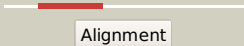
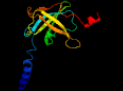
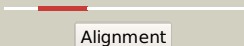

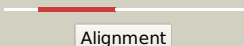












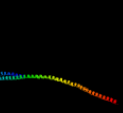
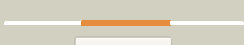
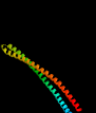

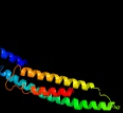
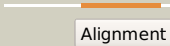

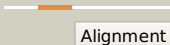
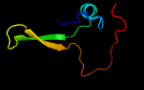
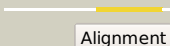
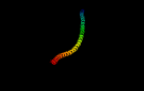
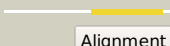
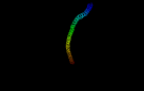
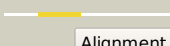
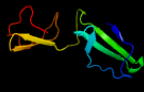
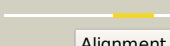
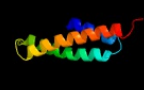
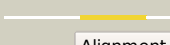

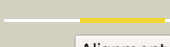
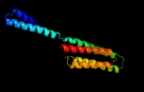
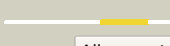

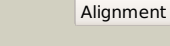
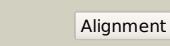
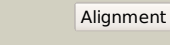
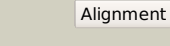



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1971_(mce3F)_2215265_2216578
Date	Mon Aug 5 13:25:07 BST 2019
Unique Job ID	183c01019a338b91

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.9	27	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		99.9	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	c5uvnB_	 Alignment		99.5	14	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnD_	 Alignment		99.5	14	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnF_	 Alignment		99.5	14	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
6	c5uvnC_	 Alignment		99.5	14	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
7	c5uvnE_	 Alignment		99.5	14	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvnA_	 Alignment		99.5	14	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c1qu7A_	 Alignment		94.7	17	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		84.3	6	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
11	c3cwgA_	 Alignment		83.6	12	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment

12	d1eq1a_	 Alignment		81.5	10	Fold: Apolipoporphin-III Superfamily: Apolipoporphin-III Family: Apolipoporphin-III
13	c2j5uB_	 Alignment		80.9	20	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
14	c3zx6A_	 Alignment		79.1	16	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
15	c2ch7A_	 Alignment		78.6	11	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
16	c2qf4A_	 Alignment		78.5	19	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		78.4	17	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
18	c5xbjA_	 Alignment		75.0	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	c2yfaA_	 Alignment		73.1	13	PDB header: receptor Chain: A: PDB Molecule: methyl-accepting chemotaxis transducer; PDBTitle: x-ray structure of mcps ligand binding domain in complex with malate
20	c2ieqC_	 Alignment		72.2	7	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
21	c3lnrA_	 Alignment	not modelled	66.9	9	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
22	c6e6aB_	 Alignment	not modelled	65.5	14	PDB header: protein binding Chain: B: PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
23	c2vs0B_	 Alignment	not modelled	59.8	15	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
24	c6evzX_	 Alignment	not modelled	59.2	9	PDB header: toxin Chain: X: PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
25	c4abxB_	 Alignment	not modelled	58.4	15	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
26	c5zhyA_	 Alignment	not modelled	58.1	8	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
27	c1kmiZ_	 Alignment	not modelled	55.3	16	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
28	c6b7nC_	 Alignment	not modelled	53.6	12	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
		 Alignment				PDB header: toxin

29	c6gy6Q_	Alignment	not modelled	50.5	9	Chain: Q: PDB Molecule: xaxa; PDBTitle: xaxab pore complex from xenorhabdus nematophila
30	c1deqF_	Alignment	not modelled	50.0	8	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
31	c2dnxA_	Alignment	not modelled	45.6	15	PDB header: transport protein Chain: A: PDB Molecule: syntaxin-12; PDBTitle: solution structure of rsgi ruh-063, an n-terminal domain of2 syntaxin 12 from human cdna
32	c5lp5F_	Alignment	not modelled	44.7	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
33	c4ut1A_	Alignment	not modelled	39.7	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
34	c4iogD_	Alignment	not modelled	34.7	11	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
35	c5u0pU_	Alignment	not modelled	32.5	14	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
36	d1h9ra2	Alignment	not modelled	32.2	16	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
37	c3ghgK_	Alignment	not modelled	32.1	7	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
38	c5n76C_	Alignment	not modelled	31.3	20	PDB header: nickel-binding protein Chain: C: PDB Molecule: coot; PDBTitle: crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
39	c1deqO_	Alignment	not modelled	28.0	7	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
40	d1h9ma2	Alignment	not modelled	26.8	28	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
41	c5wwlN_	Alignment	not modelled	26.1	15	PDB header: cell cycle Chain: N: PDB Molecule: kinetochore protein nnf1; PDBTitle: crystal structure of the schizogenesis pombe kinetochore mis12c2 subcomplex
42	c2l5bA_	Alignment	not modelled	25.7	17	PDB header: apoptosis Chain: A: PDB Molecule: activator of apoptosis harakiri; PDBTitle: solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
43	c2wpgA_	Alignment	not modelled	24.7	8	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	c5szsC_	Alignment	not modelled	24.3	8	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
45	c2kbbA_	Alignment	not modelled	23.9	14	PDB header: structural protein Chain: A: PDB Molecule: tal1n-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
46	c1ei3E_	Alignment	not modelled	23.8	7	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
47	c3ojaB_	Alignment	not modelled	23.2	14	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
48	c2y75F_	Alignment	not modelled	22.0	21	PDB header: transcription Chain: F: PDB Molecule: hth-type transcriptional regulator cymr; PDBTitle: the structure of cymr (yrzc) the global cysteine regulator of b.2 subtilis
49	c1bf5A_	Alignment	not modelled	21.6	10	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
50	c3ghgl_	Alignment	not modelled	20.9	10	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
51	c5wrgB_	Alignment	not modelled	20.5	12	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
52	c3gvmA_	Alignment	not modelled	19.4	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
53	c3j6vL_	Alignment	not modelled	18.5	19	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
54	d1h9ma1	Alignment	not modelled	18.5	20	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
55	c5dfzA_	Alignment	not modelled	18.3	11	PDB header: transferase Chain: A: PDB Molecule: vacuolar protein sorting-associated

