






















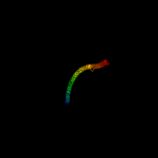
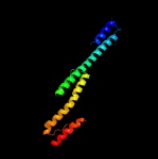
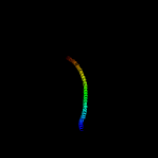
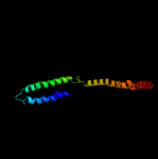
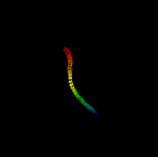
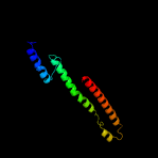
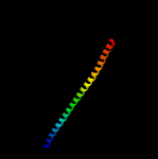
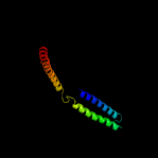


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3495c_(lprN)_3913559_3914713
Date	Fri Aug 9 18:20:17 BST 2019
Unique Job ID	a5db7062a2c67dad

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.9	23	PDB header: protein transport Chain: C; PDB Molecule: toluene tolerance efflux transporter (abc superfamily, PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
2	c5uw8C_	 Alignment		99.8	22	PDB header: transport protein Chain: C; PDB Molecule: probable phospholipid abc transporter-binding protein mlad; PDBTitle: structure of e. coli mce protein mlad, core mce domain
3	c5uvnE_	 Alignment		99.5	19	PDB header: transport protein Chain: E; PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnC_	 Alignment		99.5	19	PDB header: transport protein Chain: C; PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnA_	 Alignment		99.5	19	PDB header: transport protein Chain: A; PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
6	c5uvnF_	 Alignment		99.5	19	PDB header: transport protein Chain: F; PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
7	c5uvnB_	 Alignment		99.5	19	PDB header: transport protein Chain: B; PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvnD_	 Alignment		99.5	19	PDB header: transport protein Chain: D; PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c1qu7A_	 Alignment		91.5	12	PDB header: signaling protein Chain: A; PDB Molecule: methyl-accepting chemotaxis protein i; PDBTitle: four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
10	c2qf4A_	 Alignment		88.1	14	PDB header: structural protein Chain: A; PDB Molecule: cell shape determining protein mreC; PDBTitle: high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mreC (orthorhombic form)
11	c2wpgA_	 Alignment		86.4	6	PDB header: membrane protein Chain: A; PDB Molecule: trimeric autotransporter adhesin fragment; PDBTitle: salmonella enterica sada 479-519 fused to gcn4 adaptors (sadaK3, in-2 register fusion)

12	d1eq1a_	Alignment		85.4	15	Fold: Apolipophorin-III Superfamily: Apolipophorin-III Family: Apolipophorin-III
13	c3zx6A_	Alignment		85.3	11	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
14	c3lnrA_	Alignment		84.6	11	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
15	c2ch7A_	Alignment		83.7	9	PDB header: chemotaxis Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
16	c5u0pU_	Alignment		81.3	9	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
17	c6gajA_	Alignment		77.5	17	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t11 reovirus sigma1 coiled coil tail (iodide)
18	c6b7nC_	Alignment		76.4	12	PDB header: viral protein Chain: C: PDB Molecule: spike protein; PDBTitle: cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state
19	c5zuvB_	Alignment		71.4	12	PDB header: viral protein, inhibitor Chain: B: PDB Molecule: spike glycoprotein,spike glycoprotein,inhibitor ek1; PDBTitle: crystal structure of the human coronavirus 229e hr1 motif in complex2 with pan-covs inhibitor ek1
20	d1ykhb1	Alignment		69.9	8	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
21	c3g67A_	Alignment	not modelled	67.4	9	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
22	c4tkoB_	Alignment	not modelled	66.9	20	PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
23	c6nzkB_	Alignment	not modelled	66.2	18	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
24	c1deqO_	Alignment	not modelled	66.1	14	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
25	c2qjhA_	Alignment	not modelled	65.3	11	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
26	c4rh7A_	Alignment	not modelled	64.0	9	PDB header: motor protein Chain: A: PDB Molecule: green fluorescent protein/cytoplasmic dynein 2 heavy chain PDBTitle: crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
27	c4abxB_	Alignment	not modelled	63.3	8	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
28	c3vkhA_	Alignment	not modelled	62.4	11	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain

29	c6nb3B_	Alignment	not modelled	62.1	22	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing Ica60 antibody fab fragment2 (state 1)
30	c3cwgA_	Alignment	not modelled	61.6	9	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
31	c6gapB_	Alignment	not modelled	59.5	9	PDB header: viral protein Chain: B: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t3d reovirus sigma1 coiled coil tail and body
32	c1degF_	Alignment	not modelled	58.7	7	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
33	c6cs2A_	Alignment	not modelled	57.5	11	PDB header: viral protein/hydrolase Chain: A: PDB Molecule: spike glycoprotein,fibritin; PDBTitle: sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
34	c3jclC_	Alignment	not modelled	56.0	15	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
35	c2j5uB_	Alignment	not modelled	52.4	11	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
36	c5x5bB_	Alignment	not modelled	52.1	11	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
37	c1cz5A_	Alignment	not modelled	52.0	13	PDB header: hydrolase Chain: A: PDB Molecule: vcp-like atpase; PDBTitle: nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
38	c5xlrC_	Alignment	not modelled	50.2	11	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
39	c5cwsj_	Alignment	not modelled	50.0	7	PDB header: protein transport Chain: J: PDB Molecule: nucleoporin nup49; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
40	d1st6a4	Alignment	not modelled	49.2	7	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
41	c5wrgB_	Alignment	not modelled	48.0	13	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
42	c4njIA_	Alignment	not modelled	47.9	12	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
43	c1bf5A_	Alignment	not modelled	43.3	6	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
44	c1ei3E_	Alignment	not modelled	42.8	7	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
45	c2vs0B_	Alignment	not modelled	41.8	5	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
46	c4lwsB_	Alignment	not modelled	41.2	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
47	c3ojaB_	Alignment	not modelled	41.1	14	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
48	c5i08A_	Alignment	not modelled	40.6	14	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
49	c3zbhC_	Alignment	not modelled	39.8	10	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
50	c4iogD_	Alignment	not modelled	39.8	11	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
51	c2d4yA_	Alignment	not modelled	38.5	9	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
52	c2pjhB_	Alignment	not modelled	37.0	10	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: strctural model of the p97 n domain- npl4 ubd complex
53	c5zhyA_	Alignment	not modelled	35.1	13	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
54	c2bezC_	Alignment	not modelled	34.3	13	PDB header: viral protein Chain: C: PDB Molecule: e2 glycoprotein; PDBTitle: structure of a proteolitically resistant core from the severe acute2 respiratory syndrome coronavirus s2 fusion protein

55	c3ghgI_	Alignment	not modelled	33.8	9	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
56	c4lwsA_	Alignment	not modelled	33.7	10	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
57	c4ut1A_	Alignment	not modelled	32.9	9	PDB header: motor protein Chain: A: PDB Molecule: flagellar hook-associated protein; PDBTitle: the structure of the flagellar hook junction protein flgk2 from burkholderia pseudomallei
58	c5j0hA_	Alignment	not modelled	32.4	17	PDB header: de novo protein Chain: A: PDB Molecule: design construct 2l6hc3_13; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
59	c6e6aB_	Alignment	not modelled	31.5	11	PDB header: protein binding Chain: B: PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
60	c3ghgK_	Alignment	not modelled	30.8	14	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
61	c5xbjA_	Alignment	not modelled	29.7	7	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar hook-associated protein flgk; PDBTitle: the structure of the flagellar hook junction protein hap1 (flgk) from2 campylobacter jejuni
62	c5lskD_	Alignment	not modelled	29.7	9	PDB header: cell cycle Chain: D: PDB Molecule: kinetochore-associated protein dsn1 homolog; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
63	d1st6a3	Alignment	not modelled	28.9	10	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
64	c1kmiZ_	Alignment	not modelled	27.5	7	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
65	c5cwsC_	Alignment	not modelled	27.5	13	PDB header: protein transport Chain: C: PDB Molecule: nucleoporin nsp1; PDBTitle: crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
66	d2vzsa2	Alignment	not modelled	27.1	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
67	d1wa8a1	Alignment	not modelled	27.0	13	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
68	c1wywB_	Alignment	not modelled	26.5	12	PDB header: viral protein Chain: B: PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
69	c4wsrA_	Alignment	not modelled	25.9	15	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: the crystal structure of hemagglutinin form a/chicken/new york/14677-2 13/1998
70	c1ei3C_	Alignment	not modelled	25.8	6	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
71	c2kbbA_	Alignment	not modelled	25.6	11	PDB header: structural protein Chain: A: PDB Molecule: talin-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
72	d1v5va1	Alignment	not modelled	25.1	15	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
73	c6gaoC_	Alignment	not modelled	25.0	12	PDB header: viral protein Chain: C: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail and body
74	c4modB_	Alignment	not modelled	24.8	21	PDB header: viral protein Chain: B: PDB Molecule: hr1 of s protein, linker, hr2 of s protein; PDBTitle: structure of the mers-cov fusion core
75	c5szsC_	Alignment	not modelled	24.2	13	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: glycan shield and epitope masking of a coronavirus spike protein2 observed by cryo-electron microscopy
76	c5j65A_	Alignment	not modelled	24.1	14	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry6aa; PDBTitle: crystal structure of trypsin activated cry6aa
77	c5j9qH_	Alignment	not modelled	23.6	6	PDB header: transferase Chain: H: PDB Molecule: chromatin modification-related protein yng2; PDBTitle: crystal structure of the nua4 core complex
78	c2ieqC_	Alignment	not modelled	23.4	15	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
79	c3pltB_	Alignment	not modelled	23.2	11	PDB header: structural protein Chain: B: PDB Molecule: sphingolipid long chain base-responsive protein lsp1; PDBTitle: crystal structure of lsp1 from saccharomyces cerevisiae
80	c5zkgB_	Alignment	not modelled	22.5	17	PDB header: ligase Chain: B: PDB Molecule: aminoacyl-trna synthetase-interacting multifunctional PDBTitle: crystal structure of c-terminal domain of plasmodium vivax p43

