
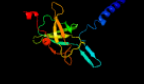





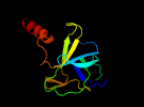









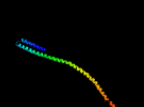

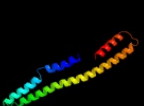

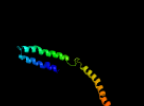
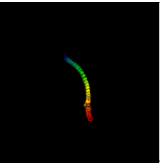
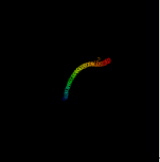
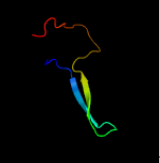
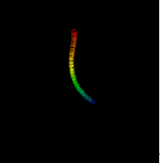
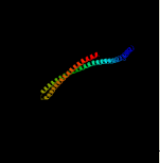
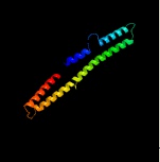
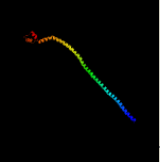
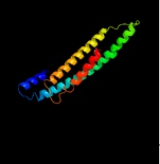
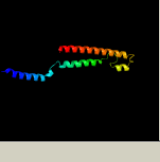


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD0593\_(lprL)\_692027\_693235  
 Date Fri Jul 26 01:50:15 BST 2019  
 Unique Job ID 3e13662818e567b4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ic4C_</a>	 Alignment		99.9	24	<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	28	<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="#">c5uvnB_</a>	 Alignment		99.3	17	<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
4	<a href="#">c5uvnF_</a>	 Alignment		99.3	17	<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="#">c5uvnA_</a>	 Alignment		99.3	17	<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
6	<a href="#">c5uvnE_</a>	 Alignment		99.3	17	<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
7	<a href="#">c5uvnC_</a>	 Alignment		99.3	17	<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
8	<a href="#">c5uvnD_</a>	 Alignment		99.3	17	<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
9	<a href="#">c1qu7A_</a>	 Alignment		87.5	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
10	<a href="#">c2d4yA_</a>	 Alignment		86.0	16	<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)
11	<a href="#">c5u0pU_</a>	 Alignment		82.3	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

12	<a href="#">c2qihA</a>	Alignment		82.0	4	<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
13	<a href="#">c3zx6A</a>	Alignment		79.6	15	<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="#">c2j5uB</a>	Alignment		75.7	14	<b>PDB header:</b> cell shape regulation <b>Chain:</b> B: <b>PDB Molecule:</b> mrec protein; <b>PDBTitle:</b> mrec lysteria monocytogenes
15	<a href="#">c2ch7A</a>	Alignment		75.7	10	<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
16	<a href="#">c3g67A</a>	Alignment		75.2	14	<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
17	<a href="#">c5xbjA</a>	Alignment		73.9	13	<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
18	<a href="#">c4rh7A</a>	Alignment		70.8	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="#">c3cwqA</a>	Alignment		70.0	7	<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
20	<a href="#">c5szsC</a>	Alignment		69.2	11	<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
21	<a href="#">c4ut1A</a>	Alignment	not modelled	69.0	13	<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
22	<a href="#">c3vkhA</a>	Alignment	not modelled	68.8	8	<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="#">c2wpgA</a>	Alignment	not modelled	68.4	5	<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 (sada3, in-2 register fusion)
24	<a href="#">c1deqF</a>	Alignment	not modelled	65.4	10	<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)
25	<a href="#">c5x5bB</a>	Alignment	not modelled	64.8	6	<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
26	<a href="#">c3jclC</a>	Alignment	not modelled	61.3	11	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
27	<a href="#">d1h9ra2</a>	Alignment	not modelled	60.7	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain
28	<a href="#">c6b7nC</a>	Alignment	not modelled	60.1	10	<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

29	<a href="#">c6nzkB</a>	Alignment	not modelled	59.6	8	<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
30	<a href="#">c3lnrA</a>	Alignment	not modelled	59.4	16	<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
31	<a href="#">c2qf4A</a>	Alignment	not modelled	58.2	13	<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)
32	<a href="#">c5xlrC</a>	Alignment	not modelled	58.0	6	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> structure of sars-cov spike glycoprotein
33	<a href="#">d1eq1a</a>	Alignment	not modelled	57.7	16	<b>Fold:</b> Apolipophorin-III <b>Superfamily:</b> Apolipophorin-III <b>Family:</b> Apolipophorin-III
34	<a href="#">c5i08A</a>	Alignment	not modelled	57.5	7	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein, envelope glycoprotein chimera; <b>PDBTitle:</b> prefusion structure of a human coronavirus spike protein
35	<a href="#">c6nb3B</a>	Alignment	not modelled	54.9	13	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
36	<a href="#">c5x5fC</a>	Alignment	not modelled	51.3	13	<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
37	<a href="#">c1ei3C</a>	Alignment	not modelled	51.2	10	<b>PDB header:</b> blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
38	<a href="#">c1kmiZ</a>	Alignment	not modelled	50.1	10	<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
39	<a href="#">c5wrgB</a>	Alignment	not modelled	49.6	6	<b>PDB header:</b> virus like particle <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> sars-cov spike glycoprotein
40	<a href="#">d1h9ma2</a>	Alignment	not modelled	49.1	32	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BIMOP, duplicated molybdate-binding domain
41	<a href="#">c5lp5F</a>	Alignment	not modelled	48.9	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 (ppb2) and mrec from2 helicobacter pylori
42	<a href="#">c3ghgl</a>	Alignment	not modelled	48.3	8	<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
43	<a href="#">d1guta</a>	Alignment	not modelled	48.3	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> Molybdate/tungstate binding protein MOP
44	<a href="#">c4abxB</a>	Alignment	not modelled	47.7	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
45	<a href="#">c4zzkA</a>	Alignment	not modelled	46.6	17	<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
46	<a href="#">d1h9ma1</a>	Alignment	not modelled	44.7	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BIMOP, duplicated molybdate-binding domain
47	<a href="#">d1ykhb1</a>	Alignment	not modelled	43.0	8	<b>Fold:</b> Mediator hinge subcomplex-like <b>Superfamily:</b> Mediator hinge subcomplex-like <b>Family:</b> CSE2-like
48	<a href="#">c3dyjA</a>	Alignment	not modelled	42.3	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> tal1n-1; <b>PDBTitle:</b> crystal structure of a talin rod fragment
49	<a href="#">c1degO</a>	Alignment	not modelled	40.6	10	<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)
50	<a href="#">c6cs2A</a>	Alignment	not modelled	40.5	6	<b>PDB header:</b> viral protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein,fibrin; <b>PDBTitle:</b> sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
51	<a href="#">d1st6a5</a>	Alignment	not modelled	39.5	11	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
52	<a href="#">c4n21E</a>	Alignment	not modelled	39.3	10	<b>PDB header:</b> viral protein <b>Chain:</b> E: <b>PDB Molecule:</b> gp2 ectodomain; <b>PDBTitle:</b> crystal structure of the gp2 core domain from the california academy2 of science virus
53	<a href="#">c1ei3E</a>	Alignment	not modelled	39.1	12	<b>PDB header:</b> blood clotting <b>Chain:</b> E: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
54	<a href="#">c5lskD</a>	Alignment	not modelled	38.1	13	<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 <b>Fold:</b> Common fold of diphtheria toxin/transcription

55	<a href="#">d1x9la_</a>	Alignment	not modelled	36.2	22	factors/cytochrome f <b>Superfamily:</b> DR1885-like metal-binding protein <b>Family:</b> DR1885-like metal-binding protein
56	<a href="#">d2uub1</a>	Alignment	not modelled	36.0	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
57	<a href="#">c4tkoB_</a>	Alignment	not modelled	35.9	14	<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
58	<a href="#">c3j6vL_</a>	Alignment	not modelled	34.9	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
59	<a href="#">c1bf5A_</a>	Alignment	not modelled	34.9	11	<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
60	<a href="#">c2kbbA_</a>	Alignment	not modelled	34.9	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> stalin-1; <b>PDBTitle:</b> nmr structure of the talin rod domain, 1655-1822
61	<a href="#">c2k6zA_</a>	Alignment	not modelled	34.8	20	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein ttha1943; <b>PDBTitle:</b> solution structures of copper loaded form pcua (trans2 conformation of the peptide bond involving the nitrogen of3 p14)
62	<a href="#">c3c12A_</a>	Alignment	not modelled	34.4	20	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> flagellar protein; <b>PDBTitle:</b> crystal structure of flgd from xanthomonas campestris:2 insights into the hook capping essential for flagellar3 assembly
63	<a href="#">c6e6aB_</a>	Alignment	not modelled	34.2	11	<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
64	<a href="#">c1zn1L_</a>	Alignment	not modelled	32.5	16	<b>PDB header:</b> biosynthetic/structural protein/rna <b>Chain:</b> L: <b>PDB Molecule:</b> 30s ribosomal protein s12; <b>PDBTitle:</b> coordinates of rrf fitted into cryo-em map of the 70s post-termination2 complex
65	<a href="#">c3zk0A_</a>	Alignment	not modelled	31.5	13	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> sco3965; <b>PDBTitle:</b> the crystal structure of a cu(i) metallochaperone from2 streptomyces lividans in its apo form
66	<a href="#">d1st6a4</a>	Alignment	not modelled	31.4	4	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
67	<a href="#">c5zuvB_</a>	Alignment	not modelled	31.0	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
68	<a href="#">c2vs0B_</a>	Alignment	not modelled	30.9	11	<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
69	<a href="#">c5yfpD_</a>	Alignment	not modelled	29.5	7	<b>PDB header:</b> exocytosis <b>Chain:</b> D: <b>PDB Molecule:</b> exocyst complex component sec8; <b>PDBTitle:</b> cryo-em structure of the exocyst complex
70	<a href="#">c3ojaB_</a>	Alignment	not modelled	28.5	10	<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
71	<a href="#">c1h9mB_</a>	Alignment	not modelled	27.3	28	<b>PDB header:</b> binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> molybdenum-binding-protein; <b>PDBTitle:</b> two crystal structures of the cytoplasmic molybdate-binding protein2 modg suggest a novel cooperative binding mechanism and provide3 insights into ligand-binding specificity. pegrown form with4 molybdate bound
72	<a href="#">d1i94I_</a>	Alignment	not modelled	26.9	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
73	<a href="#">c1h9sA_</a>	Alignment	not modelled	26.4	16	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum transport protein mode; <b>PDBTitle:</b> molybdate bound complex of dimop domain of mode from e.coli
74	<a href="#">c4iogD_</a>	Alignment	not modelled	26.1	11	<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
75	<a href="#">d1v5va1</a>	Alignment	not modelled	25.9	17	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
76	<a href="#">c2ieqC_</a>	Alignment	not modelled	25.6	7	<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
77	<a href="#">d2qall1</a>	Alignment	not modelled	25.0	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
78	<a href="#">d1hcia4</a>	Alignment	not modelled	24.9	10	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
79	<a href="#">c5j65A_</a>	Alignment	not modelled	24.8	8	<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
80	<a href="#">c5yfpG_</a>	Alignment	not modelled	24.8	15	<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

