
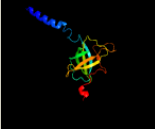







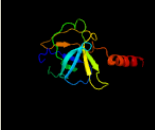





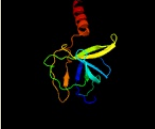

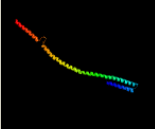

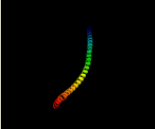

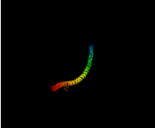
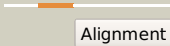
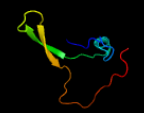
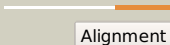
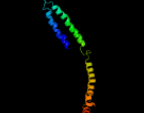
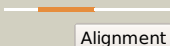
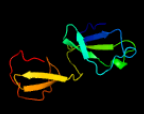
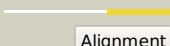

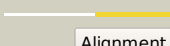
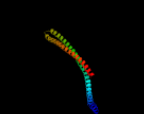
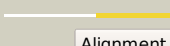
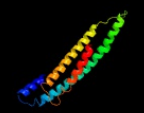
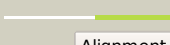

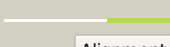
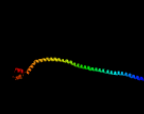
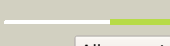
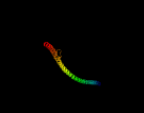
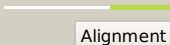

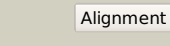
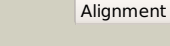
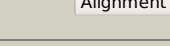

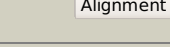
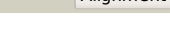


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0173_(lprK)_204063_205235
 Date Tue Jul 23 14:50:22 BST 2019
 Unique Job ID bb8345a820c54c21

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.9	20	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	26	PDB header: transport protein Chain: C: PDB Molecule: probable phospholipid abc transporter-binding protein mlad; PDBTitle: structure of e. coli mce protein mlad, core mce domain
3	c5uvnD_	 Alignment		99.5	12	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnF_	 Alignment		99.5	12	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		99.5	12	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	12	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		99.5	12	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvnB_	 Alignment		99.5	12	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c1qu7A_	 Alignment		89.7	13	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	c2wpgA_	 Alignment		88.4	10	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)
11	c3zx6A_	 Alignment		84.0	14	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant

12	c2j5uB_	 Alignment		82.4	13	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
13	c5u0pU_	 Alignment		82.3	11	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
14	c2qf4A_	 Alignment		81.5	13	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)
15	c3lnrA_	 Alignment		78.9	13	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
16	c3g67A_	 Alignment		77.3	12	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
17	c3cwgA_	 Alignment		70.6	9	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
18	d1eq1a_	 Alignment		68.4	11	Fold: Apolipoprotein-III Superfamily: Apolipoprotein-III Family: Apolipoprotein-III
19	c4rh7A_	 Alignment		66.2	7	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
20	c2qihA_	 Alignment		66.0	9	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
21	c6gajA_	 Alignment	not modelled	65.2	17	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)
22	c2ch7A_	 Alignment	not modelled	65.1	7	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
23	c3vkhA_	 Alignment	not modelled	62.5	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
24	c5xbjA_	 Alignment	not modelled	58.7	12	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
25	c5lp5F_	 Alignment	not modelled	58.4	16	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
26	c5lskD_	 Alignment	not modelled	55.4	11	PDB header: cell cycle Chain: D: PDB Molecule: kinetochore-associated protein dsn1 homolog; PDBTitle: crystal structure of the human kinetochore mis12-cenp-c complex
27	c1deqO_	 Alignment	not modelled	55.3	16	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
28	c1deqF_	 Alignment	not modelled	54.3	5	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at

						~42 angstrom resolution)
29	c2vs0B_	Alignment	not modelled	53.2	11	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
30	d1st6a4	Alignment	not modelled	52.0	18	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
31	d1h9ra2	Alignment	not modelled	51.9	24	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
32	c4tkoB_	Alignment	not modelled	49.0	13	PDB header: membrane protein Chain: B: PDB Molecule: emra; PDBTitle: structure of the periplasmic adaptor protein emra
33	d1v5va1	Alignment	not modelled	44.7	14	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
34	c3gvmA_	Alignment	not modelled	42.3	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
35	c2d4yA_	Alignment	not modelled	40.9	11	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
36	c5n76C_	Alignment	not modelled	40.4	15	PDB header: nickel-binding protein Chain: C: PDB Molecule: coot; PDBTitle: crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
37	c6b7nC_	Alignment	not modelled	39.7	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
38	d1h9ma2	Alignment	not modelled	39.2	28	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
39	c1bf5A_	Alignment	not modelled	39.1	8	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
40	d1guta_	Alignment	not modelled	38.8	16	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
41	c4zzkA_	Alignment	not modelled	38.8	14	PDB header: motor protein Chain: A: PDB Molecule: basal-body rod modification protein flgd; PDBTitle: crystal structure of truncated flgd (monoclinic form) from the human2 pathogen helicobacter pylori
42	c4iogD_	Alignment	not modelled	38.4	14	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
43	c1ei3E_	Alignment	not modelled	35.1	9	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
44	c4ut1A_	Alignment	not modelled	34.3	12	PDB header: motor protein Chain: A: PDB Molecule: flagellar hook-associated protein; PDBTitle: the structure of the flagellar hook junction protein flgk2 from burkholderia pseudomallei
45	d1ykhl1	Alignment	not modelled	34.0	15	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
46	c5cwsj_	Alignment	not modelled	33.6	9	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
47	d1h9ma1	Alignment	not modelled	33.0	26	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
48	c3ojaB_	Alignment	not modelled	30.1	10	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
49	c4abxB_	Alignment	not modelled	28.4	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
50	c5zuvB_	Alignment	not modelled	28.2	11	PDB header: viral protein, inhibitor Chain: B: PDB Molecule: spike glycoprotein,spike glycoprotein,inhibitor ek1; PDBTitle: crystal structure of the human coronavirus 229e hr1 motif in complex2 with pan-covs inhibitor ek1
51	c1kmiZ_	Alignment	not modelled	27.6	17	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
52	c6nb3B_	Alignment	not modelled	27.6	15	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
53	c1ei3C_	Alignment	not modelled	25.8	11	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
54	d2uubl1	Alignment	not modelled	25.6	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like

55	d1st6a3	Alignment	not modelled	25.4	10	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
56	c3j6vL_	Alignment	not modelled	25.0	13	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
57	c6gapB_	Alignment	not modelled	24.9	12	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
58	c5wrgB_	Alignment	not modelled	24.4	13	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
59	c3c12A_	Alignment	not modelled	24.3	21	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
60	d1wosa1	Alignment	not modelled	24.1	14	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
61	c1zn1L_	Alignment	not modelled	22.2	6	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
62	c3ghgK_	Alignment	not modelled	21.9	16	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
63	c5j2IB_	Alignment	not modelled	19.3	17	PDB header: de novo protein Chain: B: PDB Molecule: protein design 214hc2_11; PDBTitle: de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
64	d2vzsa2	Alignment	not modelled	18.8	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: beta-Galactosidase/glucuronidase domain Family: beta-Galactosidase/glucuronidase domain
65	d1i94I_	Alignment	not modelled	18.5	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
66	c4modB_	Alignment	not modelled	18.4	14	PDB header: viral protein Chain: B: PDB Molecule: hr1 of s protein, linker, hr2 of s protein; PDBTitle: structure of the mers-cov fusion core
67	c1h9sA_	Alignment	not modelled	18.2	24	PDB header: transcription regulator Chain: A: PDB Molecule: molybdenum transport protein mode; PDBTitle: molybdate bound complex of dimop domain of mode from e.coli
68	c4lwsB_	Alignment	not modelled	18.0	14	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
69	d2qall1	Alignment	not modelled	17.8	6	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
70	c3m9hB_	Alignment	not modelled	17.6	12	PDB header: chaperone Chain: B: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa
71	c1v5vA_	Alignment	not modelled	17.1	17	PDB header: transferase Chain: A: PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of a component of glycine cleavage system: t-protein2 from pyrococcus horikoshii ot3 at 1.5 a resolution
72	d1fr3a_	Alignment	not modelled	17.0	18	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
73	c3dyjA_	Alignment	not modelled	16.9	9	PDB header: structural protein Chain: A: PDB Molecule: tal1n-1; PDBTitle: crystal structure a talin rod fragment
74	c5yfpG_	Alignment	not modelled	16.8	15	PDB header: exocytosis Chain: G: PDB Molecule: exocyst complex component exo70; PDBTitle: cryo-em structure of the exocyst complex
75	c6cfzD_	Alignment	not modelled	16.7	15	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
76	d1x9la_	Alignment	not modelled	15.6	17	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: DR1885-like metal-binding protein Family: DR1885-like metal-binding protein
77	c4njIA_	Alignment	not modelled	15.4	7	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
78	c6gaoC_	Alignment	not modelled	15.2	11	PDB header: viral protein Chain: C: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail and body
79	c2bezC_	Alignment	not modelled	15.0	6	PDB header: viral protein Chain: C: PDB Molecule: e2 glycoprotein; PDBTitle: structure of a proteolytically resistant core from the severe acute2 respiratory syndrome coronavirus s2 fusion protein
80	c1cz5A_	Alignment	not modelled	14.9	11	PDB header: hydrolase Chain: A: PDB Molecule: vcp-like atpase; PDBTitle: nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
81	c2nr9A_	Alignment	not modelled	14.9	15	PDB header: viral protein Chain: A: PDB Molecule: baseplate assembly protein v;

81	c5qr6A_	Alignment	not modelled	14.5	15	PDBTitle: crystal structure of the bacteriophage p2 membrane-piercing protein2 gpv
82	d1st6a5	Alignment	not modelled	13.9	16	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
83	c6nzkB_	Alignment	not modelled	13.9	10	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
84	c5xlrC_	Alignment	not modelled	13.7	7	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
85	c1zvzA_	Alignment	not modelled	13.5	9	PDB header: protein binding Chain: A: PDB Molecule: vinculin; PDBTitle: vinculin head (0-258) in complex with the talin rod residue2 820-844
86	c4lwsA_	Alignment	not modelled	13.3	6	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
87	c5wwlN_	Alignment	not modelled	13.1	9	PDB header: cell cycle Chain: N: PDB Molecule: kinetochore protein nnf1; PDBTitle: crystal structure of the schizogenesis pombe kinetochore mis12c2 subcomplex
88	c5zhyA_	Alignment	not modelled	13.1	11	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
89	d1k0ha_	Alignment	not modelled	12.9	6	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: gpFII-like
90	c3zbhC_	Alignment	not modelled	12.8	10	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
91	c2k6zA_	Alignment	not modelled	12.6	14	PDB header: metal transport Chain: A: PDB Molecule: putative uncharacterized protein ttha1943; PDBTitle: solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
92	c5tpjA_	Alignment	not modelled	12.6	5	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
93	c3ur1C_	Alignment	not modelled	12.6	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.
94	c3ghgl_	Alignment	not modelled	12.2	11	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
95	c6grjG_	Alignment	not modelled	11.6	17	PDB header: toxin Chain: G: PDB Molecule: ahlb; PDBTitle: structure of the ahlb pore of the tripartite alpha-pore forming toxin,2 ahl, from aeromonas hydrophila.
96	c3ipdB_	Alignment	not modelled	11.5	12	PDB header: exocytosis Chain: B: PDB Molecule: syntaxin-1a; PDBTitle: helical extension of the neuronal snare complex into the2 membrane, spacegroup i 21 21 21
97	c3htrB_	Alignment	not modelled	11.4	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized prc-barrel domain protein; PDBTitle: crystal structure of prc-barrel domain protein from2 rhodospseudomonas palustris
98	c4s37F_	Alignment	not modelled	11.3	10	PDB header: metal binding protein Chain: F: PDB Molecule: phage baseplate protein; PDBTitle: crystal structure of r2 pyocin membrane-piercing spike
99	d1h9ra1	Alignment	not modelled	11.0	18	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain