




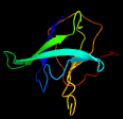

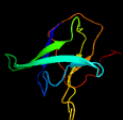

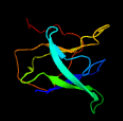



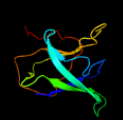

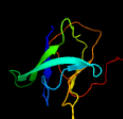



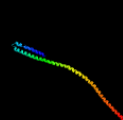


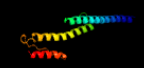
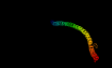
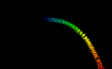

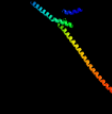
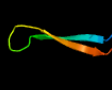
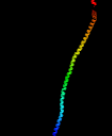
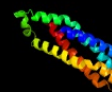
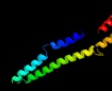


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0170\_(mce1B)\_199893\_200933  
 Date Tue Jul 23 14:50:22 BST 2019  
 Unique Job ID 4ca1867f4e1a6497

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ic4C_</a>	 Alignment		99.9	27	<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		99.8	24	<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="#">c5uvnA_</a>	 Alignment		99.5	21	<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
4	<a href="#">c5uvnF_</a>	 Alignment		99.5	21	<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
5	<a href="#">c5uvnC_</a>	 Alignment		99.5	21	<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
6	<a href="#">c5uvnD_</a>	 Alignment		99.5	21	<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
7	<a href="#">c5uvnB_</a>	 Alignment		99.5	21	<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="#">c5uvnE_</a>	 Alignment		99.5	21	<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
9	<a href="#">c3g67A_</a>	 Alignment		92.2	13	<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
10	<a href="#">c1qu7A_</a>	 Alignment		89.5	13	<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
11	<a href="#">c6b7nC_</a>	 Alignment		87.3	9	<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

12	<a href="#">c3lnrA_</a>	Alignment		85.0	8	<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
13	<a href="#">c3zx6A_</a>	Alignment		77.9	12	<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
14	<a href="#">c2ch7A_</a>	Alignment		75.8	9	<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
15	<a href="#">c2qf4A_</a>	Alignment		75.3	17	<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)
16	<a href="#">c3ojaB_</a>	Alignment		68.5	12	<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/apl1c complex
17	<a href="#">c2j5uB_</a>	Alignment		67.3	13	<b>PDB header:</b> cell shape regulation <b>Chain:</b> B: <b>PDB Molecule:</b> mrec protein; <b>PDBTitle:</b> mrec lysteria monocytogenes
18	<a href="#">c4rh7A_</a>	Alignment		66.8	7	<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
19	<a href="#">c6e6aB_</a>	Alignment		65.2	17	<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
20	<a href="#">c2d4yA_</a>	Alignment		64.9	8	<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)
21	<a href="#">c2wpgA_</a>	Alignment	not modelled	64.1	9	<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)
22	<a href="#">c1deqF_</a>	Alignment	not modelled	63.4	12	<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)
23	<a href="#">c3vkhA_</a>	Alignment	not modelled	63.2	7	<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
24	<a href="#">c3cwgA_</a>	Alignment	not modelled	62.9	11	<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
25	<a href="#">c5lp5F_</a>	Alignment	not modelled	61.6	13	<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
26	<a href="#">c5zuvB_</a>	Alignment	not modelled	59.6	8	<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
27	<a href="#">c6gajA_</a>	Alignment	not modelled	55.9	13	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t11 reovirus sigma1 coiled coil tail (iodide)
28	<a href="#">c6nh3B_</a>	Alignment	not modelled	55.2	9	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein;

28	<a href="#">c0ub5B</a>	Alignment	not modelled	53.2	9	<b>PDBTitle:</b> mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1) <b>PDB header:</b> hydrolase
29	<a href="#">c3j99M</a>	Alignment	not modelled	54.7	10	<b>Chain:</b> M: <b>PDB Molecule:</b> synaptosomal-associated protein 25; <b>PDBTitle:</b> structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state iib)
30	<a href="#">c2ieqC</a>	Alignment	not modelled	53.2	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 n163 spike2 glycoprotein
31	<a href="#">c5szsC</a>	Alignment	not modelled	52.8	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
32	<a href="#">c4iogD</a>	Alignment	not modelled	51.2	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
33	<a href="#">c3zbc</a>	Alignment	not modelled	41.5	16	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
34	<a href="#">c6grjG</a>	Alignment	not modelled	40.9	10	<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.
35	<a href="#">c1deqO</a>	Alignment	not modelled	40.1	11	<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)
36	<a href="#">c1ei3E</a>	Alignment	not modelled	39.0	7	<b>PDB header:</b> blood clotting <b>Chain:</b> E: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
37	<a href="#">c4wsrA</a>	Alignment	not modelled	37.3	15	<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
38	<a href="#">c6gapB</a>	Alignment	not modelled	36.8	12	<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
39	<a href="#">c6f0kA</a>	Alignment	not modelled	36.8	17	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c family protein; <b>PDBTitle:</b> alternative complex iii
40	<a href="#">c6evzX</a>	Alignment	not modelled	36.7	13	<b>PDB header:</b> toxin <b>Chain:</b> X: <b>PDB Molecule:</b> non-hemolytic enterotoxin lytic component I1; <b>PDBTitle:</b> the cytotoxin maka from vibrio cholerae
41	<a href="#">c5xbjA</a>	Alignment	not modelled	36.6	10	<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
42	<a href="#">d1v5va1</a>	Alignment	not modelled	36.5	15	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
43	<a href="#">d1pj5a1</a>	Alignment	not modelled	35.2	10	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
44	<a href="#">c3gvmA</a>	Alignment	not modelled	33.4	8	<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="#">c5u0pU</a>	Alignment	not modelled	32.7	10	<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
46	<a href="#">c1ei3C</a>	Alignment	not modelled	32.4	5	<b>PDB header:</b> blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
47	<a href="#">c4nj1A</a>	Alignment	not modelled	32.3	10	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> s protein; <b>PDBTitle:</b> crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
48	<a href="#">c2vs0B</a>	Alignment	not modelled	30.9	14	<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
49	<a href="#">c1t98B</a>	Alignment	not modelled	30.1	11	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome partition protein mukf; <b>PDBTitle:</b> crystal structure of mukf(1-287)
50	<a href="#">c1kmiZ</a>	Alignment	not modelled	29.4	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
51	<a href="#">c2wr2B</a>	Alignment	not modelled	29.3	15	<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
52	<a href="#">c4ut1A</a>	Alignment	not modelled	29.3	8	<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
53	<a href="#">c1v5vA</a>	Alignment	not modelled	29.0	14	<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
54	<a href="#">c4fiuC</a>	Alignment	not modelled	27.3	11	<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

55	<a href="#">c4abxB_</a>	Alignment	not modelled	26.0	8	<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
56	<a href="#">c4mc5C_</a>	Alignment	not modelled	25.1	9	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> crystal structure of a subtype h18 hemagglutinin homologue from2 a/flat-faced bat/peru/033/2010 (h18n11)
57	<a href="#">c1worA_</a>	Alignment	not modelled	25.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminomethyltransferase; <b>PDBTitle:</b> crystal structure of t-protein of the glycine cleavage2 system
58	<a href="#">c5dmaA_</a>	Alignment	not modelled	24.8	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna helicase pcra; <b>PDBTitle:</b> crystal structure of c-terminal tudor domain in pcra/uvrd helicase
59	<a href="#">d1wa8a1</a>	Alignment	not modelled	24.5	11	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
60	<a href="#">c1ha0A_</a>	Alignment	not modelled	24.5	9	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hemagglutinin precursor); <b>PDBTitle:</b> hemagglutinin precursor ha0
61	<a href="#">c5xl9B_</a>	Alignment	not modelled	24.4	9	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> the structure of hemagglutinin g228s mutant from an avian-origin h4n62 influenza virus in complex with avian receptor analog lsta
62	<a href="#">c4lwsB_</a>	Alignment	not modelled	23.8	8	<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
63	<a href="#">c3bt6B_</a>	Alignment	not modelled	23.4	10	<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
64	<a href="#">c5zhyA_</a>	Alignment	not modelled	23.3	13	<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
65	<a href="#">c1mqjB_</a>	Alignment	not modelled	22.9	8	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin ha2 chain; <b>PDBTitle:</b> bha of ukr/63
66	<a href="#">c2ql2B_</a>	Alignment	not modelled	22.4	10	<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 <b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain <b>Family:</b> Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
67	<a href="#">d1szia_</a>	Alignment	not modelled	21.7	12	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> a structure-based mechanism of sars virus membrane fusion
68	<a href="#">c1zvaA_</a>	Alignment	not modelled	20.8	15	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> a structure-based mechanism of sars virus membrane fusion
69	<a href="#">c1jsdB_</a>	Alignment	not modelled	19.8	12	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> haemagglutinin (ha2 chain); <b>PDBTitle:</b> crystal structure of swine h9 haemagglutinin
70	<a href="#">d1jcb3</a>	Alignment	not modelled	19.7	28	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
71	<a href="#">d1st6a4</a>	Alignment	not modelled	19.0	13	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
72	<a href="#">c2wrhl_</a>	Alignment	not modelled	17.8	15	<b>PDB header:</b> viral protein <b>Chain:</b> I: <b>PDB Molecule:</b> hemagglutinin ha2 chain; <b>PDBTitle:</b> structure of h1 duck albert hemagglutinin with human2 receptor
73	<a href="#">c1ru7B_</a>	Alignment	not modelled	17.5	13	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> 1934 human h1 hemagglutinin
74	<a href="#">c2qihA_</a>	Alignment	not modelled	17.2	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
75	<a href="#">c1hgeD_</a>	Alignment	not modelled	17.1	9	<b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> hemagglutinin, (g135r), ha1 chain; <b>PDBTitle:</b> binding of influenza virus hemagglutinin to analogs of its cell-2 surface receptor, sialic acid: analysis by proton nuclear magnetic3 resonance spectroscopy and x-ray crystallography
76	<a href="#">c6cv0C_</a>	Alignment	not modelled	17.0	8	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
77	<a href="#">c1yx2B_</a>	Alignment	not modelled	16.8	19	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aminomethyltransferase; <b>PDBTitle:</b> crystal structure of the probable aminomethyltransferase2 from bacillus subtilis
78	<a href="#">d1wosa1</a>	Alignment	not modelled	15.7	13	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
79	<a href="#">c2iakA_</a>	Alignment	not modelled	15.3	13	<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)
80	<a href="#">c1wyyB_</a>	Alignment	not modelled	15.2	16	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> post-fusion hairpin conformation of the sars coronavirus

					spike2 glycoprotein
81	<a href="#">c3izcN_</a>	Alignment	not modelled	15.0	20 <b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein rpl14 (I14e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
82	<a href="#">d1eq1a_</a>	Alignment	not modelled	14.9	13 <b>Fold:</b> Apolipoporphin-III <b>Superfamily:</b> Apolipoporphin-III <b>Family:</b> Apolipoporphin-III
83	<a href="#">c4lwsA_</a>	Alignment	not modelled	14.7	6 <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
84	<a href="#">c6nzkB_</a>	Alignment	not modelled	14.1	10 <b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> spike surface glycoprotein; <b>PDBTitle:</b> structural basis for human coronavirus attachment to sialic acid2 receptors
85	<a href="#">c3pe0B_</a>	Alignment	not modelled	13.7	7 <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
86	<a href="#">c1wncE_</a>	Alignment	not modelled	13.5	14 <b>PDB header:</b> viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> crystal structure of the sars-cov spike protein fusion core
87	<a href="#">c5x5bB_</a>	Alignment	not modelled	13.5	8 <b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> prefusion structure of sars-cov spike glycoprotein, conformation 2
88	<a href="#">c5x5fC_</a>	Alignment	not modelled	13.3	11 <b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> s protein; <b>PDBTitle:</b> prefusion structure of mers-cov spike glycoprotein, conformation 2
89	<a href="#">c4a19F_</a>	Alignment	not modelled	12.8	25 <b>PDB header:</b> ribosome <b>Chain:</b> F: <b>PDB Molecule:</b> rpl14; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rrna and3 proteins of molecule 2.
90	<a href="#">d1xmec1</a>	Alignment	not modelled	12.8	21 <b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Bacterial ba3 type cytochrome c oxidase subunit IIa <b>Family:</b> Bacterial ba3 type cytochrome c oxidase subunit IIa
91	<a href="#">c3bvdC_</a>	Alignment	not modelled	12.8	21 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide 2a; <b>PDBTitle:</b> structure of surface-engineered cytochrome ba3 oxidase from thermus2 thermophilus under xenon pressure, 100psi 5min
92	<a href="#">c5wrgB_</a>	Alignment	not modelled	12.7	8 <b>PDB header:</b> virus like particle <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> sars-cov spike glycoprotein
93	<a href="#">c3iz5N_</a>	Alignment	not modelled	12.6	29 <b>PDB header:</b> ribosome <b>Chain:</b> N: <b>PDB Molecule:</b> 60s ribosomal protein I14 (I14e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
94	<a href="#">c5b0oB_</a>	Alignment	not modelled	12.5	35 <b>PDB header:</b> hydrolase/motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> flagellum-specific atp synthase; <b>PDBTitle:</b> structure of the flih-flii complex
95	<a href="#">d1wa8b1</a>	Alignment	not modelled	12.5	8 <b>Fold:</b> Ferritin-like <b>Superfamily:</b> EsxAB dimer-like <b>Family:</b> ESAT-6 like
96	<a href="#">c3j3bM_</a>	Alignment	not modelled	12.5	17 <b>PDB header:</b> ribosome <b>Chain:</b> M: <b>PDB Molecule:</b> 60s ribosomal protein I14; <b>PDBTitle:</b> structure of the human 60s ribosomal proteins
97	<a href="#">c3zf7P_</a>	Alignment	not modelled	12.5	21 <b>PDB header:</b> ribosome <b>Chain:</b> P: <b>PDB Molecule:</b> probable 60s ribosomal protein I14; <b>PDBTitle:</b> high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
98	<a href="#">c6gaoC_</a>	Alignment	not modelled	12.4	9 <b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t11 reovirus sigma1 coiled coil tail and body
99	<a href="#">c3ghgK_</a>	Alignment	not modelled	12.4	10 <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