
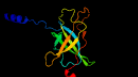


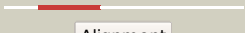










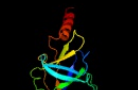



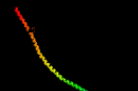

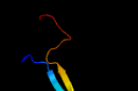

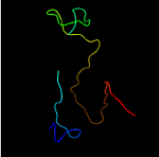



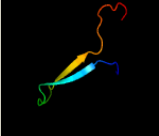
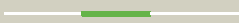
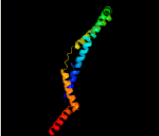


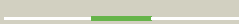






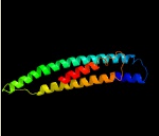

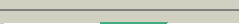

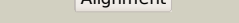
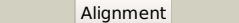
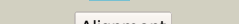
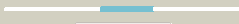



# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD0169\_(mce1A)\_198532\_199896  
 Date Tue Jul 23 14:50:22 BST 2019  
 Unique Job ID 7580e1d11f66fbdd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ic4C_</a>	 Alignment		99.9	21	<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	21	<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		99.5	19	<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="#">c5uvnC_</a>	 Alignment		99.5	19	<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="#">c5uvnF_</a>	 Alignment		99.5	19	<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
6	<a href="#">c5uvnE_</a>	 Alignment		99.5	19	<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="#">c5uvnA_</a>	 Alignment		99.5	19	<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
8	<a href="#">c5uvnB_</a>	 Alignment		99.5	19	<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		82.0	9	<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		81.8	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein i; <b>PDBTitle:</b> four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
11	<a href="#">c2j5uB_</a>	 Alignment		68.3	14	<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="#">c5jxpA_</a>	 Alignment		62.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> asp/glu-specific dipeptidyl-peptidase; <b>PDBTitle:</b> crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
13	<a href="#">d1szia_</a>	 Alignment		62.5	16	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain <b>Family:</b> Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
14	<a href="#">c2qf4A_</a>	 Alignment		58.3	17	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> cell shape determining protein mreC; <b>PDBTitle:</b> high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mreC (orthorhombic form)
15	<a href="#">c4abxB_</a>	 Alignment		55.9	13	<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
16	<a href="#">c3lnrA_</a>	 Alignment		52.4	10	<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
17	<a href="#">c5xbjA_</a>	 Alignment		50.7	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="#">c6e6aB_</a>	 Alignment		50.1	15	<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
19	<a href="#">c3q5xA_</a>	 Alignment		49.7	12	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> protein cut8; <b>PDBTitle:</b> structure of proteasome tether
20	<a href="#">c3cwgA_</a>	 Alignment		48.0	12	<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
21	<a href="#">c5lp5F_</a>	 Alignment	not modelled	47.4	17	<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
22	<a href="#">c2ch7A_</a>	 Alignment	not modelled	46.1	5	<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
23	<a href="#">c6cs2A_</a>	 Alignment	not modelled	42.8	22	<b>PDB header:</b> viral protein/hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> spike glycoprotein,fibritin; <b>PDBTitle:</b> sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
24	<a href="#">c4y01B_</a>	 Alignment	not modelled	40.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> peptidase s46; <b>PDBTitle:</b> crystal structure of dipeptidyl peptidase 11 (dpp11) from2 porphyromonas gingivalis
25	<a href="#">c4iogD_</a>	 Alignment	not modelled	38.0	15	<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
26	<a href="#">c1kmiZ_</a>	 Alignment	not modelled	35.9	14	<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
27	<a href="#">c3zx6A_</a>	 Alignment	not modelled	34.1	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
28	<a href="#">c1deqF_</a>	 Alignment	not modelled	34.0	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)

29	<a href="#">c3bt6B</a>	Alignment	not modelled	33.3	9	<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
30	<a href="#">c3ur1C</a>	Alignment	not modelled	33.1	22	<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.
31	<a href="#">c3gvmA</a>	Alignment	not modelled	33.0	14	<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
32	<a href="#">d1st6a4</a>	Alignment	not modelled	32.8	15	<b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
33	<a href="#">c4rh7A</a>	Alignment	not modelled	32.0	9	<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
34	<a href="#">c4wsrA</a>	Alignment	not modelled	31.9	11	<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
35	<a href="#">c5n77A</a>	Alignment	not modelled	31.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> magnesium transport protein cora; <b>PDBTitle:</b> crystal structure of the cytosolic domain of the cora magnesium2 channel from escherichia coli in complex with magnesium
36	<a href="#">c2wpgA</a>	Alignment	not modelled	31.8	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)
37	<a href="#">c4hw9E</a>	Alignment	not modelled	30.8	18	<b>PDB header:</b> membrane protein <b>Chain:</b> E: <b>PDB Molecule:</b> mechanosensitive channel mscs; <b>PDBTitle:</b> crystal structure of helicobacter pylori mscs (closed state)
38	<a href="#">c4lwsA</a>	Alignment	not modelled	30.6	14	<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
39	<a href="#">c2vs0B</a>	Alignment	not modelled	30.6	13	<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
40	<a href="#">c4fiuC</a>	Alignment	not modelled	30.3	12	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> the structure of hemagglutinin of h16 subtype influenza virus with2 v327g mutation
41	<a href="#">c4tkoB</a>	Alignment	not modelled	30.3	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
42	<a href="#">c6j9rA</a>	Alignment	not modelled	29.8	9	<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
43	<a href="#">c6ezvX</a>	Alignment	not modelled	29.1	13	<b>PDB header:</b> toxin <b>Chain:</b> X: <b>PDB Molecule:</b> non-hemolytic enterotoxin lytic component I1; <b>PDBTitle:</b> the cytotoxin maka from vibrio cholerae
44	<a href="#">c5u0pU</a>	Alignment	not modelled	28.9	7	<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
45	<a href="#">c2wr2B</a>	Alignment	not modelled	28.1	11	<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
46	<a href="#">c1ha0A</a>	Alignment	not modelled	28.0	11	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (hemagglutinin precursor); <b>PDBTitle:</b> hemagglutinin precursor ha0
47	<a href="#">c3j6vL</a>	Alignment	not modelled	27.9	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
48	<a href="#">c1zn1L</a>	Alignment	not modelled	27.8	24	<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
49	<a href="#">c3t9nG</a>	Alignment	not modelled	27.6	18	<b>PDB header:</b> membrane protein <b>Chain:</b> G: <b>PDB Molecule:</b> small-conductance mechanosensitive channel; <b>PDBTitle:</b> crystal structure of a membrane protein
50	<a href="#">d2uubl1</a>	Alignment	not modelled	26.9	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
51	<a href="#">c3ck6E</a>	Alignment	not modelled	24.1	9	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> putative membrane transport protein; <b>PDBTitle:</b> crystal structure of zntb cytoplasmic domain from vibrio2 parahaemolyticus rimd 2210633
52	<a href="#">c1mqjB</a>	Alignment	not modelled	23.7	12	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin ha2 chain; <b>PDBTitle:</b> bha of ukr/63
53	<a href="#">c4n21E</a>	Alignment	not modelled	23.6	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
						<b>PDB header:</b> viral protein

54	<a href="#">c6cv0C_</a>	Alignment	not modelled	22.8	5	<b>Chain:</b> C; <b>PDB Molecule:</b> spike glycoprotein; <b>PDBTitle:</b> cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
55	<a href="#">c5zhyA_</a>	Alignment	not modelled	22.5	11	<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
56	<a href="#">c6b7nC_</a>	Alignment	not modelled	22.4	13	<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
57	<a href="#">c1bf5A_</a>	Alignment	not modelled	21.6	10	<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
58	<a href="#">c5xnmj_</a>	Alignment	not modelled	21.6	18	<b>PDB header:</b> membrane protein <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> structure of unstacked c2s2m2-type psii-lhcii supercomplex from pisum2 sativum
59	<a href="#">c6gajA_</a>	Alignment	not modelled	21.4	7	<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)
60	<a href="#">c2wrhl_</a>	Alignment	not modelled	20.9	9	<b>PDB header:</b> viral protein <b>Chain:</b> I; <b>PDB Molecule:</b> hemagglutinin ha2 chain; <b>PDBTitle:</b> structure of h1 duck albert hemagglutinin with human2 receptor
61	<a href="#">d2qall1</a>	Alignment	not modelled	20.0	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
62	<a href="#">c4mc5C_</a>	Alignment	not modelled	19.9	10	<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)
63	<a href="#">c1hgeD_</a>	Alignment	not modelled	19.6	11	<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
64	<a href="#">c3a0hj_</a>	Alignment	not modelled	19.6	21	<b>PDB header:</b> electron transport <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> crystal structure of i-substituted photosystem ii complex
65	<a href="#">d2axtj1</a>	Alignment	not modelled	19.6	21	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction center protein J, Psbj <b>Family:</b> Psbj-like
66	<a href="#">c4h32L_</a>	Alignment	not modelled	19.5	12	<b>PDB header:</b> viral protein <b>Chain:</b> L; <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> the crystal structure of the hemagglutinin h17 derived the bat2 influenza a virus
67	<a href="#">c2qihA_</a>	Alignment	not modelled	19.3	10	<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
68	<a href="#">c2j0oA_</a>	Alignment	not modelled	18.9	10	<b>PDB header:</b> cell invasion <b>Chain:</b> A; <b>PDB Molecule:</b> invasin ipad; <b>PDBTitle:</b> shigella flexneri ipad
69	<a href="#">d2j0oa1</a>	Alignment	not modelled	18.9	10	<b>Fold:</b> lpad-like <b>Superfamily:</b> lpad-like <b>Family:</b> lpad-like
70	<a href="#">d1i94L_</a>	Alignment	not modelled	18.9	27	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
71	<a href="#">c3jcuJ_</a>	Alignment	not modelled	18.7	24	<b>PDB header:</b> membrane protein <b>Chain:</b> J; <b>PDB Molecule:</b> photosystem ii reaction center protein j; <b>PDBTitle:</b> cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
72	<a href="#">c3vkhA_</a>	Alignment	not modelled	18.4	12	<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
73	<a href="#">c2d4yA_</a>	Alignment	not modelled	18.0	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)
74	<a href="#">c1ru7B_</a>	Alignment	not modelled	18.0	9	<b>PDB header:</b> viral protein <b>Chain:</b> B; <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> 1934 human h1 hemagglutinin
75	<a href="#">c4ut1A_</a>	Alignment	not modelled	17.8	17	<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
76	<a href="#">c6el1F_</a>	Alignment	not modelled	17.4	8	<b>PDB header:</b> membrane protein <b>Chain:</b> F; <b>PDB Molecule:</b> yaxa; <b>PDBTitle:</b> yaxab pore complex
77	<a href="#">c3nwiC_</a>	Alignment	not modelled	17.3	9	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> zinc transport protein zntb; <b>PDBTitle:</b> the soluble domain structure of the zntb zn2+ efflux system
78	<a href="#">c4h8sA_</a>	Alignment	not modelled	17.1	7	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> dcc-interacting protein 13-beta; <b>PDBTitle:</b> crystal structure of human appl2barph domain
79	<a href="#">c6nzkB_</a>	Alignment	not modelled	16.7	17	<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
80	<a href="#">d1eq1a_</a>	Alianment	not modelled	16.5	10	<b>Fold:</b> Apolipophorin-III <b>Superfamily:</b> Apolipophorin-III

					<b>Family:</b> Apolipoprotein III
81	<a href="#">c5zuvB_</a>	Alignment	not modelled	16.4	17 <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
82	<a href="#">c3m5gD_</a>	Alignment	not modelled	16.3	8 <b>PDB header:</b> viral protein <b>Chain:</b> D: <b>PDB Molecule:</b> hemagglutinin; <b>PDBTitle:</b> crystal structure of a h7 influenza virus hemagglutinin
83	<a href="#">c2vv5D_</a>	Alignment	not modelled	16.0	21 <b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> small-conductance mechanosensitive channel; <b>PDBTitle:</b> the open structure of mscs
84	<a href="#">c3euhB_</a>	Alignment	not modelled	15.5	9 <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
85	<a href="#">d1hcia4</a>	Alignment	not modelled	15.2	2 <b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Spectrin repeat <b>Family:</b> Spectrin repeat
86	<a href="#">c3zbcC_</a>	Alignment	not modelled	15.1	17 <b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> esxa; <b>PDBTitle:</b> geobacillus thermodenitrificans esxa crystal form i
87	<a href="#">d1gd7a_</a>	Alignment	not modelled	15.0	16 <b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Myf domain
88	<a href="#">d1st6a3</a>	Alignment	not modelled	14.4	15 <b>Fold:</b> Four-helical up-and-down bundle <b>Superfamily:</b> alpha-catenin/vinculin-like <b>Family:</b> alpha-catenin/vinculin
89	<a href="#">d1t98a2</a>	Alignment	not modelled	14.2	12 <b>Fold:</b> STAT-like <b>Superfamily:</b> MukF C-terminal domain-like <b>Family:</b> MukF C-terminal domain-like
90	<a href="#">c1p68A_</a>	Alignment	not modelled	13.7	26 <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
91	<a href="#">c2kbbA_</a>	Alignment	not modelled	13.2	13 <b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> tal1n-1; <b>PDBTitle:</b> nmr structure of the talin rod domain, 1655-1822
92	<a href="#">c1jsdB_</a>	Alignment	not modelled	12.9	10 <b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> haemagglutinin (ha2 chain); <b>PDBTitle:</b> crystal structure of swine h9 haemagglutinin
93	<a href="#">c5zdiB_</a>	Alignment	not modelled	12.9	11 <b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> protein secretion chaperonin csaa; <b>PDBTitle:</b> crystal structure of csaa chaperone protein from picrophilus torridus
94	<a href="#">c3pe0B_</a>	Alignment	not modelled	12.4	11 <b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> plectin; <b>PDBTitle:</b> structure of the central region of the plakin domain of plectin
95	<a href="#">c5j2lB_</a>	Alignment	not modelled	11.7	15 <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
96	<a href="#">c1htmB_</a>	Alignment	not modelled	11.7	11 <b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> hemagglutinin ha2 chain; <b>PDBTitle:</b> structure of influenza haemagglutinin at the ph of membrane2 fusion
97	<a href="#">c2h7vD_</a>	Alignment	not modelled	11.6	15 <b>PDB header:</b> signaling protein <b>Chain:</b> D: <b>PDB Molecule:</b> protein kinase ypk1; <b>PDBTitle:</b> co-crystal structure of ypk1-rac1
98	<a href="#">c5i08A_</a>	Alignment	not modelled	11.5	16 <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
99	<a href="#">c5j65A_</a>	Alignment	not modelled	11.3	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