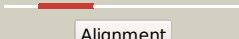
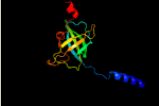
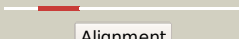
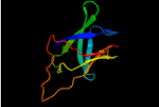
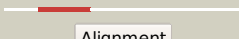


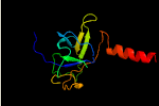









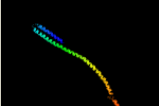



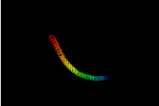
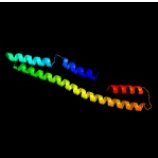

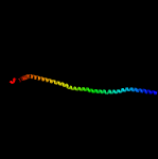

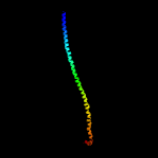
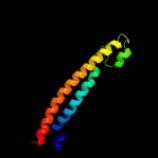
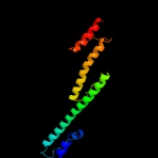
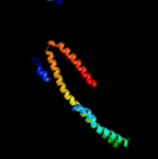



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0592_(mce2D)_690504_692030
Date	Fri Jul 26 01:50:15 BST 2019
Unique Job ID	43cb3e6f1b9534f9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ic4C_	 Alignment		99.9	25	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	28	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	c5uvnD_	 Alignment		99.4	20	PDB header: transport protein Chain: D: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
4	c5uvnA_	 Alignment		99.4	20	PDB header: transport protein Chain: A: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
5	c5uvnB_	 Alignment		99.4	20	PDB header: transport protein Chain: B: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
6	c5uvnF_	 Alignment		99.4	20	PDB header: transport protein Chain: F: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
7	c5uvnC_	 Alignment		99.4	20	PDB header: transport protein Chain: C: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
8	c5uvnE_	 Alignment		99.4	20	PDB header: transport protein Chain: E: PDB Molecule: paraquat-inducible protein b; PDBTitle: structure of e. coli mce protein pqib, periplasmic domain
9	c1qu7A_	 Alignment		94.1	13	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
10	c3g67A_	 Alignment		93.6	6	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
11	c2ch7A_	 Alignment		89.7	5	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

12	c2d4yA_	Alignment		89.4	16	PDB header: structural protein Chain: A: PDB Molecule: flagellar hook-associated protein 1; PDBTitle: crystal structure of a 49k fragment of hap1 (flgk)
13	c6b7nC_	Alignment		88.8	10	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
14	c4rh7A_	Alignment		87.2	11	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
15	c6gajA_	Alignment		86.4	11	PDB header: viral protein Chain: A: PDB Molecule: outer capsid protein sigma-1; PDBTitle: crystal structure of the t11 reovirus sigma1 coiled coil tail (iodide)
16	c3vkhA_	Alignment		83.4	14	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain
17	c3jcIC_	Alignment		79.9	11	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
18	c3lnrA_	Alignment		79.8	10	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
19	c6ezvX_	Alignment		79.8	13	PDB header: toxin Chain: X: PDB Molecule: non-hemolytic enterotoxin lytic component I1; PDBTitle: the cytotoxin maka from vibrio cholerae
20	c3zx6A_	Alignment		76.8	11	PDB header: signaling Chain: A: PDB Molecule: hamp, methyl-accepting chemotaxis protein i; PDBTitle: structure of hamp(af1503)-tsr fusion - hamp (a291v) mutant
21	c2wpgA_	Alignment	not modelled	75.8	6	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)
22	c5zuvB_	Alignment	not modelled	74.3	21	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
23	c2ieqC_	Alignment	not modelled	73.5	13	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: core structure of s2 from the human coronavirus n163 spike2 glycoprotein
24	c5u0pU_	Alignment	not modelled	72.6	13	PDB header: transcription Chain: U: PDB Molecule: mediator complex subunit 21; PDBTitle: cryo-em structure of the transcriptional mediator
25	c1deqF_	Alignment	not modelled	72.1	6	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
26	c3cwgA_	Alignment	not modelled	71.4	6	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
27	c1kmiZ_	Alignment	not modelled	70.0	16	PDB header: signaling protein Chain: Z: PDB Molecule: chemotaxis protein chez; PDBTitle: crystal structure of an e.coli chemotaxis protein, chez
28	c2j5uB_	Alignment	not modelled	69.5	18	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes

29	c4ut1A_	Alignment	not modelled	69.4	9	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
30	c6b3oB_	Alignment	not modelled	68.5	12	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
31	d1eq1a_	Alignment	not modelled	68.1	12	Fold: Apolipoporphin-III Superfamily: Apolipoporphin-III Family: Apolipoporphin-III
32	c1wyyB_	Alignment	not modelled	66.2	11	PDB header: viral protein Chain: B: PDB Molecule: e2 glycoprotein; PDBTitle: post-fusion hairpin conformation of the sars coronavirus spike2 glycoprotein
33	c5szsC_	Alignment	not modelled	65.5	15	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
34	c6e6aB_	Alignment	not modelled	63.9	13	PDB header: protein binding Chain: B: PDB Molecule: inclusion membrane protein a; PDBTitle: triclinic crystal form of inca g144a point mutant
35	c6nzkB_	Alignment	not modelled	63.6	17	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
36	c5yfpD_	Alignment	not modelled	63.0	14	PDB header: exocytosis Chain: D: PDB Molecule: exocyst complex component sec8; PDBTitle: cryo-em structure of the exocyst complex
37	d1h9ma2	Alignment	not modelled	62.6	28	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
38	c1ei3E_	Alignment	not modelled	60.0	8	PDB header: blood clotting Chain: E: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
39	c5x5bB_	Alignment	not modelled	57.9	15	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
40	d1h9ra2	Alignment	not modelled	57.2	23	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
41	c2qihA_	Alignment	not modelled	56.5	10	PDB header: cell adhesion Chain: A: PDB Molecule: protein uspa1; PDBTitle: crystal structure of 527-665 fragment of uspa1 protein from moraxella2 catarrhalis
42	c4lwsB_	Alignment	not modelled	56.2	8	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
43	d1h9ma1	Alignment	not modelled	56.0	13	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
44	c4nl6C_	Alignment	not modelled	55.3	13	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
45	c6grjG_	Alignment	not modelled	54.1	16	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.
46	c5i08A_	Alignment	not modelled	53.5	19	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
47	d1wa8a1	Alignment	not modelled	52.9	10	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
48	c1cz5A_	Alignment	not modelled	51.9	17	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)
49	c1bf5A_	Alignment	not modelled	51.5	10	PDB header: gene regulation/dna Chain: A: PDB Molecule: signal transducer and activator of transcription 1- PDBTitle: tyrosine phosphorylated stat-1/dna complex
50	c3gvmA_	Alignment	not modelled	51.1	17	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
51	c1ei3C_	Alignment	not modelled	51.0	10	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
52	c5zhyA_	Alignment	not modelled	50.0	17	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
53	c5xbjA_	Alignment	not modelled	50.0	8	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
54	c5wrgB_	Alignment	not modelled	48.6	17	PDB header: virus like particle Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: sars-cov spike glycoprotein
55	c4lwsA_	Alignment	not modelled	46.7	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein;

55	c4wvA	Alignment	not modelled	46.7	10	PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata PDB header: structural protein
56	c3a0mF	Alignment	not modelled	46.3	17	Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
57	c3euhB	Alignment	not modelled	46.1	13	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of the muke-mukf complex
58	c1zvaA	Alignment	not modelled	45.9	13	PDB header: viral protein Chain: A: PDB Molecule: e2 glycoprotein; PDBTitle: a structure-based mechanism of sars virus membrane fusion
59	c5dmaA	Alignment	not modelled	45.7	13	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna helicase pcra; PDBTitle: crystal structure of c-terminal tudor domain in pcra/uvrd helicase
60	c5xlrC	Alignment	not modelled	45.2	15	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
61	c3zbhC	Alignment	not modelled	44.6	12	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
62	d1guta	Alignment	not modelled	44.4	12	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
63	c4e40A	Alignment	not modelled	44.0	11	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: the haptoglobin-hemoglobin receptor of trypanosoma congolense
64	c3ghgI	Alignment	not modelled	44.0	9	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
65	c5n76C	Alignment	not modelled	43.1	23	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	d1ykhb1	Alignment	not modelled	42.7	10	Fold: Mediator hinge subcomplex-like Superfamily: Mediator hinge subcomplex-like Family: CSE2-like
67	c4wsrA	Alignment	not modelled	40.9	10	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: the crystal structure of hemagglutinin form a/chicken/new york/14677-2 13/1998
68	c2p22A	Alignment	not modelled	39.2	14	PDB header: transport protein Chain: A: PDB Molecule: suppressor protein stp22 of temperature-sensitive alpha- PDBTitle: structure of the yeast esct-i heterotetramer core
69	c1m1jA	Alignment	not modelled	37.6	9	PDB header: blood clotting Chain: A: PDB Molecule: fibrinogen alpha subunit; PDBTitle: crystal structure of native chicken fibrinogen with two different2 bound ligands
70	c2yfaA	Alignment	not modelled	36.6	13	PDB header: receptor Chain: A: PDB Molecule: methyl-accepting chemotaxis transducer; PDBTitle: x-ray structure of mcps ligand binding domain in complex with malate
71	c2vs0B	Alignment	not modelled	36.6	11	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
72	c3fseB	Alignment	not modelled	36.0	16	PDB header: hydrolase Chain: B: PDB Molecule: two-domain protein containing dj-1/thij/pfpi-like and PDBTitle: crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anaerobaculum variabilis3 atcc 29413 at 1.90 a resolution
73	d1fr3a	Alignment	not modelled	35.5	10	Fold: OB-fold Superfamily: MOP-like Family: Molybdate/tungstate binding protein MOP
74	c3j99M	Alignment	not modelled	34.4	7	PDB header: hydrolase Chain: M: PDB Molecule: synaptosomal-associated protein 25; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state iib)
75	c1h9mB	Alignment	not modelled	34.1	15	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
76	c1deqO	Alignment	not modelled	34.0	9	PDB header: blood clotting Chain: O: PDB Molecule: fibrinogen (beta chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
77	c6gaoC	Alignment	not modelled	33.9	12	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
78	c4iogD	Alignment	not modelled	33.8	8	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
79	c3qr8A	Alignment	not modelled	33.7	25	PDB header: viral protein Chain: A: PDB Molecule: baseplate assembly protein v; PDBTitle: crystal structure of the bacteriophage p2 membrane-piercing protein2 gpv
80	c6cs2A	Alignment	not modelled	32.9	13	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
81	c1t98B	Alignment	not modelled	32.5	20	PDB header: cell cycle Chain: B: PDB Molecule: chromosome partition protein mukf; PDBTitle: crystal structure of mukf(1-287)
82	c2qf4A	Alignment	not modelled	31.9	9	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)
83	c3ok8A	Alignment	not modelled	31.9	9	PDB header: protein binding Chain: A: PDB Molecule: brain-specific angiogenesis inhibitor 1-associated protein PDBTitle: i-bar of pinkbar
84	c1h9sA	Alignment	not modelled	31.3	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
85	c4abxB	Alignment	not modelled	31.2	15	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein recn; PDBTitle: crystal structure of deinococcus radiodurans recn coiled-2 coil domain
86	d1h9ra1	Alignment	not modelled	30.6	15	Fold: OB-fold Superfamily: MOP-like Family: BiMOP, duplicated molybdate-binding domain
87	c6gapB	Alignment	not modelled	30.4	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
88	c2d3hC	Alignment	not modelled	30.0	35	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
89	c3a19A	Alignment	not modelled	30.0	35	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
90	c5dfzA	Alignment	not modelled	29.7	11	PDB header: transferase Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 38; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
91	c5tgyA	Alignment	not modelled	28.5	17	PDB header: unknown function Chain: A: PDB Molecule: ps1; PDBTitle: nmr structure of holo-ps1
92	c3ur1C	Alignment	not modelled	28.0	5	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.
93	c4s37F	Alignment	not modelled	27.8	15	PDB header: metal binding protein Chain: F: PDB Molecule: phage baseplate protein; PDBTitle: crystal structure of r2 pyocin membrane-piercing spike
94	c1x1kF	Alignment	not modelled	27.6	46	PDB header: structural protein Chain: F: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
95	c4nj1A	Alignment	not modelled	27.4	13	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
96	d2cu6a1	Alignment	not modelled	26.8	18	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: PaaD-like
97	c2cuoF	Alignment	not modelled	26.7	23	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
98	c2cuoC	Alignment	not modelled	26.7	23	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
99	c4h8sA	Alignment	not modelled	26.1	7	PDB header: signaling protein Chain: A: PDB Molecule: dcc-interacting protein 13-beta; PDBTitle: crystal structure of human app12barph domain
100	c1bg1A	Alignment	not modelled	25.9	10	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
101	c3a19E	Alignment	not modelled	25.7	35	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
102	c3a19C	Alignment	not modelled	25.7	35	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
103	c2cuoE	Alignment	not modelled	25.2	19	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
104	c2cuoA	Alignment	not modelled	25.2	19	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
105	c2cuoD	Alignment	not modelled	25.2	19	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
						PDB header: structural protein

106	c2cuoB_	Alignment	not modelled	25.2	19	Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
107	c3ah9C_	Alignment	not modelled	25.1	19	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
108	c3ah9E_	Alignment	not modelled	25.1	19	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
109	c3ah9B_	Alignment	not modelled	25.1	19	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
110	d1v5va1	Alignment	not modelled	25.0	21	Fold: Elongation factor/aminomethyltransferase common domain Superfamily: Aminomethyltransferase beta-barrel domain Family: Aminomethyltransferase beta-barrel domain
111	c5mg8B_	Alignment	not modelled	24.8	8	PDB header: recombination Chain: B: PDB Molecule: structural maintenance of chromosomes protein 6; PDBTitle: crystal structure of the s.pombe smc5/6 hinge domain
112	c3a35B_	Alignment	not modelled	24.5	16	PDB header: luminescent protein Chain: B: PDB Molecule: lumazine protein; PDBTitle: crystal structure of lump complexed with riboflavin
113	c3ah9A_	Alignment	not modelled	24.3	20	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
114	c6dlcA_	Alignment	not modelled	23.9	21	PDB header: de novo protein Chain: A: PDB Molecule: designed protein dhd1:234_a; PDBTitle: designed protein dhd1:234_a, designed protein dhd1:234_b
115	d2vv5a1	Alignment	not modelled	23.5	26	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Mechanosensitive channel protein MscS (YggB), middle domain
116	c2d3hB_	Alignment	not modelled	23.5	36	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
117	c3a19B_	Alignment	not modelled	23.5	36	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
118	c2d3hA_	Alignment	not modelled	23.5	36	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
119	c4g2kB_	Alignment	not modelled	23.4	15	PDB header: viral protein Chain: B: PDB Molecule: general control protein gcn4, envelope glycoprotein gp2 PDBTitle: crystal structure of the marburg virus gp2 ectodomain in its post-2 fusion conformation
120	c2d3hE_	Alignment	not modelled	22.7	36	PDB header: structural protein Chain: E: 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