


















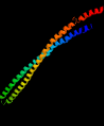



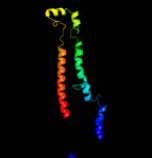
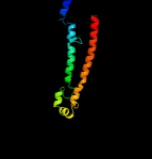
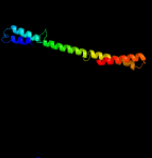
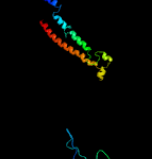
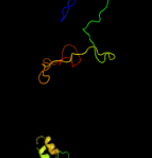

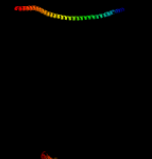
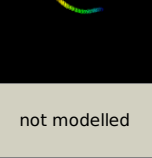


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0172_(mce1D)_202474_204066
Date	Tue Jul 23 14:50:22 BST 2019
Unique Job ID	247e971647faba62

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.9	24	PDB header: protein transport Chain: C: PDB Molecule: toluene tolerance efflux transporter (abc superfamily, PDBTitle: cryo-em structure of the a. baumannii mla complex at 8.7 a resolution
2	c5uw8C_	 Alignment		99.8	24	PDB header: transport protein Chain: C: PDB Molecule: probable phospholipid abc transporter-binding protein mlad; PDBTitle: structure of e. coli mce protein mlad, core mce domain
3	c5uvnE_	 Alignment		99.4	16	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnF_	 Alignment		99.4	16	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnD_	 Alignment		99.4	16	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
6	c5uvnA_	 Alignment		99.4	16	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
7	c5uvnC_	 Alignment		99.4	16	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvnB_	 Alignment		99.4	16	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c3g67A_	 Alignment		94.9	5	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
10	c1qu7A_	 Alignment		92.3	6	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein i; PDBTitle: four helical-bundle structure of the cytoplasmic domain of a serine2 chemotaxis receptor
11	c2d4yA_	 Alignment		91.5	16	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)

12	c6nzkB_	Alignment		91.0	9	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
13	c6nb3B_	Alignment		90.6	14	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
14	c3jclC_	Alignment		88.5	10	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
15	c5xbjA_	Alignment		88.3	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: flagellar hook-associated protein flgk; PDBTitle: the structure of the flagellar hook junction protein hap1 (flgk) from2 campylobacter jejuni
16	c5i08A_	Alignment		88.2	8	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
17	c4nl6C_	Alignment		87.0	17	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
18	c5x5bB_	Alignment		86.5	11	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
19	c3zx6A_	Alignment		86.0	9	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
20	c2qihA_	Alignment		85.9	11	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
21	c1kmiZ_	Alignment	not modelled	85.8	16	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
22	c5wrgB_	Alignment	not modelled	85.6	11	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
23	c5u0pU_	Alignment	not modelled	83.1	9	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
24	c6e6aB_	Alignment	not modelled	83.0	20	PDB header: protein binding Chain: B: PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
25	c5xlrC_	Alignment	not modelled	82.6	11	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
26	c5x5fC_	Alignment	not modelled	80.4	14	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
27	c2ch7A_	Alignment	not modelled	79.5	6	PDB header: chemotaxis Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of the cytoplasmic domain of a bacterial2 chemoreceptor from thermotoga maritima
28	c2j5uB_	Alignment	not modelled	79.3	16	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
29	c3gvmA_	Alignment	not modelled	77.2	10	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039;