81	c6ezvX	Alignment	not modelled	21.5	9	PDB header: toxin Chain: X: PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
82	c2q13A	Alignment	not modelled	19.3	5	PDB header: protein transport Chain: A: PDB Molecule: dcc-interacting protein 13 alpha; PDBTitle: crystal structure of bar-ph domain of app1
83	c5n9yB	Alignment	not modelled	18.6	13	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
84	c4n21E	Alignment	not modelled	18.2	7	PDB header: viral protein Chain: E: PDB Molecule: gp2 ectodomain; PDBTitle: crystal structure of the gp2 core domain from the california academy2 of science virus
85	c6grjG	Alignment	not modelled	18.1	17	PDB header: toxin Chain: G: PDB Molecule: ahlb; PDBTitle: structure of the ahlb pore of the tripartite alpha-pore forming toxin,2 ahl, from aeromonas hydrophila.
86	c6ewyA	Alignment	not modelled	17.6	9	PDB header: structural protein Chain: A: PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
87	c3gvmA	Alignment	not modelled	17.5	11	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
88	d1h9ra2	Alignment	not modelled	17.0	24	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
89	d1x9la	Alignment	not modelled	15.8	11	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: DR1885-like metal-binding protein Family: DR1885-like metal-binding protein
90	c5nmoA	Alignment	not modelled	15.6	14	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein smc,chromosome partition PDBTitle: structure of the bacillus subtilis smc joint domain
91	c5mg8B	Alignment	not modelled	15.6	12	PDB header: recombination Chain: B: PDB Molecule: structural maintenance of chromosomes protein 6; PDBTitle: crystal structure of the s.pombe smc5/6 hinge domain
92	d2cbia1	Alignment	not modelled	15.3	14	Fold: Hyaluronidase domain-like Superfamily: Hyaluronidase post-catalytic domain-like Family: Hyaluronidase post-catalytic domain-like
93	c3j99M	Alignment	not modelled	15.2	9	PDB header: hydrolase Chain: M: PDB Molecule: synaptosomal-associated protein 25; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state iiib)
94	c5e7pA	Alignment	not modelled	14.8	13	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
95	c5gasN	Alignment	not modelled	14.7	13	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
96	d1fl0a	Alignment	not modelled	14.6	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Myf domain
97	c5j21B	Alignment	not modelled	14.2	14	PDB header: de novo protein Chain: B: PDB Molecule: protein design 2l4hc2_11; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
98	d2cp6a1	Alignment	not modelled	14.0	22	Fold: SH3-like barrel Superfamily: Cap-Gly domain Family: Cap-Gly domain
99	c1t5eB	Alignment	not modelled	14.0	14	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa