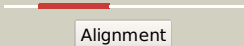
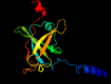
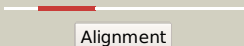

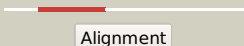



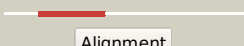

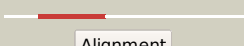
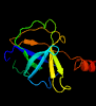
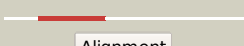
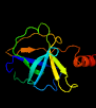



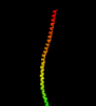
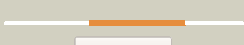
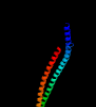


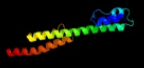

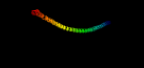

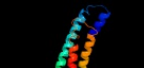


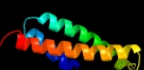
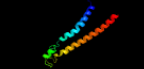


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3499c_(mce4A)_3918177_3919379
 Date Fri Aug 9 18:20:17 BST 2019
 Unique Job ID 551d5c34483ec732

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.8	17	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		99.5	17	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	c5uvnB_	 Alignment		99.2	19	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnF_	 Alignment		99.2	19	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnC_	 Alignment		99.2	19	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
6	c5uvnA_	 Alignment		99.2	19	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
7	c5uvnE_	 Alignment		99.2	19	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvnD_	 Alignment		99.2	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		90.5	7	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		88.3	11	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
11	c6b7nC_	 Alignment		81.5	11	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

12	c3lnrA_	Alignment		81.1	14	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
13	c2j5uB_	Alignment		68.8	14	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
14	c2ch7A_	Alignment		66.2	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
15	c5lp5F_	Alignment		63.0	23	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
16	c3cwgA_	Alignment		58.8	14	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
17	c2qf4A_	Alignment		57.8	16	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)
18	c5xbjA_	Alignment		57.2	14	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
19	d1st6a4	Alignment		53.4	12	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
20	c6nb3B_	Alignment		50.5	12	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing Ica60 antibody fab fragment2 (state 1)
21	c4abxB_	Alignment	not modelled	46.3	12	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
22	c5u0pU_	Alignment	not modelled	46.0	11	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
23	c1kmiZ_	Alignment	not modelled	45.1	15	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
24	c5zhyA_	Alignment	not modelled	44.6	7	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
25	c5szsC_	Alignment	not modelled	44.0	11	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
26	c6nzkB_	Alignment	not modelled	41.7	14	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
27	c1ei3E_	Alignment	not modelled	41.1	6	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
28	c2d4yA_	Alignment	not modelled	40.5	13	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
						PDB header: membrane protein

29	c4tkoB_	Alignment	not modelled	39.4	18	Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
30	c5x5bB_	Alignment	not modelled	39.3	10	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
31	c6cv0C_	Alignment	not modelled	37.5	9	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
32	c5dmaA_	Alignment	not modelled	37.3	20	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pcrA; PDBTitle: crystal structure of c-terminal tudor domain in pcrA/uvrd helicase
33	c3zx6A_	Alignment	not modelled	36.9	6	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
34	c5zuvB_	Alignment	not modelled	36.7	16	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
35	c5i08A_	Alignment	not modelled	35.7	12	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
36	c3jclC_	Alignment	not modelled	34.9	10	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
37	d1h9ma2	Alignment	not modelled	34.2	29	Fold: OB-fold Superfamily: MOP-like Family: BIMOP, duplicated molybdate-binding domain
38	c5n77A_	Alignment	not modelled	33.4	15	PDB header: transport protein Chain: A: PDB Molecule: magnesium transport protein cora; PDBTitle: crystal structure of the cytosolic domain of the cora magnesium2 channel from escherichia coli in complex with magnesium
39	c3j6vL_	Alignment	not modelled	33.2	18	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
40	c2jo1A_	Alignment	not modelled	32.4	26	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
41	c5n76C_	Alignment	not modelled	32.1	21	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
42	c2jp3A_	Alignment	not modelled	31.9	22	PDB header: transcription Chain: A: PDB Molecule: fxyd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
43	d1h9ra2	Alignment	not modelled	31.4	20	Fold: OB-fold Superfamily: MOP-like Family: BIMOP, duplicated molybdate-binding domain
44	c6e6aB_	Alignment	not modelled	31.4	16	PDB header: protein binding Chain: B: PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
45	c1zn1L_	Alignment	not modelled	31.1	26	PDB header: biosynthetic/structural protein/rna Chain: L: PDB Molecule: 30s ribosomal protein s12; PDBTitle: coordinates of rrf fitted into cryo-em map of the 70s post-termination2 complex
46	c3ok8A_	Alignment	not modelled	30.8	13	PDB header: protein binding Chain: A: PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: i-bar of pinkbar
47	d2uubl1	Alignment	not modelled	30.7	35	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
48	c3gvmA_	Alignment	not modelled	30.0	9	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
49	c3ghgK_	Alignment	not modelled	29.6	9	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
50	c5x5fC_	Alignment	not modelled	29.4	13	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
51	d1h9ma1	Alignment	not modelled	28.9	12	Fold: OB-fold Superfamily: MOP-like Family: BIMOP, duplicated molybdate-binding domain
52	c2mkvA_	Alignment	not modelled	27.7	35	PDB header: transport protein Chain: A: PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
53	c2ieqC_	Alignment	not modelled	26.9	20	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
						PDB header: unknown function

54	c4lwsA	Alignment	not modelled	26.7	9	Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
55	c1ei3C	Alignment	not modelled	25.9	11	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
56	c4wsrA	Alignment	not modelled	25.3	8	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: the crystal structure of hemagglutinin form a/chicken/new york/14677-2 13/1998
57	d2qall1	Alignment	not modelled	25.3	26	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
58	c4h8sA	Alignment	not modelled	25.2	13	PDB header: signaling protein Chain: A: PDB Molecule: dcc-interacting protein 13-beta; PDBTitle: crystal structure of human appl2barph domain
59	c2wpgA	Alignment	not modelled	24.8	8	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)
60	c3ur1C	Alignment	not modelled	24.4	24	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.
61	c6cs2A	Alignment	not modelled	23.5	10	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
62	d2cu6a1	Alignment	not modelled	23.4	14	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
63	d1guta	Alignment	not modelled	23.0	24	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
64	c4n21E	Alignment	not modelled	22.8	11	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
65	d1g4us1	Alignment	not modelled	22.6	17	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
66	c4c47B	Alignment	not modelled	22.2	17	PDB header: cell adhesion Chain: B: PDB Molecule: inner membrane lipoprotein; PDBTitle: salmonella enterica trimeric lipoprotein sadb
67	d1i94l	Alignment	not modelled	21.8	35	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
68	c2kg7B	Alignment	not modelled	21.8	16	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
69	c2l8sA	Alignment	not modelled	21.3	18	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
70	d1hcia4	Alignment	not modelled	21.1	3	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
71	c3bt6B	Alignment	not modelled	20.8	13	PDB header: viral protein Chain: B: PDB Molecule: influenza b hemagglutinin (ha); PDBTitle: crystal structure of influenza b virus hemagglutinin
72	c4fiuC	Alignment	not modelled	20.3	12	PDB header: viral protein Chain: C: PDB Molecule: hemagglutinin; PDBTitle: the structure of hemagglutinin of h16 subtype influenza virus with2 v327g mutation
73	c3qr8A	Alignment	not modelled	20.3	15	PDB header: viral protein Chain: A: PDB Molecule: baseplate assembly protein v; PDBTitle: crystal structure of the bacteriophage p2 membrane-piercing protein2 gpv
74	c3zbhC	Alignment	not modelled	19.9	11	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
75	c6g90Q	Alignment	not modelled	19.1	13	PDB header: splicing Chain: Q: PDB Molecule: cold sensitive u2 snrna suppressor 1; PDBTitle: prespliceosome structure provides insight into spliceosome assembly2 and regulation (map a2)
76	d1fr3a	Alignment	not modelled	19.0	12	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
77	c1ha0A	Alignment	not modelled	18.6	11	PDB header: viral protein Chain: A: PDB Molecule: protein (hemagglutinin precursor); PDBTitle: hemagglutinin precursor ha0
78	c2wrhl	Alignment	not modelled	18.5	10	PDB header: viral protein Chain: I: PDB Molecule: hemagglutinin ha2 chain; PDBTitle: structure of h1 duck albert hemagglutinin with human2 receptor
79	c2wr2B	Alignment	not modelled	18.4	9	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin; PDBTitle: structure of influenza h2 avian hemagglutinin with avian2 receptor
						PDB header: structural protein