29	c3gvnA	Alignment	not modelled	77.2	10	PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae PDB header: viral protein
30	c2ieqC	Alignment	not modelled	77.2	14	Chain: C; PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus nl63 spike2 glycoprotein
31	c4abxB	Alignment	not modelled	75.9	18	PDB header: dna binding protein Chain: B; PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
32	c6gaiA	Alignment	not modelled	75.8	12	PDB header: viral protein Chain: A; PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
33	c3ghgK	Alignment	not modelled	74.9	13	PDB header: blood clotting Chain: K; PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
34	c6b7nC	Alignment	not modelled	74.7	15	PDB header: viral protein Chain: C; PDB Molecule: spike protein; PDBTitle: cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state
35	d1eq1a	Alignment	not modelled	71.4	10	Fold: Apolipophorin-III Superfamily: Apolipophorin-III Family: Apolipophorin-III
36	c4ut1A	Alignment	not modelled	69.8	12	PDB header: motor protein Chain: A; PDB Molecule: flagellar hook-associated protein; PDBTitle: the structure of the flagellar hook junction protein flgk2 from burkholderia pseudomallei
37	c2wpgA	Alignment	not modelled	68.5	9	PDB header: membrane protein Chain: A; PDB Molecule: trimeric autotransporter adhesin fragment; PDBTitle: salmonella enterica sada 479-519 fused to gcn4 adaptors (sadaK3, in-2 register fusion)
38	c6cs2A	Alignment	not modelled	68.4	11	PDB header: viral protein/hydrolase Chain: A; PDB Molecule: spike glycoprotein,fibrin; PDBTitle: sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
39	c5zhyA	Alignment	not modelled	67.4	13	PDB header: viral protein Chain: A; PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
40	c6cv0C	Alignment	not modelled	66.9	12	PDB header: viral protein Chain: C; PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
41	c5yfpD	Alignment	not modelled	66.0	15	PDB header: exocytosis Chain: D; PDB Molecule: exocyst complex component sec8; PDBTitle: cryo-em structure of the exocyst complex
42	d1ykhb1	Alignment	not modelled	65.4	8	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
43	c3euhB	Alignment	not modelled	64.1	13	PDB header: cell cycle Chain: B; PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of the muke-mukf complex
44	c3cwgA	Alignment	not modelled	62.6	7	PDB header: transcription Chain: A; PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
45	c2yfaA	Alignment	not modelled	61.2	15	PDB header: receptor Chain: A; PDB Molecule: methyl-accepting chemotaxis transducer; PDBTitle: x-ray structure of mcps ligand binding domain in complex with malate
46	c4lwsB	Alignment	not modelled	58.4	10	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
47	c6ezvX	Alignment	not modelled	56.0	8	PDB header: toxin Chain: X; PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
48	c4iogD	Alignment	not modelled	54.4	18	PDB header: unknown function Chain: D; PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. sterne
49	d1h9ma2	Alignment	not modelled	53.3	24	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
50	c3ok8A	Alignment	not modelled	52.7	8	PDB header: protein binding Chain: A; PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: i-bar of pinkbar
51	d1h9ra2	Alignment	not modelled	52.4	20	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
52	c6grjG	Alignment	not modelled	51.5	18	PDB header: toxin Chain: G; PDB Molecule: ahlb; PDBTitle: structure of the ahlb pore of the tripartite alpha-pore forming toxin,2 ahl, from aeromonas hydrophila.
53	c1wyyB	Alignment	not modelled	50.8	14	PDB header: viral protein Chain: B; PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
54	c3uunA	Alignment	not modelled	50.2	9	PDB header: structural protein Chain: A; PDB Molecule: dystrophin; PDBTitle: crystal structure of n-terminal first spectrin repeat of dystrophin
55	c1dggF	Alignment	not modelled	48.9	6	PDB header: blood clotting Chain: F; PDB Molecule: fibrinogen (gamma chain);

55	c10eqf_	Alignment	not modelled	48.9	0	PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
56	c3zbc_	Alignment	not modelled	48.8	8	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
57	d1wa8a1	Alignment	not modelled	48.4	9	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
58	c2qf4A_	Alignment	not modelled	48.1	6	PDB header: structural protein Chain: A: PDB Molecule: cell shape determining protein mrec; PDBTitle: high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
59	c5szsC_	Alignment	not modelled	46.6	12	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: glycan shield and epitope masking of a coronavirus spike protein2 observed by cryo-electron microscopy
60	d1h9ma1	Alignment	not modelled	44.2	12	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
61	d1guta_	Alignment	not modelled	43.5	12	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
62	c5dmaA_	Alignment	not modelled	43.2	16	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pcrA; PDBTitle: crystal structure of c-terminal tudor domain in pcrA/uvrD helicase
63	c1cz5A_	Alignment	not modelled	42.7	12	PDB header: hydrolase Chain: A: PDB Molecule: vcp-like atpase; PDBTitle: nmr structure of vat-n: the n-terminal domain of vat (vcp-2 like atpase of thermoplasma)
64	c6gaoC_	Alignment	not modelled	42.7	13	PDB header: viral protein Chain: C: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t11 reovirus sigma1 coiled coil tail and body
65	c5n76C_	Alignment	not modelled	42.0	15	PDB header: nickel-binding protein Chain: C: PDB Molecule: coot; PDBTitle: crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
66	c4e40A_	Alignment	not modelled	41.7	10	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the haptoglobin-hemoglobin receptor of trypanosoma congolense
67	c1ei3C_	Alignment	not modelled	40.7	10	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
68	c4n21E_	Alignment	not modelled	40.4	12	PDB header: viral protein Chain: E: PDB Molecule: gp2 ectodomain; PDBTitle: crystal structure of the gp2 core domain from the california academy2 of science virus
69	c1bf5A_	Alignment	not modelled	38.4	11	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
70	c5n9yB_	Alignment	not modelled	38.0	14	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
71	c5zuvB_	Alignment	not modelled	35.7	23	PDB header: viral protein, inhibitor Chain: B: PDB Molecule: spike glycoprotein, spike glycoprotein, inhibitor ek1; PDBTitle: crystal structure of the human coronavirus 229e hr1 motif in complex2 with pan-covs inhibitor ek1
72	c2vs0B_	Alignment	not modelled	35.4	5	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
73	c5j65A_	Alignment	not modelled	35.3	14	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry6aa; PDBTitle: crystal structure of trypsin activated cry6aa
74	c2p22A_	Alignment	not modelled	35.0	11	PDB header: transport protein Chain: A: PDB Molecule: suppressor protein stp22 of temperature-sensitive alpha- PDBTitle: structure of the yeast esct-i heterotetramer core
75	c4rh7A_	Alignment	not modelled	34.9	10	PDB header: motor protein Chain: A: PDB Molecule: green fluorescent protein/cytoplasmic dynein 2 heavy chain PDBTitle: crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
76	c1ei3E_	Alignment	not modelled	34.0	15	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
77	c1h9mB_	Alignment	not modelled	33.7	21	PDB header: binding protein Chain: B: PDB Molecule: molybdenum-binding-protein; PDBTitle: two crystal structures of the cytoplasmic molybdate-binding protein2 modg suggest a novel cooperative binding mechanism and provide3 insights into ligand-binding specificity. peg-grown form with4 molybdate bound
78	c3rq9B_	Alignment	not modelled	30.5	22	PDB header: tse2-binding protein Chain: B: PDB Molecule: type vi secretion immunity protein; PDBTitle: structure of tsi2, a tse2-immunity protein from pseudomonas aeruginosa
79	c6b3oB_	Alignment	not modelled	30.4	11	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
80	c3a08B_	Alignment	not modelled	29.7	57	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide;

80	c3a06B	Alignment	not modelled	29.7	57	PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal PDB header: structural protein
81	c3a08A	Alignment	not modelled	29.7	57	Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
82	c3qr8A	Alignment	not modelled	29.4	15	PDB header: viral protein Chain: A: PDB Molecule: baseplate assembly protein v; PDBTitle: crystal structure of the bacteriophage p2 membrane-piercing protein2 gpv
83	c1deqO	Alignment	not modelled	28.9	11	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
84	c2d3hB	Alignment	not modelled	27.4	57	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
85	c3a19B	Alignment	not modelled	27.4	57	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
86	c2d3hA	Alignment	not modelled	27.4	57	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
87	c4hw9E	Alignment	not modelled	27.2	18	PDB header: membrane protein Chain: E: PDB Molecule: mechanosensitive channel mscs; PDBTitle: crystal structure of helicobacter pylori mscs (closed state)
88	c2p7nA	Alignment	not modelled	26.9	16	PDB header: cell invasion Chain: A: PDB Molecule: pathogenicity island 1 effector protein; PDBTitle: crystal structure of the pathogenicity island 1 effector protein from2 chromobacterium violaceum. northeast structural genomics consortium3 (nesgc) target cvr69.
89	c3pwxB	Alignment	not modelled	26.9	11	PDB header: structural protein Chain: B: PDB Molecule: putative flagellar hook-associated protein; PDBTitle: structure of putative flagellar hook-associated protein from vibrio2 parahaemolyticus
90	c3stqC	Alignment	not modelled	26.6	22	PDB header: toxin Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: hypothetical protein pa2703 pseudomonas aeruginosa pao1
91	d1fr3a	Alignment	not modelled	26.4	10	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
92	d1st6a3	Alignment	not modelled	25.9	7	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
93	c1h9sA	Alignment	not modelled	25.5	20	PDB header: transcription regulator Chain: A: PDB Molecule: molybdenum transport protein mode; PDBTitle: molybdate bound complex of dimop domain of mode from e.coli
94	d1st6a4	Alignment	not modelled	25.3	10	Fold: Four-helical up-and-down bundle Superfamily: alpha-catenin/vinculin-like Family: alpha-catenin/vinculin
95	c4s37F	Alignment	not modelled	24.9	10	PDB header: metal binding protein Chain: F: PDB Molecule: phage baseplate protein; PDBTitle: crystal structure of r2 pyocin membrane-piercing spike
96	d1y2oa1	Alignment	not modelled	24.1	6	Fold: BAR/IMD domain-like Superfamily: BAR/IMD domain-like Family: IMD domain
97	c4jf3A	Alignment	not modelled	24.1	17	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: crystal structure of the mpmv tm retroviral fusion core
98	c2d3hC	Alignment	not modelled	23.4	57	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
99	c3a19A	Alignment	not modelled	23.4	57	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
100	c2akfC	Alignment	not modelled	23.2	39	PDB header: protein binding Chain: C: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1
101	c2akfA	Alignment	not modelled	23.2	39	PDB header: protein binding Chain: A: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1
102	c2akfB	Alignment	not modelled	23.2	39	PDB header: protein binding Chain: B: PDB Molecule: coronin-1a; PDBTitle: crystal structure of the coiled-coil domain of coronin 1
103	c3zrwB	Alignment	not modelled	22.9	15	PDB header: signaling protein Chain: B: PDB Molecule: af1503 protein, osmolarity sensor protein envz; PDBTitle: the structure of the dimeric hamp-dhp fusion a291v mutant
104	d1quua1	Alignment	not modelled	22.7	16	Fold: Spectrin repeat-like Superfamily: Spectrin repeat Family: Spectrin repeat
105	c4lwsA	Alignment	not modelled	22.5	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora

					curvata
106	c2kbbA_	Alignment	not modelled	22.3	10 PDB header: structural protein Chain: A: PDB Molecule: tal1n-1; PDBTitle: nmr structure of the talin rod domain, 1655-1822
107	c1zvaA_	Alignment	not modelled	22.2	8 PDB header: viral protein Chain: A: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of sars virus membrane fusion
108	c3ur1C_	Alignment	not modelled	21.9	3 PDB header: immune system Chain: C: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: 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.
109	d2vv5a1	Alignment	not modelled	21.3	19 Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
110	d1h9ra1	Alignment	not modelled	21.2	15 Fold: OB-fold Superfamily: MOP-like Family: BIMOP, duplicated molybdate-binding domain
111	c4jgsL_	Alignment	not modelled	20.9	12 PDB header: viral protein Chain: I: PDB Molecule: mlv-related proviral env polyprotein; PDBTitle: crystal structure of the xmrv tm retroviral fusion core
112	c4p71B_	Alignment	not modelled	20.8	24 PDB header: ligase Chain: B: PDB Molecule: phenylalanine--trna ligase beta subunit; PDBTitle: apo phers from p. aeuriginosa
113	d1s94a_	Alignment	not modelled	20.8	8 Fold: STAT-like Superfamily: t-snare proteins Family: t-snare proteins
114	c1s94A_	Alignment	not modelled	20.8	8 PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: s-syntaxin; PDBTitle: crystal structure of the habc domain of neuronal syntaxin from the2 squid loligo pealei
115	c6gapB_	Alignment	not modelled	20.6	12 PDB header: viral protein Chain: B: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t3d reovirus sigma1 coiled coil tail and body
116	c4njiA_	Alignment	not modelled	20.6	13 PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
117	c1zv8I_	Alignment	not modelled	20.5	13 PDB header: viral protein Chain: I: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of sars virus membrane fusion
118	c1wncE_	Alignment	not modelled	20.4	11 PDB header: viral protein Chain: E: PDB Molecule: e2 glycoprotein; PDBTitle: crystal structure of the sars-cov spike protein fusion core
119	c3j6vL_	Alignment	not modelled	20.2	18 PDB header: ribosome Chain: L: PDB Molecule: 28s ribosomal protein s12, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome