
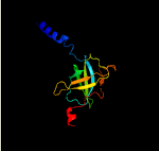
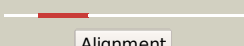














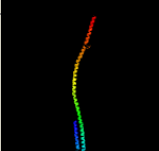
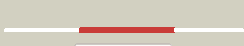
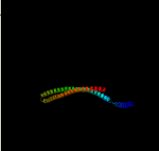

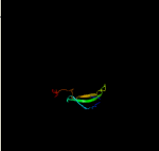


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD1969\_(mce3D)\_2212863\_2214134  
 Date Mon Aug 5 13:25:07 BST 2019  
 Unique Job ID 82cca60e296178ec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ic4C_</a>	 Alignment		99.8	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		99.7	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="#">c5uvnD_</a>	 Alignment		99.4	12	<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
4	<a href="#">c5uvnA_</a>	 Alignment		99.4	12	<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="#">c5uvnE_</a>	 Alignment		99.4	12	<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
6	<a href="#">c5uvnB_</a>	 Alignment		99.4	12	<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
7	<a href="#">c5uvnF_</a>	 Alignment		99.4	12	<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
8	<a href="#">c5uvnC_</a>	 Alignment		99.4	12	<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
9	<a href="#">c1qu7A_</a>	 Alignment		93.8	11	<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="#">c3g67A_</a>	 Alignment		92.4	8	<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
11	<a href="#">c2j5uB_</a>	 Alignment		83.3	12	<b>PDB header:</b> cell shape regulation <b>Chain:</b> B: <b>PDB Molecule:</b> mrec protein; <b>PDBTitle:</b> mrec lysteria monocytogenes

12	<a href="#">c2ch7A_</a>	Alignment		81.3	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
13	<a href="#">c2d4yA_</a>	Alignment		77.8	9	<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)
14	<a href="#">c6e6aB_</a>	Alignment		74.1	14	<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
15	<a href="#">c5szsC_</a>	Alignment		72.8	13	<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
16	<a href="#">c5u0pU_</a>	Alignment		72.7	12	<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
17	<a href="#">c2qihA_</a>	Alignment		72.3	12	<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
18	<a href="#">c1ei3C_</a>	Alignment		71.3	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
19	<a href="#">c3lnrA_</a>	Alignment		70.2	9	<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
20	<a href="#">c6nzkB_</a>	Alignment		70.2	12	<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
21	<a href="#">c3ghgI_</a>	Alignment	not modelled	69.7	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
22	<a href="#">c4tkoB_</a>	Alignment	not modelled	67.8	15	<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
23	<a href="#">c3jclC_</a>	Alignment	not modelled	66.5	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
24	<a href="#">c3zx6A_</a>	Alignment	not modelled	64.4	13	<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
25	<a href="#">c2yfaA_</a>	Alignment	not modelled	64.2	13	<b>PDB header:</b> receptor <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis transducer; <b>PDBTitle:</b> x-ray structure of mcps ligand binding domain in complex with malate
26	<a href="#">c5i08A_</a>	Alignment	not modelled	63.9	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
27	<a href="#">c5x5bB_</a>	Alignment	not modelled	62.1	9	<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
28	<a href="#">c2wpgA_</a>	Alignment	not modelled	61.2	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)
29	<a href="#">c2ieqC</a>	Alignment	not modelled	61.0	15	<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
30	<a href="#">c5xlrC</a>	Alignment	not modelled	59.9	9	<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="#">c6cs2A</a>	Alignment	not modelled	58.7	9	<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
32	<a href="#">c4njiA</a>	Alignment	not modelled	57.6	17	<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
33	<a href="#">c5n76C</a>	Alignment	not modelled	56.9	15	<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
34	<a href="#">c5wrgB</a>	Alignment	not modelled	56.7	9	<b>PDB header:</b> virus like particle <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> sars-cov spike glycoprotein
35	<a href="#">c2vs0B</a>	Alignment	not modelled	55.8	7	<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
36	<a href="#">d1ykhb1</a>	Alignment	not modelled	55.6	9	<b>Fold:</b> Mediator hinge subcomplex-like <b>Superfamily:</b> Mediator hinge subcomplex-like <b>Family:</b> CSE2-like
37	<a href="#">c1bf5A</a>	Alignment	not modelled	54.7	8	<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
38	<a href="#">c6b7nC</a>	Alignment	not modelled	54.3	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
39	<a href="#">c6nb3B</a>	Alignment	not modelled	53.1	12	<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)
40	<a href="#">c5x5fC</a>	Alignment	not modelled	52.5	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
41	<a href="#">c1deqO</a>	Alignment	not modelled	52.5	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)
42	<a href="#">c6gaiA</a>	Alignment	not modelled	52.0	15	<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)
43	<a href="#">c4iogD</a>	Alignment	not modelled	51.5	19	<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
44	<a href="#">c5dmaA</a>	Alignment	not modelled	51.1	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
45	<a href="#">c4ut1A</a>	Alignment	not modelled	50.6	16	<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
46	<a href="#">c2qf4A</a>	Alignment	not modelled	49.7	8	<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)
47	<a href="#">c2l8sA</a>	Alignment	not modelled	48.7	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-1; <b>PDBTitle:</b> solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
48	<a href="#">c4rh7A</a>	Alignment	not modelled	48.6	6	<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
49	<a href="#">c1deqF</a>	Alignment	not modelled	47.2	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)
50	<a href="#">d1h9ra2</a>	Alignment	not modelled	46.6	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain
51	<a href="#">d1h9ma2</a>	Alignment	not modelled	45.4	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain
52	<a href="#">c1kmiZ</a>	Alignment	not modelled	45.4	15	<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
53	<a href="#">c6b3oB</a>	Alignment	not modelled	45.3	11	<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
54	<a href="#">c2ha7C</a>	Alignment	not modelled	44.4	17	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> e2 glycoprotein;

