	d1mf7a_	Alignment	not modelled	92.4	5	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
62	d1n3ya_	Alignment	not modelled	91.4	11	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
63	c1u8cB_	Alignment	not modelled	86.5	13	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
64	c6nmiF_	Alignment	not modelled	85.1	14	PDB header: transcription Chain: F: PDB Molecule: general transcription factor tiih subunit 3, p34; PDBTitle: cryo-em structure of the human tiih core complex
65	c3ijeB_	Alignment	not modelled	84.4	12	PDB header: protein binding Chain: B: PDB Molecule: integrin beta-3; PDBTitle: crystal structure of the complete integrin alphavbeta3 ectodomain plus2 an alpha/beta transmembrane fragment
66	c5y59B_	Alignment	not modelled	84.1	14	PDB header: protein binding Chain: B: PDB Molecule: atp-dependent dna helicase ii subunit 2; PDBTitle: crystal structure of ku80 and sir4
67	c5y58D_	Alignment	not modelled	81.9	18	PDB header: rna binding protein Chain: D: PDB Molecule: atp-dependent dna helicase ii subunit 2; PDBTitle: crystal structure of ku70/80 and tic1
68	c1pd0A_	Alignment	not modelled	74.0	18	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the copii coat subunit, sec24,2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
69	c3k6sB_	Alignment	not modelled	65.1	9	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-2; PDBTitle: structure of integrin alphaxbeta2 ectodomain
70	c6gvwD_	Alignment	not modelled	59.7	5	PDB header: signaling protein Chain: D: PDB Molecule: brisc and brca1-a complex member 1; PDBTitle: crystal structure of the brca1-a complex
71	c3eh2B_	Alignment	not modelled	55.1	17	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24c; PDBTitle: crystal structure of the human copii-coat protein sec24c
72	c4pn7A_	Alignment	not modelled	51.3	12	PDB header: transcription Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of the tiih p34 n-terminal domain
73	c3eg9B_	Alignment	not modelled	46.3	18	PDB header: protein transport Chain: B: PDB Molecule: sec24 related gene family, member d; PDBTitle: crystal structure of the mammalian copii-coat protein sec23/24 bound2 to the transport signal sequence of membrin
74	c4zy8D_	Alignment	not modelled	24.0	19	PDB header: transport protein Chain: D: PDB Molecule: protein Ist4; PDBTitle: k. lactis Ist4 longin domain
75	d1np7a2	Alignment	not modelled	21.8	15	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
76	d1chma1	Alignment	not modelled	21.8	11	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain
77	c1m2vB_	Alignment	not modelled	21.8	19	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
78	d1owla2	Alignment	not modelled	20.3	17	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
79	c4v34A_	Alignment	not modelled	18.7	13	PDB header: transferase Chain: A: PDB Molecule: alanyl-trna-dependent l-alanyl-phosphatidylglycerol PDBTitle: the structure of a-pgs from pseudomonas aeruginosa (semet derivative)
80	c3egxB_	Alignment	not modelled	18.1	12	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24a; PDBTitle: crystal structure of the mammalian copii-coat protein sec23a/24a2 complexed with the snare protein sec22b and bound to the transport3 signal sequence of the snare protein bet1
						PDB header: ribosome Chain: C: PDB Molecule: 50s ribosomal protein l2; PDBTitle: crystal structure of the bacterial ribosome from

81	c2z4lC_	Alignment	not modelled	16.7	16	escherichia coli in2 complex with paromomycin and ribosome recycling factor (rrf). this3 file contains the 50s subunit of the first 70s ribosome, with4 paromomycin and rrf bound. the entire crystal structure contains two5 70s ribosomes and is described in remark 400.
82	c1m2oA_	Alignment	not modelled	16.3	12	PDB header: protein transport/signaling protein Chain: A: PDB Molecule: protein transport protein sec23; PDBTitle: crystal structure of the sec23-sar1 complex
83	d2qtva3	Alignment	not modelled	16.3	15	Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
84	c5oqj4_	Alignment	not modelled	15.5	12	PDB header: transcription Chain: 4: PDB Molecule: rna polymerase ii transcription factor b subunit 4; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
85	c5iy63_	Alignment	not modelled	12.3	12	PDB header: transcription, transferase/dna Chain: 3: PDB Molecule: general transcription factor iih subunit 3; PDBTitle: human holo-pic in the closed state
86	c3s29C_	Alignment	not modelled	11.7	10	PDB header: transferase Chain: C: PDB Molecule: sucrose synthase 1; PDBTitle: the crystal structure of sucrose synthase-1 from arabidopsis thaliana2 and its functional implications.
87	d1rl2a2	Alignment	not modelled	10.9	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
88	c5es8A_	Alignment	not modelled	10.1	13	PDB header: ligase Chain: A: PDB Molecule: linear gramicidin synthetase subunit a; PDBTitle: crystal structure of the initiation module of lgra in the thiolation2 state
89	d1q77a_	Alignment	not modelled	10.1	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
90	c6mrrA_	Alignment	not modelled	9.7	17	PDB header: de novo protein Chain: A: PDB Molecule: foldit1; PDBTitle: de novo designed protein foldit1
91	c3kyzA_	Alignment	not modelled	9.4	24	PDB header: transferase Chain: A: PDB Molecule: sensor protein pfes; PDBTitle: the crystal structure of the sensor domain of two-component2 sensor pfes from pseudomonas aeruginosa pa01
92	c5d0nA_	Alignment	not modelled	9.1	9	PDB header: transferase Chain: A: PDB Molecule: pyruvate, phosphate dikinase regulatory protein, PDBTitle: crystal structure of maize pdrp bound with amp
93	c5udwB_	Alignment	not modelled	8.1	21	PDB header: transferase Chain: B: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel
94	c2rrlA_	Alignment	not modelled	8.0	11	PDB header: protein transport Chain: A: PDB Molecule: flagellar hook-length control protein; PDBTitle: solution structure of the c-terminal domain of the fliik
95	d2zjra2	Alignment	not modelled	8.0	13	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
96	d1kr4a_	Alignment	not modelled	7.9	10	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Divalent ion tolerance proteins CutA (CutA1)
97	c4yhwa_	Alignment	not modelled	7.7	6	PDB header: splicing Chain: A: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: yeast prp3 (296-469) in complex with fragment of u4/u6 di-snrna
98	c3qocD_	Alignment	not modelled	7.6	3	PDB header: hydrolase Chain: D: PDB Molecule: putative metallopeptidase; PDBTitle: crystal structure of n-terminal domain (creatinase/prolidase like2 domain) of putative metallopeptidase from corynebacterium diphtheriae
99	c2wfbA_	Alignment	not modelled	7.6	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