
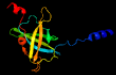









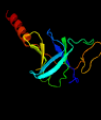



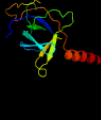

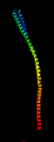




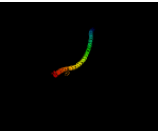

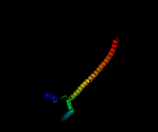
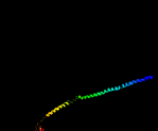
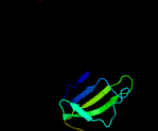

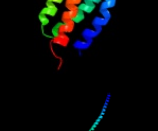




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3498c_(mce4B)_3917125_3918177
Date	Fri Aug 9 18:20:17 BST 2019
Unique Job ID	5d42bb844e85bd1f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.9	28	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	26	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	c5uvnD_	 Alignment		99.5	21	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnE_	 Alignment		99.5	21	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnF_	 Alignment		99.5	21	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
6	c5uvnA_	 Alignment		99.5	21	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
7	c5uvnC_	 Alignment		99.5	21	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvnB_	 Alignment		99.5	21	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c1qu7A_	 Alignment		93.5	10	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		93.3	12	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
11	c2ch7A_	 Alignment		85.5	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

12	c3zx6A_	Alignment		85.2	8	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
13	c4tkoB_	Alignment		81.9	12	PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
14	c3ojaB_	Alignment		81.1	7	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
15	c1deqO_	Alignment		79.0	13	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
16	c2qf4A_	Alignment		77.9	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)
17	d1st6a4	Alignment		75.8	14	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
18	c1ei3E_	Alignment		75.0	12	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
19	c6ezvX_	Alignment		73.4	16	PDB header: toxin Chain: X: PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
20	c2d4yA_	Alignment		73.1	9	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
21	c3lnrA_	Alignment	not modelled	72.3	12	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
22	c3cwgA_	Alignment	not modelled	67.2	10	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
23	c6gajA_	Alignment	not modelled	66.1	16	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)
24	c4rh7A_	Alignment	not modelled	65.8	11	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
25	c1deqF_	Alignment	not modelled	64.8	7	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
26	c6b7nC_	Alignment	not modelled	64.1	9	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
27	c3vkhA_	Alignment	not modelled	63.6	10	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
28	c2j5uB_	Alignment	not modelled	61.6	11	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
						PDB header: signaling protein

29	c1kmiZ_	Alignment	not modelled	58.8	8	Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
30	c3j99M_	Alignment	not modelled	58.6	12	PDB header: hydrolase Chain: M: PDB Molecule: synaptosomal-associated protein 25; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state iib)
31	c5xbjA_	Alignment	not modelled	56.6	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
32	c4ut1A_	Alignment	not modelled	55.7	12	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
33	c4iogD_	Alignment	not modelled	55.7	12	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
34	d1eq1a_	Alignment	not modelled	55.4	6	Fold: Apolipophorin-III Superfamily: Apolipophorin-III Family: Apolipophorin-III
35	c2vs0B_	Alignment	not modelled	53.1	8	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
36	c6o7ua_	Alignment	not modelled	51.5	9	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
37	c2qihA_	Alignment	not modelled	51.3	10	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
38	c5zuvB_	Alignment	not modelled	50.3	11	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
39	c5j65A_	Alignment	not modelled	49.2	13	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry6aa; PDBTitle: crystal structure of trypsin activated cry6aa
40	c2ieqC_	Alignment	not modelled	49.1	10	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
41	c6f0kA_	Alignment	not modelled	48.1	13	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
42	c1ei3C_	Alignment	not modelled	45.5	10	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
43	c2wpgA_	Alignment	not modelled	44.5	11	PDB header: membrane protein Chain: A: PDB Molecule: trimeric autotransporter adhesin fragment; PDBTitle: salmonella enterica sada 479-519 fused to gcn4 adaptors (sada3, in-2 register fusion)
44	c2gl2B_	Alignment	not modelled	37.5	9	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
45	c5u0pU_	Alignment	not modelled	36.1	9	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
46	c2dq3A_	Alignment	not modelled	35.2	14	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of aq_298
47	c6gapB_	Alignment	not modelled	34.9	14	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
48	c1bf5A_	Alignment	not modelled	34.2	8	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
49	c4abxB_	Alignment	not modelled	31.6	18	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
50	d1ykhl1	Alignment	not modelled	30.5	10	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
51	c5szsC_	Alignment	not modelled	30.4	12	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
52	d1v5va1	Alignment	not modelled	30.3	18	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
53	c4wy4B_	Alignment	not modelled	27.9	11	PDB header: membrane protein Chain: B: PDB Molecule: syntaxin-17; PDBTitle: crystal structure of autophagic snare complex
54	c6ewyA_	Alignment	not modelled	27.6	12	PDB header: structural protein Chain: A: PDB Molecule: peptidoglycan endopeptidase ripa; PDBTitle: ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
						PDB header: hydrolase/motor protein

55	c5b0oB_	Alignment	not modelled	27.2	29	Chain: B; PDB Molecule: flagellum-specific atp synthase; PDBTitle: structure of the flih-flii complex
56	c5i08A_	Alignment	not modelled	25.2	13	PDB header: viral protein Chain: A; PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
57	d1h9ra2	Alignment	not modelled	24.5	20	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
58	c3jcIC_	Alignment	not modelled	24.4	15	PDB header: viral protein Chain: C; PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
59	c5e5wB_	Alignment	not modelled	24.0	12	PDB header: hydrolase Chain: B; PDB Molecule: hemagglutinin-esterase; PDBTitle: hemagglutinin-esterase-fusion mutant structure of influenza d virus
60	c6e6aB_	Alignment	not modelled	23.7	13	PDB header: protein binding Chain: B; PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
61	c6gaoC_	Alignment	not modelled	23.4	7	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
62	c4njIA_	Alignment	not modelled	23.1	9	PDB header: viral protein Chain: A; PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
63	c5cwsj_	Alignment	not modelled	22.6	10	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
64	c1cz5A_	Alignment	not modelled	22.4	12	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)
65	c6gy8B_	Alignment	not modelled	21.7	8	PDB header: toxin Chain: B; PDB Molecule: xaxa; PDBTitle: crystal structure of xaxa from xenorhabdus nematophila
66	c3ghgK_	Alignment	not modelled	21.5	9	PDB header: blood clotting Chain: K; PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
67	d1h9ma2	Alignment	not modelled	20.9	26	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
68	c5x5fC_	Alignment	not modelled	20.8	12	PDB header: viral protein Chain: C; PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
69	c5wwlN_	Alignment	not modelled	20.8	12	PDB header: cell cycle Chain: N; PDB Molecule: kinetochore protein nnf1; PDBTitle: crystal structure of the schizogenesis pombe kinetochore mis12c2 subcomplex
70	c2q13A_	Alignment	not modelled	20.6	8	PDB header: protein transport Chain: A; PDB Molecule: dcc-interacting protein 13 alpha; PDBTitle: crystal structure of bar-ph domain of appl1
71	c3ipdB_	Alignment	not modelled	19.8	8	PDB header: exocytosis Chain: B; PDB Molecule: syntaxin-1a; PDBTitle: helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
72	c4qkvB_	Alignment	not modelled	19.7	15	PDB header: transcription Chain: B; PDB Molecule: polymerase i and transcript release factor; PDBTitle: crystal structure of the mouse cavin1 hr1 domain
73	c5wrgB_	Alignment	not modelled	19.0	13	PDB header: virus like particle Chain: B; PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
74	c3iv1F_	Alignment	not modelled	18.9	10	PDB header: hydrolase Chain: F; PDB Molecule: tumor susceptibility gene 101 protein; PDBTitle: coiled-coil domain of tumor susceptibility gene 101
75	c4modB_	Alignment	not modelled	18.7	12	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
76	c6nzkB_	Alignment	not modelled	18.5	15	PDB header: viral protein Chain: B; PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
77	c5zhyA_	Alignment	not modelled	18.3	7	PDB header: viral protein Chain: A; PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
78	c6grjG_	Alignment	not modelled	18.2	15	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.
79	c4lwsA_	Alignment	not modelled	17.9	6	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
80	c4qkwB_	Alignment	not modelled	17.8	15	PDB header: signaling protein Chain: B; PDB Molecule: muscle-related coiled-coil protein; PDBTitle: crystal structure of the zebrafish cavin4a hr1 domain
81	c3gvmA_	Alignment	not modelled	17.2	15	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein

						from streptococcus2 agalactiae
82	c3j6vL_	Alignment	not modelled	17.2	14	PDB header: ribosome Chain: L: PDB Molecule: 28s ribosomal protein s12, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
83	c5x5bB_	Alignment	not modelled	16.9	12	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
84	c3zbhC_	Alignment	not modelled	16.3	9	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
85	c5dmaA_	Alignment	not modelled	16.2	27	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pcra; PDBTitle: crystal structure of c-terminal tudor domain in pcra/uvrd helicase
86	c3j9vC_	Alignment	not modelled	16.1	17	PDB header: hydrolase Chain: C: PDB Molecule: v-type proton atpase catalytic subunit a; PDBTitle: yeast v-atpase state 3
87	c3jszA_	Alignment	not modelled	15.8	19	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: legionella pneumophila glucosyltransferase lgt1 n293a with udp-glc
88	d1guta_	Alignment	not modelled	15.7	20	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
89	d1h9ma1	Alignment	not modelled	15.6	18	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
90	c4e40A_	Alignment	not modelled	15.6	11	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the haptoglobin-hemoglobin receptor of trypanosoma congolense
91	c3dyjA_	Alignment	not modelled	15.1	7	PDB header: structural protein Chain: A: PDB Molecule: tal1n-1; PDBTitle: crystal structure a talin rod fragment
92	c5xlrC_	Alignment	not modelled	15.1	12	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
93	d1xmec1	Alignment	not modelled	14.6	32	Fold: Single transmembrane helix Superfamily: Bacterial ba3 type cytochrome c oxidase subunit IIa Family: Bacterial ba3 type cytochrome c oxidase subunit IIa
94	c3bvdC_	Alignment	not modelled	14.6	32	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome c oxidase polypeptide 2a; PDBTitle: structure of surface-engineered cytochrome ba3 oxidase from thermus2 thermophilus under xenon pressure, 100psi 5min
95	c3vr5C_	Alignment	not modelled	14.5	19	PDB header: hydrolase Chain: C: PDB Molecule: v-type sodium atpase catalytic subunit a; PDBTitle: crystal structure of nucleotide-free enterococcus hirae v1-atpase2 [ev1(l)]
96	c5n76C_	Alignment	not modelled	14.3	15	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
97	c1v5vA_	Alignment	not modelled	14.2	17	PDB header: transferase Chain: A: PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of a component of glycine cleavage system: t-protein2 from pyrococcus horikoshii ot3 at 1.5 a resolution
98	c3ghgl_	Alignment	not modelled	14.1	8	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
99	d2uubl1	Alignment	not modelled	13.7	25	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like