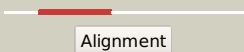

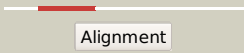



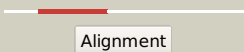

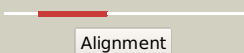

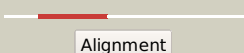
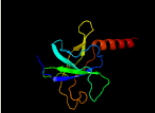




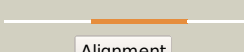
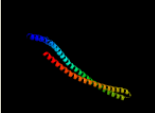
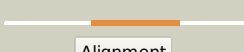
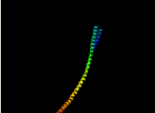
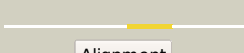

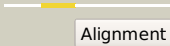
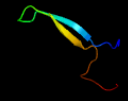
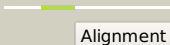

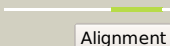
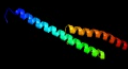


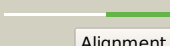
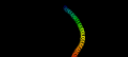
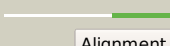
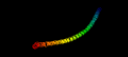
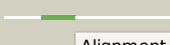
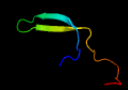
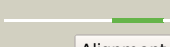


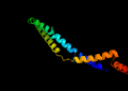
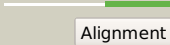

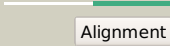
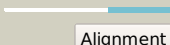
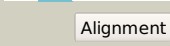
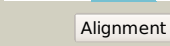
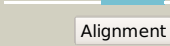
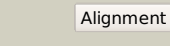


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0589_(mce2A)_686824_688038
Date	Fri Jul 26 01:50:14 BST 2019
Unique Job ID	3cbe45e44be458cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.8	22	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		99.6	18	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		99.3	14	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnC_	 Alignment		99.3	14	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnE_	 Alignment		99.3	14	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
6	c5uvnA_	 Alignment		99.3	14	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		99.3	14	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		99.3	14	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		89.8	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		85.0	12	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein i; PDBTitle: four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
11	d1st6a4	 Alignment		78.2	13	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin

12	c2j5uB_	 Alignment		73.7	11	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
13	c2qf4A_	 Alignment		66.8	11	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)
14	c3lnrA_	 Alignment		63.8	10	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
15	c5xbjA_	 Alignment		63.0	13	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
16	c3zx6A_	 Alignment		59.0	7	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
17	c2ch7A_	 Alignment		58.9	5	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
18	c5lp5F_	 Alignment		57.1	19	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
19	c2ieqC_	 Alignment		56.9	15	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
20	c4abxB_	 Alignment		55.8	10	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
21	c1kmiZ_	 Alignment	not modelled	54.7	10	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
22	c3cwgA_	 Alignment	not modelled	52.6	10	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
23	c6e6aB_	 Alignment	not modelled	40.8	13	PDB header: protein binding Chain: B: PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
24	d1ykhb1	 Alignment	not modelled	39.8	6	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
25	c3j6vL_	 Alignment	not modelled	39.1	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
26	c5n77A_	 Alignment	not modelled	38.9	13	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
27	c1deqF_	 Alignment	not modelled	37.6	11	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
28	c2d4yA_	 Alignment	not modelled	37.6	8	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)