55	c3ur2A_	Alignment	not modelled	18.3	11	protein 38; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
56	d2uub1	Alignment	not modelled	17.6	34	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
57	c4nj1A_	Alignment	not modelled	17.5	13	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
58	c4n21E_	Alignment	not modelled	17.4	12	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
59	d2j0oa1	Alignment	not modelled	17.4	9	Fold: lpaD-like Superfamily: lpaD-like Family: lpaD-like
60	c2j0oa_	Alignment	not modelled	17.4	9	PDB header: cell invasion Chain: A: PDB Molecule: invasin ipad; PDBTitle: shigella flexneri ipad
61	d1quua1	Alignment	not modelled	17.0	13	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
62	c5i08A_	Alignment	not modelled	16.9	11	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
63	c6gajA_	Alignment	not modelled	16.8	12	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)
64	c2mpnA_	Alignment	not modelled	16.7	23	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
65	c2mpnB_	Alignment	not modelled	16.7	23	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
66	c5x5bB_	Alignment	not modelled	16.4	11	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
67	c4lwsA_	Alignment	not modelled	16.2	11	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
68	c3ur1C_	Alignment	not modelled	16.2	8	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.
69	c5gasN_	Alignment	not modelled	16.0	15	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
70	d1s94a_	Alignment	not modelled	15.7	11	Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
71	c1s94A_	Alignment	not modelled	15.7	11	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: s-syntaxin; PDBTitle: crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
72	c2d4yA_	Alignment	not modelled	15.7	12	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
73	d1szia_	Alignment	not modelled	14.8	8	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
74	c2wr2B_	Alignment	not modelled	14.4	5	PDB header: viral protein Chain: B: PDB Molecule: hemagglutinin; PDBTitle: structure of influenza h2 avian hemagglutinin with avian2 receptor
75	c5cwsj_	Alignment	not modelled	14.3	7	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
76	c3c12A_	Alignment	not modelled	14.3	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar protein; PDBTitle: crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
77	c1zn1L_	Alignment	not modelled	14.0	28	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
78	d1wa8a1	Alignment	not modelled	13.9	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
79	d1i94I_	Alignment	not modelled	13.8	34	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
80	c1yv1B_	Alignment	not modelled	13.4	8	PDB header: signaling protein Chain: B: PDB Molecule: signal transducer and activator of transcription PDBTitle: structure of unphosphorylated stat1

81	c4wsrA_	Alignment	not modelled	13.3	3	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: the crystal structure of hemagglutinin form a/chicken/new york/14677-2 13/1998
82	d1hcia4	Alignment	not modelled	13.2	7	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
83	c1bg1A_	Alignment	not modelled	13.0	13	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
84	c3vkhA_	Alignment	not modelled	13.0	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
85	c4gkvB_	Alignment	not modelled	12.8	16	PDB header: transcription Chain: B: PDB Molecule: polymerase i and transcript release factor; PDBTitle: crystal structure of the mouse cavin1 hr1 domain
86	c1zvaA_	Alignment	not modelled	12.3	14	PDB header: viral protein Chain: A: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of sars virus membrane fusion
87	d2cu6a1	Alignment	not modelled	12.3	9	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
88	d2j9ua1	Alignment	not modelled	12.3	11	Fold: Four-helical up-and-down bundle Superfamily: VPS28 C-terminal domain-like Family: VPS28 C-terminal domain-like
89	c6gy8B_	Alignment	not modelled	12.2	14	PDB header: toxin Chain: B: PDB Molecule: xaxa; PDBTitle: crystal structure of xaxa from xenorhabdus nematophila
90	c6cfzG_	Alignment	not modelled	11.9	9	PDB header: nuclear protein Chain: G: PDB Molecule: hsk3; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
91	c1ei3C_	Alignment	not modelled	11.7	9	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
92	c3euhB_	Alignment	not modelled	11.7	10	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of the muke-mukf complex
93	c6gapB_	Alignment	not modelled	11.6	15	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
94	c2j9wB_	Alignment	not modelled	11.6	10	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
95	c1h9sA_	Alignment	not modelled	11.3	16	PDB header: transcription regulator Chain: A: PDB Molecule: molybdenum transport protein mode; PDBTitle: molybdate bound complex of dimop domain of mode from e.coli
96	c4lwsB_	Alignment	not modelled	11.2	11	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
97	c4f7gB_	Alignment	not modelled	10.9	13	PDB header: cell adhesion Chain: B: PDB Molecule: tal1n-1; PDBTitle: crystal structure of talin autoinhibition complex
98	c1eboE_	Alignment	not modelled	10.7	15	PDB header: viral protein Chain: E: PDB Molecule: ebola virus envelope protein chimera consisting PDBTitle: crystal structure of the ebola virus membrane-fusion2 subunit, gp2, from the envelope glycoprotein ectodomain
99	c4mc5C_	Alignment	not modelled	10.5	4	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)