
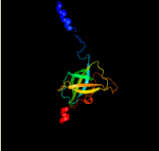

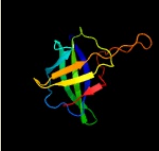
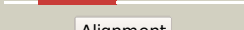
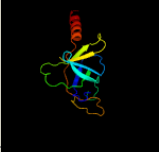

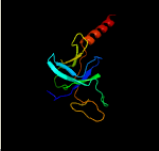

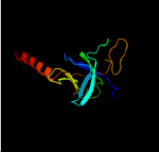

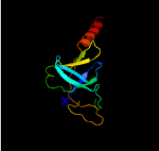

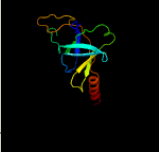

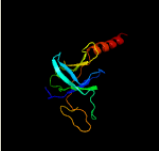
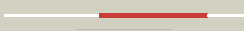
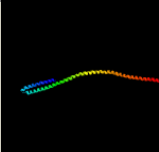

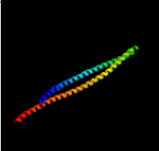

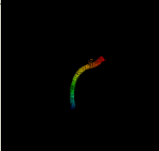

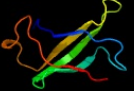





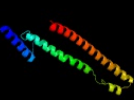







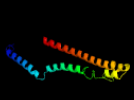












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1967_(mce3B)_2210609_2211637
Date	Mon Aug 5 13:25:06 BST 2019
Unique Job ID	f323759b99af3cc9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.9	32	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	27	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	26	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnA_	 Alignment		99.5	26	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnD_	 Alignment		99.5	26	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
6	c5uvnF_	 Alignment		99.5	26	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	26	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvnC_	 Alignment		99.5	26	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c1qu7A_	 Alignment		93.5	13	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	c3g67A_	 Alignment		91.6	10	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein i; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
11	c3zx6A_	 Alignment		87.6	16	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant

12	c4tkoB_	 Alignment		85.2	15	PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
13	c4lwsA_	 Alignment		74.8	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c6ezvX_	 Alignment		73.5	11	PDB header: toxin Chain: X: PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
15	c6b7nC_	 Alignment		71.8	14	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
16	c3cwgA_	 Alignment		69.8	8	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
17	c2vs0B_	 Alignment		68.6	11	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
18	c2ch7A_	 Alignment		67.2	10	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
19	c6nzkB_	 Alignment		67.0	10	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
20	c3ojaB_	 Alignment		65.8	10	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
21	c2wpgA_	 Alignment	not modelled	65.6	9	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)
22	c6gajA_	 Alignment	not modelled	63.9	12	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
23	c5x5bB_	 Alignment	not modelled	63.9	8	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
24	c1deqF_	 Alignment	not modelled	63.0	8	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
25	c4iogD_	 Alignment	not modelled	63.0	7	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
26	c3j99M_	 Alignment	not modelled	62.9	8	PDB header: hydrolase Chain: M: PDB Molecule: synaptosomal-associated protein 25; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state iiib)
27	c1kmiZ_	 Alignment	not modelled	62.4	18	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
28	c2ieqC_	 Alignment	not modelled	61.1	13	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus n163 spike2 glycoprotein

29	c6cs2A	Alignment	not modelled	60.6	8	PDB header: viral protein/hydrolase Chain: A: PDB Molecule: spike glycoprotein,fibrin; PDBTitle: sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
30	c3jclC	Alignment	not modelled	60.3	12	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
31	c3ghgl	Alignment	not modelled	59.0	10	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
32	c5xbjA	Alignment	not modelled	58.7	9	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
33	c3zbhC	Alignment	not modelled	58.4	10	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
34	c5i08A	Alignment	not modelled	57.6	10	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
35	c6nb3B	Alignment	not modelled	56.7	8	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
36	c1deqO	Alignment	not modelled	55.3	15	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
37	c4rh7A	Alignment	not modelled	55.0	10	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
38	d1st6a4	Alignment	not modelled	54.8	8	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
39	c4abxB	Alignment	not modelled	54.0	17	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
40	c2qf4A	Alignment	not modelled	53.9	10	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)
41	c4ut1A	Alignment	not modelled	53.1	13	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
42	c5wrgB	Alignment	not modelled	53.1	8	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
43	c2j5uB	Alignment	not modelled	53.0	8	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
44	d1wa8a1	Alignment	not modelled	52.8	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
45	d1szia	Alignment	not modelled	51.5	12	Fold: Four-helical up-and-down bundle Superfamily: Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain Family: Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
46	c5xlrC	Alignment	not modelled	51.3	8	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
47	c1ei3E	Alignment	not modelled	49.3	13	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
48	c5u0pU	Alignment	not modelled	46.8	9	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
49	c2ql2B	Alignment	not modelled	44.8	10	PDB header: cell adhesion Chain: B: PDB Molecule: adhesion a; PDBTitle: crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
50	d1eq1a	Alignment	not modelled	44.4	11	Fold: Apolipoporphin-III Superfamily: Apolipoporphin-III Family: Apolipoporphin-III
51	c2d4yA	Alignment	not modelled	44.2	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	c5szsC	Alignment	not modelled	40.9	9	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
53	c6ewyA	Alignment	not modelled	38.9	15	PDB header: structural protein Chain: A: PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
54	c3ur1C	Alianment	not modelled	36.4	6	PDB header: immune system Chain: C: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: the structure of a ternary complex between chea

						domains p4 and p5 with2 chew and with a truncated fragment of tm14, a chemoreceptor analog3 from thermotoga maritima.
55	c6gapB	Alignment	not modelled	36.2	11	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
56	c4qkvB	Alignment	not modelled	34.1	13	PDB header: transcription Chain: B: PDB Molecule: polymerase i and transcript release factor; PDBTitle: crystal structure of the mouse cavin1 hr1 domain
57	c6e6aB	Alignment	not modelled	32.9	14	PDB header: protein binding Chain: B: PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
58	c2qihA	Alignment	not modelled	32.2	8	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
59	c4qkwB	Alignment	not modelled	31.5	13	PDB header: signaling protein Chain: B: PDB Molecule: muscle-related coiled-coil protein; PDBTitle: crystal structure of the zebrafish cavin4a hr1 domain
60	c3lnrA	Alignment	not modelled	31.4	9	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
61	c5x5fC	Alignment	not modelled	30.1	9	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
62	d1v5va1	Alignment	not modelled	29.9	16	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
63	c3gvmA	Alignment	not modelled	29.2	14	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
64	c4pdxB	Alignment	not modelled	28.6	13	PDB header: hydrolase Chain: B: PDB Molecule: putative alkyl/aryl-sulfatase yjcs; PDBTitle: crystal structure of escherchia coli uncharacterized protein yjcs
65	c4nurB	Alignment	not modelled	27.6	16	PDB header: hydrolase Chain: B: PDB Molecule: psdsa; PDBTitle: crystal structure of thermostable alkylsulfatase sdsap from2 pseudomonas sp. s9
66	c2yheD	Alignment	not modelled	26.7	9	PDB header: hydrolase Chain: D: PDB Molecule: sec-alkyl sulfatase; PDBTitle: structure determination of the stereoselective inverting sec-2 alkylsulfatase pisa1 from pseudomonas sp.
67	c5lskD	Alignment	not modelled	26.7	14	PDB header: cell cycle Chain: D: PDB Molecule: kinetochore-associated protein dsn1 homolog; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
68	d1st6a3	Alignment	not modelled	26.4	13	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
69	c6grjG	Alignment	not modelled	26.1	12	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.
70	c1ei3C	Alignment	not modelled	24.2	6	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
71	d1k0ha	Alignment	not modelled	24.2	22	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: gpFII-like
72	d2cfua2	Alignment	not modelled	23.7	13	Fold: Metallo-hydrolase/oxidoreductase Superfamily: Metallo-hydrolase/oxidoreductase Family: Alkylsulfatase-like
73	c3jszA	Alignment	not modelled	23.2	11	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: legionella pneumophila glucosyltransferase lgt1. n293a with udp-glc
74	c2dq3A	Alignment	not modelled	22.7	16	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
75	d1uwda	Alignment	not modelled	22.4	16	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
76	c5n76C	Alignment	not modelled	22.1	20	PDB header: nickel-binding protein Chain: C: PDB Molecule: coot; PDBTitle: crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
77	d1ykhb1	Alignment	not modelled	21.8	9	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
78	c3vkhA	Alignment	not modelled	21.7	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
79	c6b3oB	Alignment	not modelled	20.9	12	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
80	d1st6a5	Alignment	not modelled	20.5	9	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin

81	c2yfaA_	Alignment	not modelled	20.3	10	PDB header: receptor Chain: A: PDB Molecule: methyl-accepting chemotaxis transducer; PDBTitle: x-ray structure of mcps ligand binding domain in complex with malate
82	c1bf5A_	Alignment	not modelled	20.2	11	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
83	c3ghgK_	Alignment	not modelled	20.0	12	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
84	c5e5wB_	Alignment	not modelled	19.7	14	PDB header: hydrolase Chain: B: PDB Molecule: hemagglutinin-esterase; PDBTitle: hemagglutinin-esterase-fusion mutant structure of influenza d virus
85	c1yvlB_	Alignment	not modelled	19.7	11	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1
86	d1h9ra2	Alignment	not modelled	19.3	20	Fold: OB-fold Superfamily: MOP-like Family: BIMOP, duplicated molybdate-binding domain
87	c5b0oB_	Alignment	not modelled	19.2	29	PDB header: hydrolase/motor protein Chain: B: PDB Molecule: flagellum-specific atp synthase; PDBTitle: structure of the flih-flii complex
88	c1wyyB_	Alignment	not modelled	18.7	13	PDB header: viral protein Chain: B: PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
89	c5zhyA_	Alignment	not modelled	18.6	15	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
90	c1cz5A_	Alignment	not modelled	18.6	19	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)
91	d1svba1	Alignment	not modelled	18.4	16	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Class II viral fusion proteins C-terminal domain
92	c5zuvB_	Alignment	not modelled	17.7	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
93	d1g4us1	Alignment	not modelled	17.6	17	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
94	c5cwsj_	Alignment	not modelled	17.5	9	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
95	c6gaoC_	Alignment	not modelled	17.0	11	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
96	c2x3bB_	Alignment	not modelled	16.9	14	PDB header: hydrolase Chain: B: PDB Molecule: toxic extracellular endopeptidase; PDBTitle: asap1 inactive mutant e294a, an extracellular toxic zinc2 metalloendopeptidase
97	c5lp5F_	Alignment	not modelled	16.9	18	PDB header: hydrolase/antibiotic Chain: F: PDB Molecule: rod shape-determining protein (mrec); PDBTitle: complex between penicillin-binding protein (pbp2) and mrec from2 helicobacter pylori
98	c4njIA_	Alignment	not modelled	16.7	12	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
99	c4modB_	Alignment	not modelled	16.4	10	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