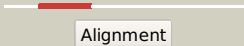
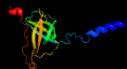
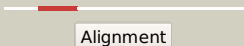

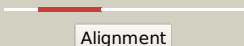
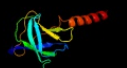

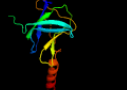


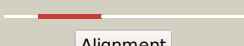
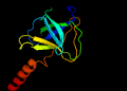



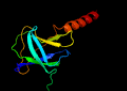

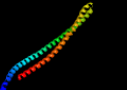

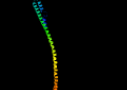

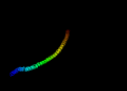
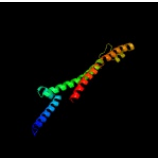
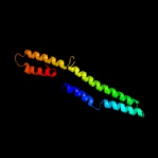
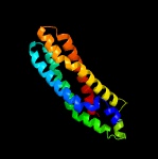
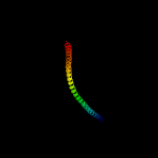
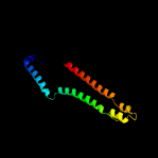

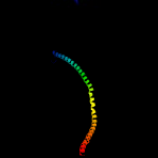

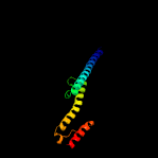


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0171\_(mce1C)\_200930\_202477  
 Date Tue Jul 23 14:50:22 BST 2019  
 Unique Job ID 96ed4d8289548d16

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		99.7	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="#">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
4	<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
5	<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
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="#">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
8	<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
9	<a href="#">c3g67A_</a>	 Alignment		96.5	10	<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		96.2	8	<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="#">c2ch7A_</a>	 Alignment		95.8	13	<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

12	<a href="#">c5szsC_</a>	Alignment		95.0	17	<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
13	<a href="#">c2d4yA_</a>	Alignment		94.7	13	<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		94.7	13	<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="#">c2wpgA_</a>	Alignment		94.5	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 (sadak3, in-2 register fusion)
16	<a href="#">c6nzkB_</a>	Alignment		94.4	16	<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
17	<a href="#">c6b7nC_</a>	Alignment		94.2	17	<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
18	<a href="#">c1ei3C_</a>	Alignment		94.0	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="#">c6gajA_</a>	Alignment		94.0	19	<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)
20	<a href="#">c3lnrA_</a>	Alignment		93.9	11	<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
21	<a href="#">c2ieqC_</a>	Alignment	not modelled	93.5	14	<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
22	<a href="#">c5xbjA_</a>	Alignment	not modelled	93.4	6	<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
23	<a href="#">c4abxB_</a>	Alignment	not modelled	93.1	14	<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
24	<a href="#">c1ei3E_</a>	Alignment	not modelled	92.8	16	<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="#">c1deqO_</a>	Alignment	not modelled	92.8	14	<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)
26	<a href="#">c2dq3A_</a>	Alignment	not modelled	92.8	13	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of aq_298
27	<a href="#">c6ezvX_</a>	Alignment	not modelled	92.7	10	<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
28	<a href="#">c6nb3B_</a>	Alignment	not modelled	92.7	15	<b>PDB header:</b> virus <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> mers-cov complex with human neutralizing Ica60 antibody fab fragment2 (state 1) <b>PDB header:</b> viral protein

29	<a href="#">c5i08A_</a>	Alignment	not modelled	92.6	15	<b>Chain:</b> A: <b>PDB Molecule:</b> spike glycoprotein, envelope glycoprotein chimera; <b>PDBTitle:</b> prefusion structure of a human coronavirus spike protein
30	<a href="#">c5x5bB_</a>	Alignment	not modelled	92.6	11	<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
31	<a href="#">c2p22A_</a>	Alignment	not modelled	92.4	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> suppressor protein stp22 of temperature-sensitive alpha- <b>PDBTitle:</b> structure of the yeast escrt-i heterotetramer core
32	<a href="#">c6gapB_</a>	Alignment	not modelled	92.2	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
33	<a href="#">c3cwgA_</a>	Alignment	not modelled	92.1	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
34	<a href="#">c6cs2A_</a>	Alignment	not modelled	91.7	11	<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
35	<a href="#">c3jclC_</a>	Alignment	not modelled	91.6	15	<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
36	<a href="#">c1degF_</a>	Alignment	not modelled	91.0	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)
37	<a href="#">c2bbjB_</a>	Alignment	not modelled	91.0	13	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein; <b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
38	<a href="#">c4ut1A_</a>	Alignment	not modelled	91.0	15	<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
39	<a href="#">c3zx6A_</a>	Alignment	not modelled	90.8	7	<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
40	<a href="#">c5xlrC_</a>	Alignment	not modelled	89.9	11	<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
41	<a href="#">c6gy8B_</a>	Alignment	not modelled	89.1	11	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> xaxa; <b>PDBTitle:</b> crystal structure of xaxa from xenorhabdus nematophila
42	<a href="#">c2qihA_</a>	Alignment	not modelled	89.0	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
43	<a href="#">c5dfzA_</a>	Alignment	not modelled	88.7	13	<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.
44	<a href="#">c1wyyB_</a>	Alignment	not modelled	88.7	22	<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
45	<a href="#">c6b3oB_</a>	Alignment	not modelled	88.5	20	<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
46	<a href="#">c5u0pU_</a>	Alignment	not modelled	87.8	16	<b>PDB header:</b> transcription <b>Chain:</b> U: <b>PDB Molecule:</b> mediator complex subunit 21; <b>PDBTitle:</b> cryo-em structure of the transcriptional mediator
47	<a href="#">d1ykbh1</a>	Alignment	not modelled	87.8	13	<b>Fold:</b> Mediator hinge subcomplex-like <b>Superfamily:</b> Mediator hinge subcomplex-like <b>Family:</b> CSE2-like
48	<a href="#">c5zhyA_</a>	Alignment	not modelled	87.8	9	<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
49	<a href="#">c4rh7A_</a>	Alignment	not modelled	87.7	11	<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
50	<a href="#">c3ojaB_</a>	Alignment	not modelled	87.3	13	<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
51	<a href="#">c5wrgB_</a>	Alignment	not modelled	87.1	11	<b>PDB header:</b> virus like particle <b>Chain:</b> B: <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> sars-cov spike glycoprotein
52	<a href="#">c1kmiZ_</a>	Alignment	not modelled	87.1	13	<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="#">c4nl6C_</a>	Alignment	not modelled	86.9	15	<b>PDB header:</b> splicing <b>Chain:</b> C: <b>PDB Molecule:</b> survival motor neuron protein; <b>PDBTitle:</b> structure of the full-length form of the protein smn found in healthy2 patients
54	<a href="#">c5nmoA_</a>	Alignment	not modelled	86.8	15	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein smc,chromosome partition <b>PDBTitle:</b> structure of the bacillus subtilis smc joint domain

55	<a href="#">c1quuA</a>	Alignment	not modelled	85.7	14	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> human skeletal muscle alpha-actinin 2; <b>PDBTitle:</b> crystal structure of two central spectrin-like repeats from alpha-2 actinin
56	<a href="#">c5lskD</a>	Alignment	not modelled	85.4	17	<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
57	<a href="#">c2nrjA</a>	Alignment	not modelled	85.3	15	<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
58	<a href="#">c4e40A</a>	Alignment	not modelled	85.3	8	<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
59	<a href="#">c6grjG</a>	Alignment	not modelled	85.0	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.
60	<a href="#">c5j65A</a>	Alignment	not modelled	84.5	11	<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
61	<a href="#">c3ghgI</a>	Alignment	not modelled	83.8	7	<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
62	<a href="#">c3ghgK</a>	Alignment	not modelled	83.3	14	<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
63	<a href="#">c3j99M</a>	Alignment	not modelled	82.1	12	<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)
64	<a href="#">c5cwsC</a>	Alignment	not modelled	81.9	10	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> nucleoporin nsp1; <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
65	<a href="#">c2gl2B</a>	Alignment	not modelled	81.0	12	<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
66	<a href="#">d1eq1a</a>	Alignment	not modelled	80.9	13	<b>Fold:</b> Apolipophorin-III <b>Superfamily:</b> Apolipophorin-III <b>Family:</b> Apolipophorin-III
67	<a href="#">c5yfpG</a>	Alignment	not modelled	78.4	13	<b>PDB header:</b> exocytosis <b>Chain:</b> G: <b>PDB Molecule:</b> exocyst complex component exo70; <b>PDBTitle:</b> cryo-em structure of the exocyst complex
68	<a href="#">c6gaoC</a>	Alignment	not modelled	78.1	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
69	<a href="#">d1g4us1</a>	Alignment	not modelled	78.0	15	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Bacterial GAP domain <b>Family:</b> Bacterial GAP domain
70	<a href="#">c5cwsJ</a>	Alignment	not modelled	78.0	8	<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
71	<a href="#">d1st6a4</a>	Alignment	not modelled	77.1	17	<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="#">c6el1F</a>	Alignment	not modelled	76.5	14	<b>PDB header:</b> membrane protein <b>Chain:</b> F: <b>PDB Molecule:</b> yaxa; <b>PDBTitle:</b> yaxab pore complex
73	<a href="#">d1quua1</a>	Alignment	not modelled	74.6	15	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
74	<a href="#">c2efrB</a>	Alignment	not modelled	73.6	13	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1 alpha chain; <b>PDBTitle:</b> crystal structure of the c-terminal tropomyosin fragment with n- and2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
75	<a href="#">c4a7fB</a>	Alignment	not modelled	73.4	10	<b>PDB header:</b> structural protein/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tropomyosin 1 alpha; <b>PDBTitle:</b> structure of the actin-tropomyosin-myosin complex (rigor atm 3)
76	<a href="#">c5gasN</a>	Alignment	not modelled	73.2	12	<b>PDB header:</b> hydrolase <b>Chain:</b> N: <b>PDB Molecule:</b> archaeal/vacuolar-type h+-atpase subunit i; <b>PDBTitle:</b> thermus thermophilus v/a-atpase, conformation 2
77	<a href="#">c2xzrA</a>	Alignment	not modelled	73.1	8	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> immunoglobulin-binding protein eibd; <b>PDBTitle:</b> escherichia coli immunoglobulin-binding protein eibd 391-438 fused2 to gcn4 adaptors
78	<a href="#">c3lxbB</a>	Alignment	not modelled	72.9	9	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> spectrin beta chain, erythrocyte; <b>PDBTitle:</b> crystal structure of the erythrocyte spectrin tetramerization domain2 complex
79	<a href="#">c1u5pA</a>	Alignment	not modelled	72.4	11	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> spectrin alpha chain, brain; <b>PDBTitle:</b> crystal structure of repeats 15 and 16 of chicken brain2 alpha spectrin
						<b>PDB header:</b> viral protein

80	<a href="#">c4fiuC</a>	Alignment	not modelled	71.3	13	<b>Chain:</b> C: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> the structure of hemagglutinin of h16 subtype influenza virus with2 v327g mutation
81	<a href="#">c2fxmB</a>	Alignment	not modelled	70.2	14	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> myosin heavy chain, cardiac muscle beta isoform; <b>PDBTitle:</b> structure of the human beta-myosin s2 fragment
82	<a href="#">c2yfaA</a>	Alignment	not modelled	70.1	9	<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
83	<a href="#">c2bezC</a>	Alignment	not modelled	69.9	25	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> e2 glycoprotein; <b>PDBTitle:</b> structure of a proteolitically resistant core from the severe acute2 respiratory syndrome coronavirus s2 fusion protein
84	<a href="#">c5zuvB</a>	Alignment	not modelled	68.9	18	<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
85	<a href="#">c1z23A</a>	Alignment	not modelled	68.4	14	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> crk-associated substrate; <b>PDBTitle:</b> the serine-rich domain from crk-associated substrate2 (p130cas)
86	<a href="#">c2dq0A</a>	Alignment	not modelled	68.3	9	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> seryl-trna synthetase; <b>PDBTitle:</b> crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
87	<a href="#">c5j4oA</a>	Alignment	not modelled	67.8	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> spectrin alpha chain, erythrocytic 1; <b>PDBTitle:</b> structure of human erythrocytic spectrin alpha chain repeats 16-17
88	<a href="#">c4wsrA</a>	Alignment	not modelled	66.9	17	<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
89	<a href="#">d1hcia4</a>	Alignment	not modelled	66.2	7	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
90	<a href="#">c2d3eD</a>	Alignment	not modelled	66.1	10	<b>PDB header:</b> contractile protein <b>Chain:</b> D: <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1 alpha chain; <b>PDBTitle:</b> crystal structure of the c-terminal fragment of rabbit skeletal alpha-2 tropomyosin
91	<a href="#">c3dtpA</a>	Alignment	not modelled	65.6	13	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain chimera of smooth and cardiac muscle; <b>PDBTitle:</b> tarantula heavy meromyosin obtained by flexible docking to tarantula2 muscle thick filament cryo-em 3d-map
92	<a href="#">c2wr2B</a>	Alignment	not modelled	64.4	13	<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
93	<a href="#">c3vkhA</a>	Alignment	not modelled	64.3	14	<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
94	<a href="#">c3gvmA</a>	Alignment	not modelled	61.8	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
95	<a href="#">c3bt6B</a>	Alignment	not modelled	61.1	7	<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
96	<a href="#">c4n21E</a>	Alignment	not modelled	60.2	11	<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
97	<a href="#">c1ha0A</a>	Alignment	not modelled	59.7	10	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hemagglutinin precursor); <b>PDBTitle:</b> hemagglutinin precursor ha0
98	<a href="#">c4l1bB</a>	Alignment	not modelled	59.5	7	<b>PDB header:</b> signaling protein/transferase/inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> crystal structure of p110alpha complexed with nish2 of p85alpha
99	<a href="#">c4mc5C</a>	Alignment	not modelled	58.8	16	<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)
100	<a href="#">c2q13A</a>	Alignment	not modelled	58.6	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
101	<a href="#">c5wwlN</a>	Alignment	not modelled	58.6	12	<b>PDB header:</b> cell cycle <b>Chain:</b> N: <b>PDB Molecule:</b> kinetochore protein nnf1; <b>PDBTitle:</b> crystal structure of the schizogenesis pombe kinetochore mis12c2 subcomplex
102	<a href="#">c2dnxA</a>	Alignment	not modelled	58.5	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> syntaxin-12; <b>PDBTitle:</b> solution structure of rsgi ruh-063, an n-terminal domain of2 syntaxin 12 from human cdna
103	<a href="#">c6j9rA</a>	Alignment	not modelled	58.2	10	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> brain tumor protein; <b>PDBTitle:</b> coiled-coil domain of drosophila trim protein brat
104	<a href="#">c4lwsA</a>	Alignment	not modelled	58.0	11	<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
						<b>PDB header:</b> transferase