54	<a href="#">c2ue2C</a>	Alignment	not modelled	44.4	17	<b>PDB header:</b> structure of a proteolitically resistant core from the severe acute2 respiratory syndrome coronavirus s2 fusion protein <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
55	<a href="#">c3cwgA</a>	Alignment	not modelled	44.2	11	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> Molybdate/tungstate binding protein MOP
56	<a href="#">d1guta</a>	Alignment	not modelled	43.7	16	<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
57	<a href="#">c5zuvB</a>	Alignment	not modelled	43.4	13	<b>PDB header:</b> blood clotting <b>Chain:</b> E: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
58	<a href="#">c1ei3E</a>	Alignment	not modelled	42.6	8	<b>Fold:</b> Apolipophorin-III <b>Superfamily:</b> Apolipophorin-III <b>Family:</b> Apolipophorin-III
59	<a href="#">d1eq1a</a>	Alignment	not modelled	41.8	11	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> BiMOP, duplicated molybdate-binding domain
60	<a href="#">d1h9ma1</a>	Alignment	not modelled	41.2	8	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> platelet integrin alfaib-beta3 transmembrane-cytoplasmic2 heterocomplex
61	<a href="#">c2kncA</a>	Alignment	not modelled	36.7	18	<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
62	<a href="#">c6cv0C</a>	Alignment	not modelled	36.3	9	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
63	<a href="#">d2uubl1</a>	Alignment	not modelled	35.7	28	<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
64	<a href="#">c3j6vL</a>	Alignment	not modelled	35.0	19	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Cap-Gly domain <b>Family:</b> Cap-Gly domain
65	<a href="#">d2cp6a1</a>	Alignment	not modelled	34.5	19	<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)
66	<a href="#">c1cz5A</a>	Alignment	not modelled	34.2	12	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> chromosome partition protein mukf; <b>PDBTitle:</b> crystal structure of the muke-mukf complex
67	<a href="#">c3euhB</a>	Alignment	not modelled	33.6	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
68	<a href="#">c4abxB</a>	Alignment	not modelled	32.9	17	<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
69	<a href="#">c1zn1L</a>	Alignment	not modelled	32.4	22	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iib) transmembrane segment
70	<a href="#">c2k1aA</a>	Alignment	not modelled	31.8	19	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
71	<a href="#">c2akfB</a>	Alignment	not modelled	31.3	21	<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
72	<a href="#">c3qr8A</a>	Alignment	not modelled	31.1	20	<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
73	<a href="#">c4e40A</a>	Alignment	not modelled	30.6	9	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
74	<a href="#">c2akfC</a>	Alignment	not modelled	30.3	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
75	<a href="#">c2akfA</a>	Alignment	not modelled	30.3	21	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> coronin-1a; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of coronin 1
76	<a href="#">c1wywB</a>	Alignment	not modelled	30.1	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
77	<a href="#">c5xbjA</a>	Alignment	not modelled	28.9	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
78	<a href="#">c5lp5F</a>	Alignment	not modelled	28.1	23	<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
79	<a href="#">c4modB</a>	Alignment	not modelled	27.1	13	<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
80	<a href="#">c1bg1A</a>	Alignment	not modelled	26.9	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

81	<a href="#">c4lwsA</a>	Alignment	not modelled	26.7	13	<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="#">c2pjhB</a>	Alignment	not modelled	26.1	21	<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
83	<a href="#">c3zbhC</a>	Alignment	not modelled	26.0	15	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
84	<a href="#">c2jp3A</a>	Alignment	not modelled	25.8	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fyxd domain-containing ion transport regulator 4; <b>PDBTitle:</b> solution structure of the human fxyd4 (chif) protein in sds2 micelles
85	<a href="#">d1i94I</a>	Alignment	not modelled	25.7	28	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
86	<a href="#">c4n21E</a>	Alignment	not modelled	25.4	14	<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
87	<a href="#">c4s37F</a>	Alignment	not modelled	24.7	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> F: <b>PDB Molecule:</b> phage baseplate protein; <b>PDBTitle:</b> crystal structure of r2 pyocin membrane-piercing spike
88	<a href="#">c2mkvA</a>	Alignment	not modelled	24.3	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit gamma; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd2b in micelles
89	<a href="#">c5j65A</a>	Alignment	not modelled	24.2	10	<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
90	<a href="#">d2qall1</a>	Alignment	not modelled	24.1	26	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
91	<a href="#">c4xa3A</a>	Alignment	not modelled	24.0	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
92	<a href="#">c1gl2C</a>	Alignment	not modelled	23.7	15	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> vesicle transport v-snare protein vti1-like 1; <b>PDBTitle:</b> crystal structure of an endosomal snare core complex
93	<a href="#">c3a35B</a>	Alignment	not modelled	23.6	16	<b>PDB header:</b> luminescent protein <b>Chain:</b> B: <b>PDB Molecule:</b> lumazine protein; <b>PDBTitle:</b> crystal structure of lump complexed with riboflavin
94	<a href="#">d1quua1</a>	Alignment	not modelled	23.1	13	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
95	<a href="#">c5ue0A</a>	Alignment	not modelled	23.0	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ct622 protein; <b>PDBTitle:</b> 1.90 a resolution structure of ct622 c-terminal domain from chlamydia2 trachomatis
96	<a href="#">c5dfzA</a>	Alignment	not modelled	22.7	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 38; <b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.
97	<a href="#">c2jo1A</a>	Alignment	not modelled	22.5	4	<b>PDB header:</b> hydrolase regulator <b>Chain:</b> A: <b>PDB Molecule:</b> phospholemman; <b>PDBTitle:</b> structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
98	<a href="#">c3ojaB</a>	Alignment	not modelled	22.5	9	<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
99	<a href="#">d1v5va1</a>	Alignment	not modelled	22.0	19	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> Aminomethyltransferase beta-barrel domain <b>Family:</b> Aminomethyltransferase beta-barrel domain
100	<a href="#">c5mg8B</a>	Alignment	not modelled	21.7	4	<b>PDB header:</b> recombination <b>Chain:</b> B: <b>PDB Molecule:</b> structural maintenance of chromosomes protein 6; <b>PDBTitle:</b> crystal structure of the s.pombe smc5/6 hinge domain
101	<a href="#">c6gaoC</a>	Alignment	not modelled	21.7	7	<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 t1l reovirus sigma1 coiled coil tail and body
102	<a href="#">c5tpjA</a>	Alignment	not modelled	21.4	5	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> denovo ntf2; <b>PDBTitle:</b> crystal structure of a de novo designed protein with curved beta-sheet
103	<a href="#">c1h9sA</a>	Alignment	not modelled	21.2	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
104	<a href="#">c2zxeG</a>	Alignment	not modelled	21.2	20	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> G: <b>PDB Molecule:</b> phospholemman-like protein; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
105	<a href="#">c2q13A</a>	Alignment	not modelled	21.0	9	<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
106	<a href="#">c4lwsB</a>	Alignment	not modelled	20.9	11	<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
107	<a href="#">c2beqA_</a>	Alignment	not modelled	20.9	12 <b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> structure of a proteolytically resistant core from the severe acute2 respiratory syndrome coronavirus s2 fusion protein
108	<a href="#">d2cu6a1</a>	Alignment	not modelled	20.9	27 <b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Fe-S cluster assembly (FSCA) domain-like <b>Family:</b> PaaD-like
109	<a href="#">c6ezvX_</a>	Alignment	not modelled	20.8	16 <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
110	<a href="#">c5yfpG_</a>	Alignment	not modelled	20.4	12 <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