
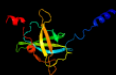
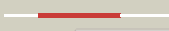








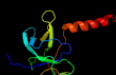

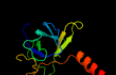


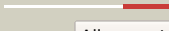
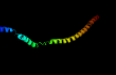



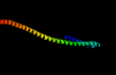


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0590_(mce2B)_688035_688862
Date	Fri Jul 26 01:50:14 BST 2019
Unique Job ID	5a2fb324602148dd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ic4C_</a>	 Alignment		99.9	28	<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		99.7	23	<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		99.5	18	<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="#">c5uvnC_</a>	 Alignment		99.5	18	<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
5	<a href="#">c5uvnD_</a>	 Alignment		99.5	18	<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="#">c5uvnF_</a>	 Alignment		99.5	18	<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
7	<a href="#">c5uvnE_</a>	 Alignment		99.5	18	<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
8	<a href="#">c5uvnA_</a>	 Alignment		99.5	18	<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
9	<a href="#">c1deqF_</a>	 Alignment		91.1	13	<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)
10	<a href="#">c1qu7A_</a>	 Alignment		90.3	7	<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="#">c3g67A_</a>	 Alignment		89.7	7	<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

12	<a href="#">c2qf4A_</a>	Alignment		89.7	14	<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)
13	<a href="#">c6b7nC_</a>	Alignment		85.7	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
14	<a href="#">c2wpgA_</a>	Alignment		79.7	7	<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)
15	<a href="#">c2j5uB_</a>	Alignment		79.5	16	<b>PDB header:</b> cell shape regulation <b>Chain:</b> B: <b>PDB Molecule:</b> mrec protein; <b>PDBTitle:</b> mrec lysteria monocytogenes
16	<a href="#">c6gajA_</a>	Alignment		79.4	14	<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)
17	<a href="#">c6nzkB_</a>	Alignment		77.0	9	<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
18	<a href="#">c5x5bB_</a>	Alignment		76.0	10	<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
19	<a href="#">c3jclC_</a>	Alignment		73.4	9	<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
20	<a href="#">c4e40A_</a>	Alignment		69.7	9	<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
21	<a href="#">c6nb3B_</a>	Alignment	not modelled	68.7	7	<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)
22	<a href="#">c1m1jA_</a>	Alignment	not modelled	67.7	17	<b>PDB header:</b> blood clotting <b>Chain:</b> A: <b>PDB Molecule:</b> fibrinogen alpha subunit; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen with two different2 bound ligands
23	<a href="#">c6cs2A_</a>	Alignment	not modelled	67.4	10	<b>PDB header:</b> viral protein/hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein,fibrinin; <b>PDBTitle:</b> sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
24	<a href="#">c1ei3E_</a>	Alignment	not modelled	66.8	9	<b>PDB header:</b> blood clotting <b>Chain:</b> E: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
25	<a href="#">c3lnrA_</a>	Alignment	not modelled	66.7	3	<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
26	<a href="#">c3vjfA_</a>	Alignment	not modelled	64.9	7	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> wa20; <b>PDBTitle:</b> crystal structure of de novo 4-helix bundle protein wa20
27	<a href="#">c1ei3C_</a>	Alignment	not modelled	63.4	8	<b>PDB header:</b> blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
28	<a href="#">c3zx6A_</a>	Alignment	not modelled	63.3	10	<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 <b>PDB header:</b> chemotaxis

29	<a href="#">c2ch7A_</a>	Alignment	not modelled	63.0	7	<b>Chain:</b> A: <b>PDB Molecule:</b> metnyl-accepting cnetotaxis protein; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
30	<a href="#">c5xlrC_</a>	Alignment	not modelled	60.6	10	<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
31	<a href="#">c6cv0C_</a>	Alignment	not modelled	58.8	10	<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
32	<a href="#">c5szsC_</a>	Alignment	not modelled	58.3	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
33	<a href="#">c3cwqA_</a>	Alignment	not modelled	55.3	9	<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
34	<a href="#">c5zhyA_</a>	Alignment	not modelled	54.1	5	<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
35	<a href="#">c5wrgB_</a>	Alignment	not modelled	51.5	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
36	<a href="#">c2gl2B_</a>	Alignment	not modelled	51.3	9	<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
37	<a href="#">c2ieqC_</a>	Alignment	not modelled	51.1	20	<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
38	<a href="#">c3ghgK_</a>	Alignment	not modelled	50.8	7	<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
39	<a href="#">c1p68A_</a>	Alignment	not modelled	49.3	13	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> de novo designed protein s-824; <b>PDBTitle:</b> solution structure of s-824, a de novo designed four helix2 bundle
40	<a href="#">c5cwsj_</a>	Alignment	not modelled	49.3	6	<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
41	<a href="#">c6b3oB_</a>	Alignment	not modelled	48.7	10	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
42	<a href="#">c5i08A_</a>	Alignment	not modelled	47.7	11	<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
43	<a href="#">c2d4yA_</a>	Alignment	not modelled	47.6	12	<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)
44	<a href="#">c1kmiZ_</a>	Alignment	not modelled	46.2	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
45	<a href="#">c1cz5A_</a>	Alignment	not modelled	45.8	12	<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)
46	<a href="#">c5b0oB_</a>	Alignment	not modelled	43.6	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
47	<a href="#">c6gaoC_</a>	Alignment	not modelled	41.4	11	<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
48	<a href="#">d1st6a4</a>	Alignment	not modelled	40.5	14	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
49	<a href="#">c5x5fC_</a>	Alignment	not modelled	40.0	16	<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
50	<a href="#">c4abxB_</a>	Alignment	not modelled	39.8	10	<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
51	<a href="#">c3ojaB_</a>	Alignment	not modelled	39.7	7	<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
52	<a href="#">c5j2lB_</a>	Alignment	not modelled	39.6	11	<b>PDB header:</b> de novo protein <b>Chain:</b> B: <b>PDB Molecule:</b> protein design 214hc2_11; <b>PDBTitle:</b> de novo design of protein homo-oligomers with modular hydrogen bond2 network-mediated specificity
53	<a href="#">c2pjhB_</a>	Alignment	not modelled	37.2	17	<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
54	<a href="#">c6ezvX_</a>	Alignment	not modelled	36.5	12	<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
55	<a href="#">c2qihA_</a>	Alignment	not modelled	36.1	10	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> protein uspa1;

55	<a href="#">c2qmA</a>	Alignment	not modelled	30.1	10	<b>PDBTitle:</b> crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis <b>PDB header:</b> gene regulation/dna
56	<a href="#">c1bf5A</a>	Alignment	not modelled	35.9	7	<b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription 1- <b>PDBTitle:</b> tyrosine phosphorylated stat-1/dna complex
57	<a href="#">c2vs0B</a>	Alignment	not modelled	35.4	10	<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
58	<a href="#">c4iogD</a>	Alignment	not modelled	34.2	14	<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
59	<a href="#">c5dmaA</a>	Alignment	not modelled	33.6	21	<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
60	<a href="#">c3ghgI</a>	Alignment	not modelled	33.4	13	<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
61	<a href="#">d1wosa1</a>	Alignment	not modelled	32.4	18	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
62	<a href="#">c4lwsB</a>	Alignment	not modelled	31.1	9	<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="#">c3zbcC</a>	Alignment	not modelled	31.0	12	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
64	<a href="#">c1kzIA</a>	Alignment	not modelled	30.3	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin synthase; <b>PDBTitle:</b> riboflavin synthase from s.pombe bound to2 carboxyethylumazine
65	<a href="#">c2nrjA</a>	Alignment	not modelled	29.4	14	<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
66	<a href="#">c3gvmA</a>	Alignment	not modelled	29.3	11	<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
67	<a href="#">c1v5vA</a>	Alignment	not modelled	29.0	15	<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
68	<a href="#">c1deqD</a>	Alignment	not modelled	28.7	14	<b>PDB header:</b> blood clotting <b>Chain:</b> D: <b>PDB Molecule:</b> fibrinogen (alpha chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
69	<a href="#">c4wy4D</a>	Alignment	not modelled	28.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> synaptosomal-associated protein 29; <b>PDBTitle:</b> crystal structure of autophagic snare complex
70	<a href="#">c3vkhA</a>	Alignment	not modelled	27.1	5	<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
71	<a href="#">c3j99M</a>	Alignment	not modelled	27.0	9	<b>PDB header:</b> hydrolase <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 iiib)
72	<a href="#">c4qkwB</a>	Alignment	not modelled	26.1	8	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> muscle-related coiled-coil protein; <b>PDBTitle:</b> crystal structure of the zebrafish cavin4a hr1 domain
73	<a href="#">c3j6vL</a>	Alignment	not modelled	25.8	15	<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
74	<a href="#">c4qkvB</a>	Alignment	not modelled	25.7	11	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase i and transcript release factor; <b>PDBTitle:</b> crystal structure of the mouse cavin1 hr1 domain
75	<a href="#">c5bn4A</a>	Alignment	not modelled	25.7	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> v-type atp synthase alpha chain; <b>PDBTitle:</b> structure of a unique atp synthase neqa-neqb in complex with anp from2 nanoarchaeum equitans
76	<a href="#">c3vr5C</a>	Alignment	not modelled	25.2	23	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> v-type sodium atpase catalytic subunit a; <b>PDBTitle:</b> crystal structure of nucleotide-free enterococcus hirae v1-atpase2 [ev1(l)]
77	<a href="#">c3ur1C</a>	Alignment	not modelled	25.1	9	<b>PDB header:</b> immune system <b>Chain:</b> C: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> 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.
78	<a href="#">c3a5dB</a>	Alignment	not modelled	25.1	30	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> v-type atp synthase alpha chain; <b>PDBTitle:</b> inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
79	<a href="#">c3j9vC</a>	Alignment	not modelled	24.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> v-type proton atpase catalytic subunit a; <b>PDBTitle:</b> yeast v-atpase state 3
80	<a href="#">c5u0pU</a>	Alignment	not modelled	24.4	9	<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
81	<a href="#">c4lwsA</a>	Alignment	not modelled	24.4	12	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein;

81	<a href="#">c4w3A_</a>	Alignment	not modelled	24.4	12	<b>PDBTitle:</b> esxa : esxb (semet) hetero-dimer from thermomonospora curvata
82	<a href="#">d1pj5a1</a>	Alignment	not modelled	23.9	10	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
83	<a href="#">d1ykhb1</a>	Alignment	not modelled	23.5	9	<b>Fold:</b> Mediator hinge subcomplex-like <b>Superfamily:</b> Mediator hinge subcomplex-like <b>Family:</b> CSE2-like
84	<a href="#">d1g7sa2</a>	Alignment	not modelled	23.4	16	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Elongation factors
85	<a href="#">c4xd7B_</a>	Alignment	not modelled	23.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase subunit alpha; <b>PDBTitle:</b> structure of thermophilic f1-atpase inhibited by epsilon subunit
86	<a href="#">d2uubl1</a>	Alignment	not modelled	22.8	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
87	<a href="#">c6iiuA_</a>	Alignment	not modelled	22.5	10	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> soluble cytochrome b562,thromboxane a2 receptor,rubredoxin, <b>PDBTitle:</b> crystal structure of the human thromboxane a2 receptor bound to2 ramatroban
88	<a href="#">c4xa3A_</a>	Alignment	not modelled	22.1	13	<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
89	<a href="#">c3htrB_</a>	Alignment	not modelled	22.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized prc-barrel domain protein; <b>PDBTitle:</b> crystal structure of prc-barrel domain protein from2 rhodospseudomonas palustris
90	<a href="#">c6npjC_</a>	Alignment	not modelled	21.9	30	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> translocator escn; <b>PDBTitle:</b> structure of the assembled atpase escn in complex with its central2 stalk esco from the enteropathogenic e. coli (epec) type iii3 secretion system
91	<a href="#">c1bg1A_</a>	Alignment	not modelled	21.9	11	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (transcription factor stat3b); <b>PDBTitle:</b> transcription factor stat3b/dna complex
92	<a href="#">c1worA_</a>	Alignment	not modelled	21.8	13	<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
93	<a href="#">d1v5va1</a>	Alignment	not modelled	21.7	18	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
94	<a href="#">c5xbjA_</a>	Alignment	not modelled	21.4	15	<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
95	<a href="#">c6e8wC_</a>	Alignment	not modelled	20.3	14	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> envelope glycoprotein gp160; <b>PDBTitle:</b> mper-tm domain of hiv-1 envelope glycoprotein (env)
96	<a href="#">c5zuvB_</a>	Alignment	not modelled	19.8	20	<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
97	<a href="#">c6rdtY_</a>	Alignment	not modelled	19.6	26	<b>PDB header:</b> proton transport <b>Chain:</b> Y: <b>PDB Molecule:</b> atp synthase subunit beta; <b>PDBTitle:</b> cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 composite map
98	<a href="#">c6gy6Q_</a>	Alignment	not modelled	19.4	12	<b>PDB header:</b> toxin <b>Chain:</b> Q: <b>PDB Molecule:</b> xaxa; <b>PDBTitle:</b> xaxab pore complex from xenorhabdus nematophila
99	<a href="#">c2dpyA_</a>	Alignment	not modelled	19.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> flagellum-specific atp synthase; <b>PDBTitle:</b> crystal structure of the flagellar type iii atpase flii