80	c2kbbA_	Alignment	not modelled	18.2	16	Chain: A; PDB Molecule: talin-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
81	c6gajA_	Alignment	not modelled	18.1	10	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)
82	c2jwyA_	Alignment	not modelled	18.0	18	PDB header: lipoprotein Chain: A; PDB Molecule: uncharacterized lipoprotein yaji; PDBTitle: solution nmr structure of uncharacterized lipoprotein yaji from <i>Escherichia coli</i> . northeast structural genomics target er540
83	c4rh7A_	Alignment	not modelled	17.8	12	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 in 2 complex with adp.vi
84	d1wosa1	Alignment	not modelled	17.7	24	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
85	c1mqjB_	Alignment	not modelled	17.5	10	PDB header: viral protein Chain: B; PDB Molecule: hemagglutinin ha2 chain; PDBTitle: bha of ukr/63
86	c6gapB_	Alignment	not modelled	17.2	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
87	c1jccC_	Alignment	not modelled	17.2	27	PDB header: membrane protein Chain: C; PDB Molecule: major outer membrane lipoprotein; PDBTitle: crystal structure of a novel alanine-zipper trimer at 1.7 Å resolution, v13a, l16a, v20a, l23a, v27a, m30a, v34a mutations
88	d1wa8b1	Alignment	not modelled	16.8	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
89	c2p22A_	Alignment	not modelled	16.8	8	PDB header: transport protein Chain: A; PDB Molecule: suppressor protein stp22 of temperature-sensitive alpha- PDBTitle: structure of the yeast escrt-i heterotetramer core
90	c1deqO_	Alignment	not modelled	16.7	10	PDB header: blood clotting Chain: O; PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 Å resolution)
91	c1hgeD_	Alignment	not modelled	16.7	11	PDB header: viral protein Chain: D; PDB Molecule: hemagglutinin, (g135r), ha1 chain; PDBTitle: binding of influenza virus hemagglutinin to analogs of its cell-2 surface receptor, sialic acid: analysis by proton nuclear magnetic resonance spectroscopy and x-ray crystallography
92	c1p84E_	Alignment	not modelled	16.7	14	PDB header: oxidoreductase Chain: E; PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
93	c4h32L_	Alignment	not modelled	16.7	11	PDB header: viral protein Chain: L; PDB Molecule: hemagglutinin; PDBTitle: the crystal structure of the hemagglutinin h17 derived from bat2 influenza a virus
94	c2zxeG_	Alignment	not modelled	16.5	16	PDB header: hydrolase/transport protein Chain: G; PDB Molecule: phospholemman-like protein; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
95	c5c70B_	Alignment	not modelled	16.2	14	PDB header: hydrolase Chain: B; PDB Molecule: glucuronidase; PDBTitle: the structure of aspergillus oryzae beta-glucuronidase
96	c6iiuA_	Alignment	not modelled	16.1	5	PDB header: signaling protein Chain: A; PDB Molecule: soluble cytochrome b562, thromboxane a2 receptor, rubredoxin, PDBTitle: crystal structure of the human thromboxane a2 receptor bound to 2 ramatroban
97	c5wrgB_	Alignment	not modelled	16.1	19	PDB header: virus like particle Chain: B; PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
98	c1ru7B_	Alignment	not modelled	15.9	10	PDB header: viral protein Chain: B; PDB Molecule: hemagglutinin; PDBTitle: 1934 human h1 hemagglutinin
99	c1hzeB_	Alignment	not modelled	15.9	14	PDB header: transferase Chain: B; PDB Molecule: riboflavin synthase alpha chain; PDBTitle: solution structure of the n-terminal domain of riboflavin synthase2 from <i>E. coli</i>