81	<a href="#">c5j2lB_</a>	Alignment	not modelled	24.4	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
82	<a href="#">c6gajA_</a>	Alignment	not modelled	24.3	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 t1l reovirus sigma1 coiled coil tail (iodide)
83	<a href="#">c3gvmA_</a>	Alignment	not modelled	23.4	9	<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
84	<a href="#">c5n76C_</a>	Alignment	not modelled	22.1	18	<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
85	<a href="#">c6el1F_</a>	Alignment	not modelled	21.9	9	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> yaxa; <b>PDBTitle:</b> yaxab pore complex
86	<a href="#">c3pwxB_</a>	Alignment	not modelled	21.8	10	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative flagellar hook-associated protein; <b>PDBTitle:</b> structure of putative flagellar hook-associated protein from vibrio2 parahaemolyticus
87	<a href="#">c3zbcC_</a>	Alignment	not modelled	21.7	10	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
88	<a href="#">c6cv0C_</a>	Alignment	not modelled	21.1	13	<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
89	<a href="#">c6ezvX_</a>	Alignment	not modelled	21.1	6	<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
90	<a href="#">c4nj1A_</a>	Alignment	not modelled	20.8	13	<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
91	<a href="#">c6grjG_</a>	Alignment	not modelled	20.3	6	<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.
92	<a href="#">c5iiaH_</a>	Alignment	not modelled	20.0	19	<b>PDB header:</b> cell adhesion <b>Chain:</b> H: <b>PDB Molecule:</b> vitelline envelope sperm lysin receptor; <b>PDBTitle:</b> crystal structure of red abalone egg ver1 repeat 3 in complex with2 sperm lysin at 1.7 a resolution (crystal form i)
93	<a href="#">d1fr3a_</a>	Alignment	not modelled	19.8	23	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> Molybdate/tungstate binding protein MOP
94	<a href="#">c2pjhB_</a>	Alignment	not modelled	19.6	9	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> strctural model of the p97 n domain- npl4 ubd complex
95	<a href="#">c5ii5A_</a>	Alignment	not modelled	19.2	33	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> maltose-binding periplasmic protein,vitelline envelope <b>PDBTitle:</b> crystal structure of red abalone ver1 repeat 1 at 1.8 a resolution
96	<a href="#">c1mg1A_</a>	Alignment	not modelled	19.1	13	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (htlv-1 gp21 ectodomain/maltose-binding protein <b>PDBTitle:</b> htlv-1 gp21 ectodomain/maltose-binding protein chimera
97	<a href="#">c4f7gB_</a>	Alignment	not modelled	19.0	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> tal1n-1; <b>PDBTitle:</b> crystal structure of talin autoinhibition complex
98	<a href="#">c5j0hA_</a>	Alignment	not modelled	17.5	24	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> design construct 2l6hc3_13; <b>PDBTitle:</b> de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
99	<a href="#">c1cz5A_</a>	Alignment	not modelled	16.2	15	<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)