



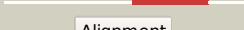

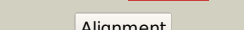

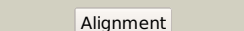





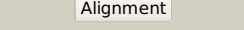

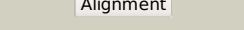

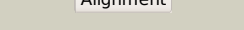

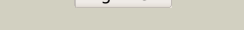



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2425c_(-)_2721876_2723318
Date	Wed Aug 7 12:50:04 BST 2019
Unique Job ID	7bdaaa052e8177e2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2i6sA_	 Alignment		99.0	16	PDB header: hydrolase Chain: A: PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
2	d2ok5a1	 Alignment		98.9	10	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
3	c4hqnb_	 Alignment		98.9	14	PDB header: cell adhesion Chain: B: PDB Molecule: sporozoite surface protein 2; PDBTitle: crystal structure of manganese-loaded plasmodium vivax trap protein
4	c4fx5A_	 Alignment		98.8	14	PDB header: blood clotting Chain: A: PDB Molecule: von willebrand factor type a; PDBTitle: von willebrand factor type a from catenulispora acidiphila
5	d1yvra2	 Alignment		98.8	15	Fold: vWA-like Superfamily: vWA-like Family: RoRNP C-terminal domain-like
6	c1rs0A_	 Alignment		98.8	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)
7	c4wfgA_	 Alignment		98.7	13	PDB header: transcription Chain: A: PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: crystal structure of tfiih subunit
8	c5iy70_	 Alignment		98.7	13	PDB header: transcription, transferase/dna Chain: 0: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the open state
9	c2nvoA_	 Alignment		98.7	17	PDB header: rna binding protein Chain: A: PDB Molecule: ro sixty-related protein, rsr; PDBTitle: crystal structure of deinococcus radiodurans ro (rsr) protein
10	c3ibsA_	 Alignment		98.7	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
11	c2ok5A_	 Alignment		98.6	11	PDB header: hydrolase Chain: A: PDB Molecule: complement factor b; PDBTitle: human complement factor b

12	c6fpzA_	Alignment		98.6	13	PDB header: structural protein Chain: A: PDB Molecule: inter-alpha-trypsin inhibitor heavy chain h1; PDBTitle: inter-alpha-inhibitor heavy chain 1, d298a
13	c4rckB_	Alignment		98.6	15	PDB header: membrane protein Chain: B: PDB Molecule: hypothetical membrane spanning protein; PDBTitle: crystal structure of uncharacterized membrane spanning protein from2 vibrio fischeri
14	c2x31F_	Alignment		98.5	17	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
15	c5a8jA_	Alignment		98.4	13	PDB header: transcription Chain: A: PDB Molecule: vwa2; PDBTitle: crystal structure of the arnb paralog vwa2 from2 sulfolobus acidocaldarius
16	c4hqfA_	Alignment		98.4	14	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin-related anonymous protein, trap; PDBTitle: crystal structure of plasmodium falciparum trap, i4 form
17	c4okuA_	Alignment		98.3	10	PDB header: cell adhesion Chain: A: PDB Molecule: micronemal protein mic2; PDBTitle: structure of toxoplasma gondii promic2
18	c1yvra_	Alignment		98.3	16	PDB header: rna binding protein Chain: A: PDB Molecule: 60-kda ss-a/ro ribonucleoprotein; PDBTitle: ro autoantigen
19	d1shux_	Alignment		98.2	17	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
20	c6o9l6_	Alignment		98.1	15	PDB header: transcription/dna Chain: 6: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
21	c2xggB_	Alignment	not modelled	98.1	13	PDB header: hydrolase Chain: B: PDB Molecule: microneme protein 2; PDBTitle: structure of toxoplasma gondii micronemal protein 2 a_i2 domain
22	c2iueA_	Alignment	not modelled	98.1	13	PDB header: membrane protein Chain: A: PDB Molecule: pactolus i-domain; PDBTitle: pactolus i-domain: functional switching of the rossmann2 fold
23	c2b2xB_	Alignment	not modelled	98.0	10	PDB header: immune system Chain: B: PDB Molecule: integrin alpha-1; PDBTitle: vla1 rdeltah i-domain complexed with a quadruple mutant of the aqc22 fab
24	c6nmiE_	Alignment	not modelled	98.0	16	PDB header: transcription Chain: E: PDB Molecule: general transcription factor iih subunit 2, p44; PDBTitle: cryo-em structure of the human tfiih core complex
25	c5oqj6_	Alignment	not modelled	98.0	15	PDB header: transcription Chain: 6: PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
26	d1v7pc_	Alignment	not modelled	98.0	12	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
27	c4b4tW_	Alignment	not modelled	98.0	11	PDB header: hydrolase Chain: W: PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
28	c2x5nA_	Alignment	not modelled	97.9	9	PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: crystal structure of the sprpn10 vwa domain
						Fold: vWA-like

29	d1jeya2	Alignment	not modelled	97.9	8	Superfamily: vWA-like Family: Ku70 subunit N-terminal domain
30	c3n2nC_	Alignment	not modelled	97.9	13	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
31	c6bxjA_	Alignment	not modelled	97.9	18	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
32	c6bxfA_	Alignment	not modelled	97.9	18	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
33	d1pt6a_	Alignment	not modelled	97.9	11	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
34	d1jeyb2	Alignment	not modelled	97.8	12	Fold: vWA-like Superfamily: vWA-like Family: Ku80 subunit N-terminal domain
35	d1n3ya_	Alignment	not modelled	97.8	15	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
36	d1ck4a_	Alignment	not modelled	97.7	9	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
37	c3jbrF_	Alignment	not modelled	97.7	18	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
38	c4cnbA_	Alignment	not modelled	97.7	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
39	c3txaA_	Alignment	not modelled	97.7	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
40	c3tw0D_	Alignment	not modelled	97.6	21	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
41	d1q0pa_	Alignment	not modelled	97.6	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
42	c5gjqW_	Alignment	not modelled	97.6	8	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
43	c5gjfF_	Alignment	not modelled	97.5	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
44	d1u0oc1	Alignment	not modelled	97.5	12	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
45	d1mf7a_	Alignment	not modelled	97.4	10	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
46	d1pd0a3	Alignment	not modelled	97.4	18	Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
47	d1ijba_	Alignment	not modelled	97.4	14	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
48	d1atza_	Alignment	not modelled	97.4	8	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
49	c4um9D_	Alignment	not modelled	97.2	18	PDB header: immune system Chain: D: PDB Molecule: integrin beta-6; PDBTitle: crystal structure of alpha v beta 6 with peptide
50	c5e6rA_	Alignment	not modelled	97.2	15	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
51	c6djpB_	Alignment	not modelled	97.1	18	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
52	c3ragA_	Alignment	not modelled	97.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein aacj_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
53	d1mjna_	Alignment	not modelled	97.0	16	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
54	c1jeyB_	Alignment	not modelled	97.0	10	PDB header: dna binding protein/dna Chain: B: PDB Molecule: ku80; PDBTitle: crystal structure of the ku heterodimer bound to dna
						PDB header: cell adhesion/blood clotting

55	c3fcuB	Alignment	not modelled	96.9	17	Chain: B: PDB Molecule: integrin beta-3; PDBTitle: structure of headpiece of integrin aiibb3 in open conformation
56	c3v4pB	Alignment	not modelled	96.9	20	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-7; PDBTitle: crystal structure of a4b7 headpiece complexed with fab act-1
57	c3gxbB	Alignment	not modelled	96.9	9	PDB header: cell adhesion Chain: B: PDB Molecule: von willebrand factor; PDBTitle: crystal structure of vwf a2 domain
58	c3vi3D	Alignment	not modelled	96.8	18	PDB header: cell adhesion/immune system Chain: D: PDB Molecule: integrin beta-1; PDBTitle: crystal structure of alpha5beta1 integrin headpiece (ligand-free form)
59	c4ihkA	Alignment	not modelled	96.7	14	PDB header: cell adhesion Chain: A: PDB Molecule: collagen alpha3(vi); PDBTitle: crystal structure of the collagen vi alpha3 n5 domain r1061q
60	d1tyeb2	Alignment	not modelled	96.6	18	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
61	c1u8cB	Alignment	not modelled	92.3	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
62	c3ijeB	Alignment	not modelled	91.9	15	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
63	c3k6sB	Alignment	not modelled	91.4	17	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-2; PDBTitle: structure of integrin alphaxbeta2 ectodomain
64	c3sftA	Alignment	not modelled	54.9	12	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
65	c6a6iG	Alignment	not modelled	50.6	14	PDB header: hydrolase Chain: G: PDB Molecule: excision repair cross-complementing rodent repair PDBTitle: crystal structure of the winged-helix domain of cockayne syndrome2 group b protein in complex with ubiquitin
66	d1jwya1	Alignment	not modelled	48.3	26	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain
67	d1jsca3	Alignment	not modelled	47.5	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
68	c6akjB	Alignment	not modelled	45.8	10	PDB header: rna binding protein Chain: B: PDB Molecule: enhancer of rudimentary homolog,yth domain-containing PDBTitle: the crystal structure of emc complex
69	c2qpuB	Alignment	not modelled	45.7	17	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
70	d1jb3a	Alignment	not modelled	42.5	12	Fold: OB-fold Superfamily: TIMP-like Family: The laminin-binding domain of agrin
71	c3b7qA	Alignment	not modelled	41.7	16	PDB header: signaling protein Chain: A: PDB Molecule: uncharacterized protein yk1091c; PDBTitle: crystal structure of yeast sec14 homolog sfh1 in complex with2 phosphatidylcholine
72	c2gdvA	Alignment	not modelled	40.7	15	PDB header: transferase Chain: A: PDB Molecule: sucrose phosphorylase; PDBTitle: sucrose phosphorylase from bifidobacterium adolescentis2 reacted with sucrose
73	d1m2ka	Alignment	not modelled	40.6	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
74	d1r7aa2	Alignment	not modelled	38.4	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
75	c2jsoA	Alignment	not modelled	35.9	25	PDB header: signaling protein Chain: A: PDB Molecule: polymyxin resistance protein pmrd; PDBTitle: antimicrobial resistance protein
76	c6irtA	Alignment	not modelled	35.5	11	PDB header: membrane protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: human lat1-4f2hc complex bound with bch
77	d1mkya3	Alignment	not modelled	33.9	38	Fold: Alpha-lytic protease prodomain-like Superfamily: Probable GTPase Der, C-terminal domain Family: Probable GTPase Der, C-terminal domain
78	c5d87A	Alignment	not modelled	33.8	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable siderophore biosynthesis protein sbna; PDBTitle: staphyloferrin b precursor biosynthetic enzyme sbna y152f/s185g2 variant
79	c5o1mA	Alignment	not modelled	31.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: rubber oxygenase; PDBTitle: structure of latex clearing protein lcp in the closed state
80	c1ydoC	Alignment	not modelled	30.8	19	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillis subtilis hmg-coa lyase, northeast2 structural genomics target sr181. PDB header: lyase

81	c2cw6B	Alignment	not modelled	30.6	14	Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
82	c3eqxB	Alignment	not modelled	30.2	16	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
83	c1ydnA	Alignment	not modelled	29.0	15	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
84	d1hlva2	Alignment	not modelled	28.7	26	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding
85	c3bleA	Alignment	not modelled	28.2	22	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in complexed with2 malonate
86	d1w6ta1	Alignment	not modelled	28.0	11	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: Enolase
87	c3eg9B	Alignment	not modelled	27.7	20	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
88	c3e59A	Alignment	not modelled	26.5	21	PDB header: transferase Chain: A: PDB Molecule: pyoverdine biosynthesis protein pvca; PDBTitle: crystal structure of the pvca (pa2254) protein from pseudomonas2 aeruginosa
89	c1oizA	Alignment	not modelled	26.4	20	PDB header: transport Chain: A: PDB Molecule: alpha-tocopherol transfer protein; PDBTitle: the molecular basis of vitamin e retention: structure of2 human alpha-tocopherol transfer protein
90	c5y59B	Alignment	not modelled	26.0	19	PDB header: protein binding Chain: B: PDB Molecule: atp-dependent dna helicase ii subunit 2; PDBTitle: crystal structure of ku80 and sir4
91	c4ov9A	Alignment	not modelled	26.0	5	PDB header: transferase Chain: A: PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
92	d1sr9a2	Alignment	not modelled	25.6	7	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
93	d1r5la2	Alignment	not modelled	24.8	18	Fold: Spollaa-like Superfamily: CRAL/TRIO domain Family: CRAL/TRIO domain
94	c1auaA	Alignment	not modelled	24.5	15	PDB header: phospholipid-binding protein Chain: A: PDB Molecule: phosphatidylinositol transfer protein sec14p; PDBTitle: phosphatidylinositol transfer protein sec14p from2 saccharomyces cerevisiae
95	c3a9iA	Alignment	not modelled	23.8	27	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermophilus2 complexed with lys
96	c2n6yA	Alignment	not modelled	23.8	22	PDB header: ligase Chain: A: PDB Molecule: hmwp2 nonribosomal peptide synthetase; PDBTitle: solution structure of holo arcp from yersiniabactin synthetase
97	c3g59A	Alignment	not modelled	23.5	13	PDB header: transferase Chain: A: PDB Molecule: fmn adenylyltransferase; PDBTitle: crystal structure of candida glabrata fmn adenylyltransferase in2 complex with atp
98	c6n0wA	Alignment	not modelled	23.2	21	PDB header: ligase Chain: A: PDB Molecule: tyrosine--trna ligase; PDBTitle: crystal structure of a tyrosine--trna ligase from elizabethkingia2 anophelis
99	d1ni8a	Alignment	not modelled	23.1	29	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
100	c2ygwB	Alignment	not modelled	23.0	14	PDB header: lyase Chain: B: PDB Molecule: malonyl-coa decarboxylase, mitochondrial; PDBTitle: crystal structure of human mcd
101	d3bz7a1	Alignment	not modelled	22.8	45	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain
102	d2ewca1	Alignment	not modelled	22.3	15	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
103	c4ksaD	Alignment	not modelled	21.7	14	PDB header: lyase Chain: D: PDB Molecule: malonyl-coa decarboxylase; PDBTitle: crystal structure of malonyl-coa decarboxylase from rhodospseudomonas2 palustris, northeast structural genomics consortium target rpr127
104	c4ksaA	Alignment	not modelled	21.3	14	PDB header: lyase Chain: A: PDB Molecule: malonyl-coa decarboxylase; PDBTitle: crystal structure of malonyl-coa decarboxylase from rhodospseudomonas2 palustris, northeast structural genomics consortium target rpr127
105	c4ksfA	Alignment	not modelled	21.0	16	PDB header: lyase Chain: A: PDB Molecule: malonyl-coa decarboxylase; PDBTitle: crystal structure of malonyl-coa decarboxylase from

					agrobacterium2 vitis, northeast structural genomics consortium target rir35
106	c1m2vB_	Alignment	not modelled	20.9	19 PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
107	c5dn8A_	Alignment	not modelled	20.8	29 PDB header: gtp-binding protein Chain: A: PDB Molecule: gtpase der; PDBTitle: 1.76 angstrom crystal structure of gtp-binding protein der from2 coxiella burnetii in complex with gdp.
108	c5dxiB_	Alignment	not modelled	20.5	12 PDB header: hydrolase Chain: B: PDB Molecule: trehalose-6-phosphate phosphatase; PDBTitle: structure of c. albicans trehalose-6-phosphate phosphatase c-terminal2 domain