105	<a href="#">c5tvbB_</a>	Alignment	not modelled	57.9	10	<b>Chain:</b> B: <b>PDB Molecule:</b> nucleoprotein tpr; <b>PDBTitle:</b> structure of the tpr oligomerization domain
106	<a href="#">c5dmaA_</a>	Alignment	not modelled	57.8	28	<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
107	<a href="#">c6gy6Q_</a>	Alignment	not modelled	57.1	10	<b>PDB header:</b> toxin <b>Chain:</b> Q: <b>PDB Molecule:</b> xaxa; <b>PDBTitle:</b> xaxab pore complex from xenorhabdus nematophila
108	<a href="#">c5ijnF_</a>	Alignment	not modelled	57.1	12	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> nuclear pore complex protein nup54; <b>PDBTitle:</b> composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
109	<a href="#">c2oevA_</a>	Alignment	not modelled	56.8	14	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death 6-interacting protein; <b>PDBTitle:</b> crystal structure of alix/aip1
110	<a href="#">c2j5uB_</a>	Alignment	not modelled	56.8	17	<b>PDB header:</b> cell shape regulation <b>Chain:</b> B: <b>PDB Molecule:</b> mrec protein; <b>PDBTitle:</b> mrec lysteria monocytogenes
111	<a href="#">c3o0zD_</a>	Alignment	not modelled	55.7	9	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> rho-associated protein kinase 1; <b>PDBTitle:</b> crystal structure of a coiled-coil domain from human rock i
112	<a href="#">c6h9xA_</a>	Alignment	not modelled	55.1	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> serine--trna ligase; <b>PDBTitle:</b> klebsiella pneumoniae seryl-trna synthetase in complex with the2 intermediate analog 5'-o-(n-(l-seryl)-sulfamoyl)adenosine
113	<a href="#">d1u5pa1</a>	Alignment	not modelled	55.0	14	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
114	<a href="#">c2ld3A_</a>	Alignment	not modelled	54.8	18	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin vi; <b>PDBTitle:</b> solution structure of myosin vi lever arm extension
115	<a href="#">c5yfpD_</a>	Alignment	not modelled	54.8	14	<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
116	<a href="#">c5lm2B_</a>	Alignment	not modelled	54.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tyrosine-protein phosphatase non-receptor type 23; <b>PDBTitle:</b> crystal structure of hd-ptp phosphatase
117	<a href="#">c4lwsB_</a>	Alignment	not modelled	54.6	6	<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
118	<a href="#">d1s35a1</a>	Alignment	not modelled	54.2	13	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
119	<a href="#">c1y8oA_</a>	Alignment	not modelled	53.6	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> [pyruvate dehydrogenase [lipoamide]] kinase isozyme 3; <b>PDBTitle:</b> crystal structure of the pdk3-l2 complex
120	<a href="#">c1hgeD_</a>	Alignment	not modelled	53.3	10	<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