29	c4rh7A_	Alignment	not modelled	37.2	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
30	d2uubl1	Alignment	not modelled	36.0	29	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
31	c2j0oA_	Alignment	not modelled	35.8	10	PDB header: cell invasion Chain: A: PDB Molecule: invasin ipad; PDBTitle: shigella flexneri ipad
32	d2j0oa1	Alignment	not modelled	35.8	10	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like
33	c1zn1L_	Alignment	not modelled	35.6	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
34	c5u0pU_	Alignment	not modelled	35.0	7	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
35	c6b7nC_	Alignment	not modelled	34.2	13	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
36	c5szsC_	Alignment	not modelled	32.6	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
37	c4hqjG_	Alignment	not modelled	32.1	13	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
38	c3kdpG_	Alignment	not modelled	32.0	13	PDB header: hydrolase Chain: G: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
39	c3kdpH_	Alignment	not modelled	32.0	13	PDB header: hydrolase Chain: H: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the sodium-potassium pump
40	c3vkhA_	Alignment	not modelled	31.8	12	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
41	c4hqjE_	Alignment	not modelled	31.4	13	PDB header: hydrolase/transport protein Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of na+,k+-atpase in the na+-bound state
42	c5zhyA_	Alignment	not modelled	30.9	9	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
43	d2qall1	Alignment	not modelled	29.8	26	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
44	c4n21E_	Alignment	not modelled	29.3	8	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
45	c5j9qH_	Alignment	not modelled	27.6	11	PDB header: transferase Chain: H: PDB Molecule: chromatin modification-related protein yng2; PDBTitle: crystal structure of the nua4 core complex
46	c2wpqA_	Alignment	not modelled	27.1	1	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)
47	d1i94L_	Alignment	not modelled	27.1	29	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
48	c2jp3A_	Alignment	not modelled	27.0	25	PDB header: transcription Chain: A: PDB Molecule: fyxd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fxyd4 (chif) protein in sds2 micelles
49	c5lskD_	Alignment	not modelled	26.8	9	PDB header: cell cycle Chain: D: PDB Molecule: kinetochore-associated protein dsn1 homolog; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
50	c2zzeG_	Alignment	not modelled	26.3	25	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
51	c6ezvX_	Alignment	not modelled	25.4	12	PDB header: toxin Chain: X: PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
52	c4ut1A_	Alignment	not modelled	24.1	8	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
53	c2jo1A_	Alignment	not modelled	23.6	25	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
						PDB header: membrane protein

54	c4tkoB_	Alignment	not modelled	23.5	17	Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
55	c2mkvA_	Alignment	not modelled	23.2	20	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
56	c4iogD_	Alignment	not modelled	23.0	15	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
57	c6cs2A_	Alignment	not modelled	21.6	11	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
58	c3w5aC_	Alignment	not modelled	21.4	17	PDB header: metal transport/membrane protein Chain: C: PDB Molecule: sarcolipin; PDBTitle: crystal structure of the calcium pump and sarcolipin from rabbit fast2 twitch skeletal muscle in the e1.mg2+ state
59	c4h1wB_	Alignment	not modelled	21.4	17	PDB header: hydrolase/hydrolase regulator Chain: B: PDB Molecule: sarcolipin; PDBTitle: e1 structure of the (sr) ca2+-atpase in complex with sarcolipin
60	c3jclC_	Alignment	not modelled	20.7	14	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
61	d1hcia4	Alignment	not modelled	20.5	7	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
62	c6cv0C_	Alignment	not modelled	20.4	7	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
63	c4wsrA_	Alignment	not modelled	19.8	10	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: the crystal structure of hemagglutinin form a/chicken/new york/14677-2 13/1998
64	c3nwiC_	Alignment	not modelled	19.6	8	PDB header: transport protein Chain: C: PDB Molecule: zinc transport protein zntb; PDBTitle: the soluble domain structure of the zntb zn2+ efflux system
65	c2wr2B_	Alignment	not modelled	19.2	13	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin; PDBTitle: structure of influenza h2 avian hemagglutinin with avian2 receptor
66	c3ck6E_	Alignment	not modelled	18.5	10	PDB header: structural protein Chain: E: PDB Molecule: putative membrane transport protein; PDBTitle: crystal structure of zntb cytoplasmic domain from vibrio2 parahaemolyticus rimd 2210633
67	c3ok8A_	Alignment	not modelled	18.5	14	PDB header: protein binding Chain: A: PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: i-bar of pinkbar
68	d1eq1a_	Alignment	not modelled	17.5	9	Fold: Apolipophorin-III Superfamily: Apolipophorin-III Family: Apolipophorin-III
69	c1ei3E_	Alignment	not modelled	17.5	8	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
70	c3n23E_	Alignment	not modelled	17.2	15	PDB header: hydrolase Chain: E: PDB Molecule: na+/k+ atpase gamma subunit transcript variant a; PDBTitle: crystal structure of the high affinity complex between ouabain and the e2p form of the sodium-potassium pump
71	d1szia_	Alignment	not modelled	17.2	16	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
72	c5zuvB_	Alignment	not modelled	16.4	13	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
73	c1bf5A_	Alignment	not modelled	15.9	10	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
74	c1p84E_	Alignment	not modelled	15.7	16	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
75	c3euhB_	Alignment	not modelled	15.0	13	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of the muke-mukf complex
76	c6cfzD_	Alignment	not modelled	14.8	18	PDB header: nuclear protein Chain: D: PDB Molecule: duo1; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
77	c3gvmA_	Alignment	not modelled	14.8	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
78	d2vzsa4	Alignment	not modelled	14.3	12	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
79	c3ghgK_	Alignment	not modelled	14.2	10	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain;

						PDBTitle: crystal structure of human fibrinogen
80	c4fiuC_	Alignment	not modelled	14.0	11	PDB header: viral protein Chain: C: PDB Molecule: hemagglutinin; PDBTitle: the structure of hemagglutinin of h16 subtype influenza virus with2 v327g mutation
81	c6ncxB_	Alignment	not modelled	13.9	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-galacturonidase; PDBTitle: crystal structure of gh2 beta-galacturonidase from eisenbergiella tayi2 bound to galacturonate
82	d1g4us1	Alignment	not modelled	13.9	15	Fold: Four-helical up-and-down bundle Superfamily: Bacterial GAP domain Family: Bacterial GAP domain
83	c2j9wB_	Alignment	not modelled	13.8	10	PDB header: protein transport Chain: B: PDB Molecule: vsps28-prov protein; PDBTitle: structural insight into the escrt-i-ii link and its role in mvb2 trafficking
84	d1g7oa1	Alignment	not modelled	13.5	12	Fold: GST C-terminal domain-like Superfamily: GST C-terminal domain-like Family: Glutathione S-transferase (GST), C-terminal domain
85	c3bt6B_	Alignment	not modelled	13.3	11	PDB header: viral protein Chain: B: PDB Molecule: influenza b hemagglutinin (ha); PDBTitle: crystal structure of influenza b virus hemagglutinin
86	c1p68A_	Alignment	not modelled	13.2	24	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed protein s-824; PDBTitle: solution structure of s-824, a de novo designed four helix2 bundle
87	c2v75A_	Alignment	not modelled	13.2	12	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear polyadenylated rna-binding protein nab2; PDBTitle: n-terminal domain of nab2
88	c4mc5C_	Alignment	not modelled	12.8	9	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)
89	c1ha0A_	Alignment	not modelled	12.7	8	PDB header: viral protein Chain: A: PDB Molecule: protein (hemagglutinin precursor); PDBTitle: hemagglutinin precursor ha0
90	c2beqA_	Alignment	not modelled	12.6	18	PDB header: viral protein Chain: A: PDB Molecule: e2 glycoprotein; PDBTitle: structure of a proteolytically resistant core from the severe acute2 respiratory syndrome coronavirus s2 fusion protein
91	c3ojaB_	Alignment	not modelled	12.4	10	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
92	c1mqIB_	Alignment	not modelled	12.2	9	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin ha2 chain; PDBTitle: bha of ukr/63
93	c2vs0B_	Alignment	not modelled	12.2	20	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
94	c2yfaA_	Alignment	not modelled	12.2	11	PDB header: receptor Chain: A: PDB Molecule: methyl-accepting chemotaxis transducer; PDBTitle: x-ray structure of mcps ligand binding domain in complex with malate
95	c6f0kA_	Alignment	not modelled	12.1	30	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
96	d2j9ua1	Alignment	not modelled	12.1	10	Fold: Four-helical up-and-down bundle Superfamily: VPS28 C-terminal domain-like Family: VPS28 C-terminal domain-like
97	c5c70B_	Alignment	not modelled	12.0	6	PDB header: hydrolase Chain: B: PDB Molecule: glucuronidase; PDBTitle: the structure of aspergillus oryzae beta-glucuronidase
98	c2mpnB_	Alignment	not modelled	11.8	19	PDB header: membrane protein Chain: B: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli
99	c2mpnA_	Alignment	not modelled	11.8	19	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli