


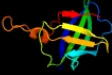





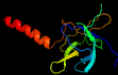



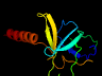



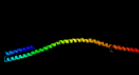




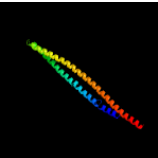

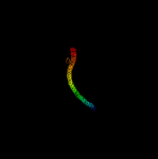
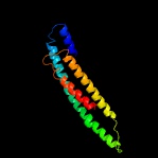


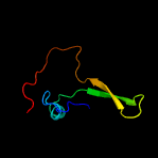

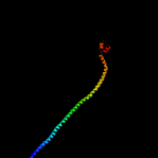


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1970_(lprM)_2214131_2215264
Date	Mon Aug 5 13:25:07 BST 2019
Unique Job ID	2a5a79517788612a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ic4C_</a>	 Alignment		99.9	25	<b>PDB header:</b> protein transport <b>Chain:</b> C; <b>PDB Molecule:</b> toluene tolerance efflux transporter (abc superfamily, <b>PDBTitle:</b> cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
2	<a href="#">c5uw8C_</a>	 Alignment		99.9	19	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> probable phospholipid abc transporter-binding protein mlad; <b>PDBTitle:</b> structure of e. coli mce protein mlad, core mce domain
3	<a href="#">c5uvnE_</a>	 Alignment		99.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> E; <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
4	<a href="#">c5uvnA_</a>	 Alignment		99.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
5	<a href="#">c5uvnD_</a>	 Alignment		99.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> D; <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
6	<a href="#">c5uvnC_</a>	 Alignment		99.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
7	<a href="#">c5uvnB_</a>	 Alignment		99.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> B; <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
8	<a href="#">c5uvnF_</a>	 Alignment		99.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> paraquat-inducible protein b; <b>PDBTitle:</b> structure of e. coli mce protein pqib, periplasmic domain
9	<a href="#">c1qu7A_</a>	 Alignment		94.0	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> methyl-accepting chemotaxis protein i; <b>PDBTitle:</b> four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
10	<a href="#">c2wpgA_</a>	 Alignment		91.3	6	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> trimeric autotransporter adhesin fragment; <b>PDBTitle:</b> salmonella enterica sada 479-519 fused to gcn4 adaptors (sadaK3, in-2 register fusion)
11	<a href="#">c2qf4A_</a>	 Alignment		89.8	12	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> cell shape determining protein mrec; <b>PDBTitle:</b> high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)

12	<a href="#">c3g67A_</a>	Alignment		87.3	11	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of a soluble chemoreceptor from thermotoga2 maritima
13	<a href="#">d1eq1a_</a>	Alignment		85.7	15	<b>Fold:</b> Apolipoprotein-III <b>Superfamily:</b> Apolipoprotein-III <b>Family:</b> Apolipoprotein-III
14	<a href="#">c3zx6A_</a>	Alignment		85.4	16	<b>PDB header:</b> signaling <b>Chain:</b> A: <b>PDB Molecule:</b> hamp, methyl-accepting chemotaxis protein i; <b>PDBTitle:</b> structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
15	<a href="#">c3cwgA_</a>	Alignment		83.5	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> unphosphorylated mouse stat3 core fragment
16	<a href="#">c3lnrA_</a>	Alignment		83.5	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> aerotaxis transducer aer2; <b>PDBTitle:</b> crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
17	<a href="#">c2ch7A_</a>	Alignment		82.3	6	<b>PDB header:</b> chemotaxis <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
18	<a href="#">c2j5uB_</a>	Alignment		78.2	15	<b>PDB header:</b> cell shape regulation <b>Chain:</b> B: <b>PDB Molecule:</b> mrec protein; <b>PDBTitle:</b> mrec lysteria monocytogenes
19	<a href="#">c1deqF_</a>	Alignment		78.0	8	<b>PDB header:</b> blood clotting <b>Chain:</b> F: <b>PDB Molecule:</b> fibrinogen (gamma chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
20	<a href="#">c4rh7A_</a>	Alignment		74.9	12	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein/cytoplasmic dynein 2 heavy chain <b>PDBTitle:</b> crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
21	<a href="#">c4tkoB_</a>	Alignment	not modelled	73.7	18	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> emra; <b>PDBTitle:</b> structure of the periplasmic adaptor protein emra
22	<a href="#">c3vkhA_</a>	Alignment	not modelled	73.5	11	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of a functional full-length dynein motor domain
23	<a href="#">c1deqO_</a>	Alignment	not modelled	73.0	15	<b>PDB header:</b> blood clotting <b>Chain:</b> O: <b>PDB Molecule:</b> fibrinogen (beta chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
24	<a href="#">c5xbjA_</a>	Alignment	not modelled	71.2	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar hook-associated protein flgk; <b>PDBTitle:</b> the structure of the flagellar hook junction protein hap1 (flgk) from2 campylobacter jejuni
25	<a href="#">c2qihA_</a>	Alignment	not modelled	71.0	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> protein uspa1; <b>PDBTitle:</b> crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
26	<a href="#">c1kmiZ_</a>	Alignment	not modelled	67.7	12	<b>PDB header:</b> signaling protein <b>Chain:</b> Z: <b>PDB Molecule:</b> chemotaxis protein chez; <b>PDBTitle:</b> crystal structure of an e.coli chemotaxis protein, chez
27	<a href="#">c5lp5F_</a>	Alignment	not modelled	64.6	22	<b>PDB header:</b> hydrolase/antibiotic <b>Chain:</b> F: <b>PDB Molecule:</b> rod shape-determining protein (mrec); <b>PDBTitle:</b> complex between penicillin-binding protein (pbp2) and mrec from2 helicobacter pylori
28	<a href="#">c3ojaB_</a>	Alignment	not modelled	61.7	8	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anopheles plasmodium-responsive leucine-rich repeat protein <b>PDBTitle:</b> crystal structure of lrim1/ap1c complex <b>PDB header:</b> viral protein

29	<a href="#">c6gajA_</a>	Alignment	not modelled	61.7	10	<b>Chain:</b> A; <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
30	<a href="#">c3ghgl_</a>	Alignment	not modelled	61.6	5	<b>PDB header:</b> blood clotting <b>Chain:</b> I; <b>PDB Molecule:</b> fibrinogen gamma chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
31	<a href="#">c5u0pU_</a>	Alignment	not modelled	61.4	16	<b>PDB header:</b> transcription <b>Chain:</b> U; <b>PDB Molecule:</b> mediator complex subunit 21; <b>PDBTitle:</b> cryo-em structure of the transcriptional mediator
32	<a href="#">c2d4yA_</a>	Alignment	not modelled	60.3	14	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> flagellar hook-associated protein 1; <b>PDBTitle:</b> crystal structure of a 49k fragment of hap1 (flgk)
33	<a href="#">d1st6a4</a>	Alignment	not modelled	59.3	14	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
34	<a href="#">c6b7nC_</a>	Alignment	not modelled	54.0	8	<b>PDB header:</b> viral protein <b>Chain:</b> C; <b>PDB Molecule:</b> spike protein; <b>PDBTitle:</b> cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state
35	<a href="#">c1bf5A_</a>	Alignment	not modelled	53.7	9	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A; <b>PDB Molecule:</b> signal transducer and activator of transcription 1- <b>PDBTitle:</b> tyrosine phosphorylated stat-1/dna complex
36	<a href="#">c5cwsj_</a>	Alignment	not modelled	53.2	10	<b>PDB header:</b> protein transport <b>Chain:</b> J; <b>PDB Molecule:</b> nucleoporin nup49; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
37	<a href="#">c1ei3E_</a>	Alignment	not modelled	46.8	10	<b>PDB header:</b> blood clotting <b>Chain:</b> E; <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
38	<a href="#">c1ei3C_</a>	Alignment	not modelled	46.5	9	<b>PDB header:</b> blood clotting <b>Chain:</b> C; <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
39	<a href="#">c5lskD_</a>	Alignment	not modelled	44.2	16	<b>PDB header:</b> cell cycle <b>Chain:</b> D; <b>PDB Molecule:</b> kinetochore-associated protein dsn1 homolog; <b>PDBTitle:</b> crystal structure of the human kinetochore mis12-cenp-c complex
40	<a href="#">c4ut1A_</a>	Alignment	not modelled	43.8	11	<b>PDB header:</b> motor protein <b>Chain:</b> A; <b>PDB Molecule:</b> flagellar hook-associated protein; <b>PDBTitle:</b> the structure of the flagellar hook junction protein flgk2 from burkholderia pseudomallei
41	<a href="#">c3zbhC_</a>	Alignment	not modelled	43.7	8	<b>PDB header:</b> unknown function <b>Chain:</b> C; <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
42	<a href="#">d1h9ra2</a>	Alignment	not modelled	42.3	32	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain
43	<a href="#">c5n76C_</a>	Alignment	not modelled	41.0	25	<b>PDB header:</b> nickel-binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> coot; <b>PDBTitle:</b> crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
44	<a href="#">c3gvmA_</a>	Alignment	not modelled	40.4	13	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein sag1039; <b>PDBTitle:</b> structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
45	<a href="#">d1st6a3</a>	Alignment	not modelled	39.8	14	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
46	<a href="#">c6gapB_</a>	Alignment	not modelled	39.5	10	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t3d reovirus sigma1 coiled coil tail and body
47	<a href="#">c3ghgK_</a>	Alignment	not modelled	39.2	17	<b>PDB header:</b> blood clotting <b>Chain:</b> K; <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
48	<a href="#">c4zzkA_</a>	Alignment	not modelled	37.3	16	<b>PDB header:</b> motor protein <b>Chain:</b> A; <b>PDB Molecule:</b> basal-body rod modification protein flgd; <b>PDBTitle:</b> crystal structure of truncated flgd (monoclinic form) from the human2 pathogen helicobacter pylori
49	<a href="#">c4abxB_</a>	Alignment	not modelled	36.1	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> dna repair protein recn; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans recn coiled-2 coil domain
50	<a href="#">d1ykbb1</a>	Alignment	not modelled	35.7	11	<b>Fold:</b> Mediator hinge subcomplex-like <b>Superfamily:</b> Mediator hinge subcomplex-like <b>Family:</b> CSE2-like
51	<a href="#">d1h9ma2</a>	Alignment	not modelled	35.4	36	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain
52	<a href="#">c5yfpG_</a>	Alignment	not modelled	34.7	13	<b>PDB header:</b> exocytosis <b>Chain:</b> G; <b>PDB Molecule:</b> exocyst complex component exo70; <b>PDBTitle:</b> cryo-em structure of the exocyst complex
53	<a href="#">c6e6aB_</a>	Alignment	not modelled	34.2	12	<b>PDB header:</b> protein binding <b>Chain:</b> B; <b>PDB Molecule:</b> inclusion membrane protein a; <b>PDBTitle:</b> triclinic crystal form of inca g144a point mutant
54	<a href="#">c4lwsB_</a>	Alignment	not modelled	33.0	13	<b>PDB header:</b> unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
55	<a href="#">d1h9ma1</a>	Alignment	not modelled	31.0	28	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like

						<b>Family:</b> BiMOP, duplicated molybdate-binding domain
56	<a href="#">c4wsrA</a>	Alignment	not modelled	29.3	11	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> the crystal structure of hemagglutinin form a/chicken/new york/14677-2 13/1998
57	<a href="#">c4iogD</a>	Alignment	not modelled	28.5	10	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> secreted protein esxb; <b>PDBTitle:</b> the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
58	<a href="#">c2vs0B</a>	Alignment	not modelled	28.5	13	<b>PDB header:</b> cell invasion <b>Chain:</b> B: <b>PDB Molecule:</b> virulence factor esxa; <b>PDBTitle:</b> structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
59	<a href="#">d1v5va1</a>	Alignment	not modelled	27.7	17	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
60	<a href="#">c2nrjA</a>	Alignment	not modelled	26.3	11	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> hbl b protein; <b>PDBTitle:</b> crystal structure of hemolysin binding component from2 bacillus cereus
61	<a href="#">c6ewyA</a>	Alignment	not modelled	26.2	9	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan endopeptidase ripa; <b>PDBTitle:</b> ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
62	<a href="#">c4modB</a>	Alignment	not modelled	25.4	17	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hr1 of s protein, linker, hr2 of s protein; <b>PDBTitle:</b> structure of the mers-cov fusion core
63	<a href="#">c5j65A</a>	Alignment	not modelled	25.0	16	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> pesticidal crystal protein cry6aa; <b>PDBTitle:</b> crystal structure of trypsin activated cry6aa
64	<a href="#">c3c12A</a>	Alignment	not modelled	24.8	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein; <b>PDBTitle:</b> crystal structure of flagd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
65	<a href="#">c5j2lB</a>	Alignment	not modelled	24.8	17	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein design 2l4hc2_11; <b>PDBTitle:</b> de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
66	<a href="#">c2ieqC</a>	Alignment	not modelled	22.7	10	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
67	<a href="#">d2vzsa2</a>	Alignment	not modelled	22.5	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> beta-Galactosidase/glucuronidase domain <b>Family:</b> beta-Galactosidase/glucuronidase domain
68	<a href="#">c4wa0A</a>	Alignment	not modelled	21.3	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> possible adhesin; <b>PDBTitle:</b> the structure of a possible adhesin c-terminal domain from2 caldicellulosiruptor kronotskyensis
69	<a href="#">c6grjG</a>	Alignment	not modelled	21.2	18	<b>PDB header:</b> toxin <b>Chain:</b> G: <b>PDB Molecule:</b> ahlb; <b>PDBTitle:</b> structure of the ahlb pore of the tripartite alpha-pore forming toxin,2 ahl, from aeromonas hydrophila.
70	<a href="#">d1wosa1</a>	Alignment	not modelled	20.9	21	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
71	<a href="#">c1qoyA</a>	Alignment	not modelled	19.9	12	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> hemolysin e; <b>PDBTitle:</b> e.coli hemolysin e (hlye, clya, shea)
72	<a href="#">c3pe0B</a>	Alignment	not modelled	19.9	11	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> plectin; <b>PDBTitle:</b> structure of the central region of the plakin domain of plectin
73	<a href="#">c1yvlB</a>	Alignment	not modelled	19.8	9	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> structure of unphosphorylated stat1
74	<a href="#">c5zuvB</a>	Alignment	not modelled	19.6	19	<b>PDB header:</b> viral protein, inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein,spike glycoprotein,inhibitor ek1; <b>PDBTitle:</b> crystal structure of the human coronavirus 229e hr1 motif in complex2 with pan-covs inhibitor ek1
75	<a href="#">d1hcia4</a>	Alignment	not modelled	19.6	11	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
76	<a href="#">c5gasN</a>	Alignment	not modelled	18.5	8	<b>PDB header:</b> hydrolase <b>Chain:</b> N: <b>PDB Molecule:</b> archaeal/vacuolar-type h+-atpase subunit i; <b>PDBTitle:</b> thermus thermophilus v/a-atpase, conformation 2
77	<a href="#">c3bt6B</a>	Alignment	not modelled	18.5	11	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> influenza b hemagglutinin (ha); <b>PDBTitle:</b> crystal structure of influenza b virus hemagglutinin
78	<a href="#">c5nmoA</a>	Alignment	not modelled	18.3	12	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein smc,chromosome partition <b>PDBTitle:</b> structure of the bacillus subtilis smc joint domain
79	<a href="#">c5lskA</a>	Alignment	not modelled	18.0	13	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> protein mis12 homolog; <b>PDBTitle:</b> crystal structure of the human kinetochore mis12-cenp-c complex
80	<a href="#">c1cz5A</a>	Alignment	not modelled	18.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> vcp-like atpase; <b>PDBTitle:</b> nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
81	<a href="#">c4lwsA</a>	Alignment	not modelled	17.7	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora

					curvata
82	<a href="#">c4xa3A_</a>	Alignment	not modelled	17.2	14 <b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp7-myh7(1361-1425)-eb1 chimera protein; <b>PDBTitle:</b> crystal structure of the coiled-coil surrounding skip 2 of myh7
83	<a href="#">c2iakA_</a>	Alignment	not modelled	17.0	8 <b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> bullous pemphigoid antigen 1, isoform 5; <b>PDBTitle:</b> crystal structure of a protease resistant fragment of the plakin2 domain of bullous pemphigoid antigen1 (bpag1)
84	<a href="#">c3j6vL_</a>	Alignment	not modelled	17.0	19 <b>PDB header:</b> ribosome <b>Chain:</b> L: <b>PDB Molecule:</b> 28s ribosomal protein s12, mitochondrial; <b>PDBTitle:</b> cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
85	<a href="#">c5szsC_</a>	Alignment	not modelled	16.7	15 <b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> glycan shield and epitope masking of a coronavirus spike protein2 observed by cryo-electron microscopy
86	<a href="#">c1ha0A_</a>	Alignment	not modelled	16.7	11 <b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hemagglutinin precursor); <b>PDBTitle:</b> hemagglutinin precursor ha0
87	<a href="#">c5wrgB_</a>	Alignment	not modelled	16.5	19 <b>PDB header:</b> virus like particle <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> sars-cov spike glycoprotein
88	<a href="#">c5zhyA_</a>	Alignment	not modelled	16.4	23 <b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein, spike glycoprotein; <b>PDBTitle:</b> structural characterization of the hcov-229e fusion core
89	<a href="#">c6ezvX_</a>	Alignment	not modelled	16.4	9 <b>PDB header:</b> toxin <b>Chain:</b> X: <b>PDB Molecule:</b> non-hemolytic enterotoxin lytic component l1; <b>PDBTitle:</b> the cytotoxin maka from vibrio cholerae
90	<a href="#">c2gl2B_</a>	Alignment	not modelled	16.3	11 <b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> adhesion a; <b>PDBTitle:</b> crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of2 bacterial adhesin fada
91	<a href="#">c4fiuC_</a>	Alignment	not modelled	16.0	10 <b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> the structure of hemagglutinin of h16 subtype influenza virus with2 v327g mutation
92	<a href="#">d1t01a1</a>	Alignment	not modelled	15.9	14 <b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
93	<a href="#">c2q13A_</a>	Alignment	not modelled	15.9	8 <b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> dcc-interacting protein 13 alpha; <b>PDBTitle:</b> crystal structure of bar-ph domain of appl1
94	<a href="#">d2uubl1</a>	Alignment	not modelled	15.7	29 <b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
95	<a href="#">c1v5vA_</a>	Alignment	not modelled	15.5	20 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminomethyltransferase; <b>PDBTitle:</b> crystal structure of a component of glycine cleavage system: t-protein2 from pyrococcus horikoshii ot3 at 1.5 a resolution
96	<a href="#">c3qr8A_</a>	Alignment	not modelled	15.2	10 <b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> baseplate assembly protein v; <b>PDBTitle:</b> crystal structure of the bacteriophage p2 membrane-piercing protein2 gpv
97	<a href="#">c2wr2B_</a>	Alignment	not modelled	15.1	12 <b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> structure of influenza h2 avian hemagglutinin with avian2 receptor
98	<a href="#">c4e40A_</a>	Alignment	not modelled	15.1	11 <b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> the haptoglobin-hemoglobin receptor of trypanosoma congolense
99	<a href="#">c6cfzD_</a>	Alignment	not modelled	14.9	10 <b>PDB header:</b> nuclear protein <b>Chain:</b> D: <b>PDB Molecule:</b> duo1; <b>PDBTitle:</b> structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface