

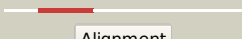

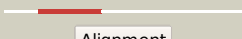




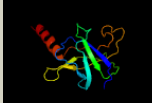


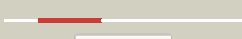



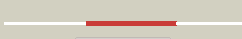
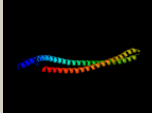

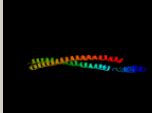


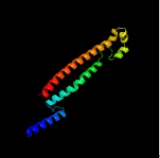
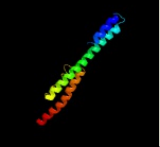
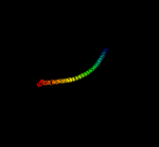
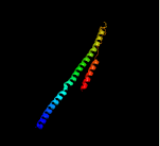

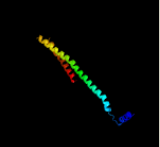
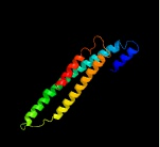
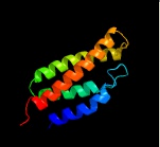
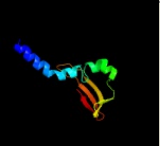


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1966_(mce3A)_2209335_2210612
 Date Mon Aug 5 13:25:06 BST 2019
 Unique Job ID 18008c7547b1f3f9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.9	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		99.7	23	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	c5uvnF_	 Alignment		99.5	18	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnE_	 Alignment		99.5	18	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnC_	 Alignment		99.5	18	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		99.5	18	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
7	c5uvnB_	 Alignment		99.5	18	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	18	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c3g67A_	 Alignment		94.5	7	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
10	c1qu7A_	 Alignment		88.2	9	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
11	c5szsC_	 Alignment		80.8	15	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

12	c6b7nC_	Alignment		79.6	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
13	c3lnrA_	Alignment		69.7	8	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
14	c2ch7A_	Alignment		67.9	12	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	c4n21E_	Alignment		62.3	15	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
16	c6gajA_	Alignment		60.3	13	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)
17	c1kmiZ_	Alignment		60.0	17	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
18	c3cwgA_	Alignment		58.3	8	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
19	d1st6a4	Alignment		57.4	16	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
20	c4hw9E_	Alignment		57.1	16	PDB header: membrane protein Chain: E: PDB Molecule: mechanosensitive channel msccs; PDBTitle: crystal structure of helicobacter pylori msccs (closed state)
21	c6cs2A_	Alignment	not modelled	55.8	13	PDB header: viral protein/hydrolase Chain: A: PDB Molecule: spike glycoprotein,fibrinin; PDBTitle: sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
22	c2kbbA_	Alignment	not modelled	55.4	18	PDB header: structural protein Chain: A: PDB Molecule: tal1n-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
23	c6nb3B_	Alignment	not modelled	55.1	18	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
24	c2qihA_	Alignment	not modelled	54.5	12	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
25	c3t9nG_	Alignment	not modelled	53.3	19	PDB header: membrane protein Chain: G: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: crystal structure of a membrane protein
26	c6cv0C_	Alignment	not modelled	52.6	16	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
27	c4rh7A_	Alignment	not modelled	49.4	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
28	c6nzkB_	Alignment	not modelled	48.0	18	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors

29	c5xbjA_	Alignment	not modelled	47.5	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar hook-associated protein flgk; PDBTitle: the structure of the flagellar hook junction protein hap1 (flgk) from <i>campylobacter jejuni</i>
30	d1ykhb1	Alignment	not modelled	47.4	6	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
31	c5zuvB_	Alignment	not modelled	47.2	24	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
32	c5u0pU_	Alignment	not modelled	44.7	8	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
33	c3ok8A_	Alignment	not modelled	44.4	9	PDB header: protein binding Chain: A: PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: i-bar of pinkbar
34	c3zx6A_	Alignment	not modelled	44.2	7	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
35	c5x5fC_	Alignment	not modelled	43.5	18	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
36	c3vkhA_	Alignment	not modelled	43.4	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
37	c5zhyA_	Alignment	not modelled	43.0	10	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
38	c5wrgB_	Alignment	not modelled	42.2	16	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
39	c4abxB_	Alignment	not modelled	40.5	11	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	c5i08A_	Alignment	not modelled	39.8	15	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
41	c2wpqA_	Alignment	not modelled	39.3	12	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)
42	c5n77A_	Alignment	not modelled	39.1	12	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
43	c3jclC_	Alignment	not modelled	37.8	20	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
44	c2ieqC_	Alignment	not modelled	37.7	15	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
45	c6b3oB_	Alignment	not modelled	35.3	22	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
46	c5x5bB_	Alignment	not modelled	33.7	11	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
47	c1wywB_	Alignment	not modelled	33.7	13	PDB header: viral protein Chain: B: PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
48	c2qf4A_	Alignment	not modelled	33.6	22	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)
49	c5xlrC_	Alignment	not modelled	33.4	13	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
50	c4e40A_	Alignment	not modelled	33.2	8	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the haptoglobin-hemoglobin receptor of trypanosoma congolense
51	c4njIA_	Alignment	not modelled	32.4	13	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
52	c2vv5D_	Alignment	not modelled	32.1	23	PDB header: membrane protein Chain: D: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: the open structure of mscs
53	c4wsrA_	Alignment	not modelled	31.3	13	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: the crystal structure of hemagglutinin form a/chicken/new

						york/14677-2 13/1998
54	d1g4us1	Alignment	not modelled	30.8	11	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
55	c2vs0B	Alignment	not modelled	30.8	14	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
56	c3gvmA	Alignment	not modelled	29.7	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
57	c6e6aB	Alignment	not modelled	29.2	10	PDB header: protein binding Chain: B: PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
58	c3j6vL	Alignment	not modelled	28.0	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
59	c5lp5F	Alignment	not modelled	27.4	38	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
60	c1zn1L	Alignment	not modelled	26.4	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
61	d1eq1a	Alignment	not modelled	26.3	12	Fold: Apolipoporphin-III Superfamily: Apolipoporphin-III Family: Apolipoporphin-III
62	d2uubl1	Alignment	not modelled	26.1	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
63	c5zkgB	Alignment	not modelled	25.9	15	PDB header: ligase Chain: B: PDB Molecule: aminoacyl-trna synthetase-interacting multifunctional PDBTitle: crystal structure of c-terminal domain of plasmodium vivax p43
64	c1deqF	Alignment	not modelled	24.7	8	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
65	c6qajB	Alignment	not modelled	23.8	4	PDB header: nuclear protein Chain: B: PDB Molecule: endolysin,transcription intermediary factor 1-beta; PDBTitle: structure of the tripartite motif of kap1/trim28
66	c1ei3E	Alignment	not modelled	22.8	13	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
67	c5xauD	Alignment	not modelled	22.8	18	PDB header: cell adhesion Chain: D: PDB Molecule: laminin subunit alpha-5; PDBTitle: crystal structure of integrin binding fragment of laminin-511
68	c4mc5C	Alignment	not modelled	22.2	10	PDB header: viral protein Chain: C: PDB Molecule: hemagglutinin; PDBTitle: crystal structure of a subtype h18 hemagglutinin homologue from2 a/flat-faced bat/peru/033/2010 (h18n11)
69	c2yfaA	Alignment	not modelled	20.6	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
70	d2qall1	Alignment	not modelled	20.6	26	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
71	c2l81A	Alignment	not modelled	19.6	10	PDB header: cell adhesion Chain: A: PDB Molecule: enhancer of filamentation 1; PDBTitle: solution nmr structure of the serine-rich domain of hef1 (enhancer of2 filamentation 1) from homo sapiens, northeast structural genomics3 consortium target hr5554a
72	d1ntga	Alignment	not modelled	18.4	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Myf domain
73	c2j9wB	Alignment	not modelled	17.9	11	PDB header: protein transport Chain: B: PDB Molecule: vps28-prov protein; PDBTitle: structural insight into the escrt-i-ii link and its role in mvb2 trafficking
74	d1i94L	Alignment	not modelled	17.9	32	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
75	c1deqO	Alignment	not modelled	17.9	12	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
76	c4fiuC	Alignment	not modelled	17.3	17	PDB header: viral protein Chain: C: PDB Molecule: hemagglutinin; PDBTitle: the structure of hemagglutinin of h16 subtype influenza virus with2 v327g mutation
77	d1hcia4	Alignment	not modelled	16.6	3	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
78	c5y4oA	Alignment	not modelled	16.4	24	PDB header: membrane protein Chain: A: PDB Molecule: low conductance mechanosensitive channel ynai; PDBTitle: cryo-em structure of mscs channel, ynai
79	c1ha0A	Alignment	not modelled	16.2	14	PDB header: viral protein Chain: A: PDB Molecule: protein (hemagglutinin precursor);

						PDBTitle: hemagglutinin precursor ha0
80	d1g7oa1	Alignment	not modelled	16.1	9	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
81	c2kg7B	Alignment	not modelled	16.1	13	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
82	d1fl0a	Alignment	not modelled	15.9	7	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Myf domain
83	c4iogD	Alignment	not modelled	15.9	10	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
84	d1oxza	Alignment	not modelled	15.6	11	Fold: Spectrin repeat-like Superfamily: GAT-like domain Family: GAT domain
85	c1oxzA	Alignment	not modelled	15.6	11	PDB header: membrane protein Chain: A: PDB Molecule: adp-ribosylation factor binding protein gga1; PDBTitle: crystal structure of the human gga1 gat domain
86	c6ezvX	Alignment	not modelled	15.4	12	PDB header: toxin Chain: X: PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
87	c3bt6B	Alignment	not modelled	15.2	17	PDB header: viral protein Chain: B: PDB Molecule: influenza b hemagglutinin (ha); PDBTitle: crystal structure of influenza b virus hemagglutinin
88	c4ut1A	Alignment	not modelled	15.2	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
89	c2bezC	Alignment	not modelled	15.1	14	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
90	c2d4yA	Alignment	not modelled	14.4	10	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
91	c2v75A	Alignment	not modelled	14.3	16	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear polyadenylated rna-binding protein nab2; PDBTitle: n-terminal domain of nab2
92	c2gl2B	Alignment	not modelled	14.3	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
93	d1szia	Alignment	not modelled	13.8	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
94	c2idxA	Alignment	not modelled	13.2	13	PDB header: transferase Chain: A: PDB Molecule: cob(i)yrinic acid a,c-diamide adenosyltransferase; PDBTitle: structure of human atp:cobalamin adenosyltransferase bound to atp.
95	c6j9rA	Alignment	not modelled	13.2	13	PDB header: translation Chain: A: PDB Molecule: brain tumor protein; PDBTitle: coiled-coil domain of drosophila trim protein brat
96	c3ur1C	Alignment	not modelled	13.1	19	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.
97	c5gasN	Alignment	not modelled	13.0	7	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
98	c4tkoB	Alignment	not modelled	13.0	15	PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
99	d2j9ua1	Alignment	not modelled	12.4	14	Fold: Four-helical up-and-down bundle Superfamily: VPS28 C-terminal domain-like Family: VPS28 C-terminal domain-like