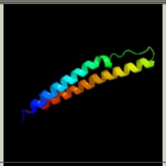
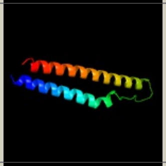
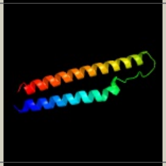
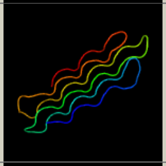
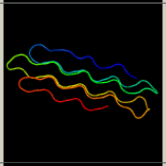
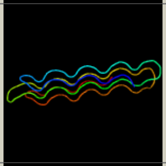
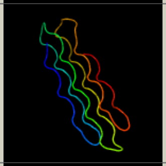
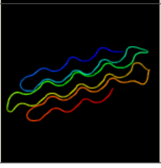
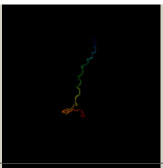
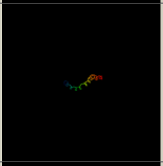
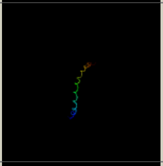
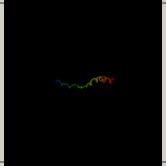
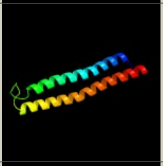
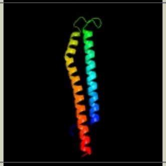
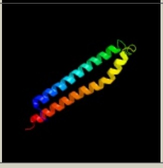
Phyre^2

Email	mdejesus@rockefeller.edu
Description	RVBD3595c_(PE_PGRS59)_4036910_4038229
Date	Fri Aug 9 18:20:28 BST 2019
Unique Job ID	3f0bd93074d02f3c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	Alignment		100.0	49	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**pe family protein pe8; **PDBTitle:** crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
2	c2g38A_	Alignment		100.0	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pe family protein; **PDBTitle:** a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38a1	Alignment		100.0	31	**Fold:**Ferritin-like **Superfamily:**PE/PPE dimer-like **Family:**PE
4	c3hqvB_	Alignment		99.5	42	**PDB header:**structural protein, contractile protein **Chain:** B: **PDB Molecule:**collagen alpha-2(i) chain; **PDBTitle:** low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
5	c1ygvA_	Alignment		99.5	32	**PDB header:**structural protein/contractile protein **Chain:** A: **PDB Molecule:**collagen i alpha 1; **PDBTitle:** the structure of collagen type i. single type i collagen2 molecule: rigid refinment
6	c1y0fB_	Alignment		99.5	31	**PDB header:**structural protein/contractile protein **Chain:** B: **PDB Molecule:**collagen i alpha 2; **PDBTitle:** the structure of collagen type i. single type i collagen2 molecule
7	c3bogB_	Alignment		98.0	40	**PDB header:**antifreeze protein **Chain:** B: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** snow flea antifreeze protein quasi-racemate
8	c3bogA_	Alignment		98.0	40	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** snow flea antifreeze protein quasi-racemate
9	c2pneA_	Alignment		97.9	40	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** crystal structure of the snow flea antifreeze protein
10	c3boiB_	Alignment		97.9	40	**PDB header:**antifreeze protein **Chain:** B: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** snow flea antifreeze protein racemate
11	c3boiA_	Alignment		97.9	40	**PDB header:**antifreeze protein **Chain:** A: **PDB Molecule:**6.5 kda glycine-rich antifreeze protein; **PDBTitle:** snow flea antifreeze protein racemate

12	c1nayC_	Alignment		94.8	34	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen-like peptide; **PDBTitle:** gpp-foldon:x-ray structure
13	c5ctdB_	Alignment		94.1	33	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen alpha-2(i) chain,collagen alpha-2(ix) chain; **PDBTitle:** crystal structure of the type ix collagen nc2 hetero-trimerization2 domain with a guest fragment a2a1a1 of type i collagen
14	c5ctiC_	Alignment		93.7	35	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen alpha-1(i) chain,collagen alpha-3(ix) chain; **PDBTitle:** crystal structure of the type ix collagen nc2 hetero-trimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
15	c5ctdA_	Alignment		93.5	37	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen alpha-1(i) chain,collagen alpha-1(ix) chain; **PDBTitle:** crystal structure of the type ix collagen nc2 hetero-trimerization2 domain with a guest fragment a2a1a1 of type i collagen
16	c4iogD_	Alignment		92.0	16	**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
17	c4wj2A_	Alignment		91.9	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**antigen mtb48; **PDBTitle:** mycobacterial protein
18	c3gvmA_	Alignment		91.0	15	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
19	d1wa8a1	Alignment		90.3	10	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
20	c2vs0B_	Alignment		87.0	17	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
21	c3zbhC_	Alignment	not modelled	86.7	17	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**esxa; **PDBTitle:** geobacillus thermodenitrificans esxa crystal form i
22	c2kg7B_	Alignment	not modelled	80.5	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**esat-6-like protein esxh; **PDBTitle:** structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
23	c2klwA_	Alignment	not modelled	79.4	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**(pkg)10; **PDBTitle:** solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions
24	c2cuoC_	Alignment	not modelled	76.4	52	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
25	c2cuoF_	Alignment	not modelled	76.4	52	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
26	c4lwsA_	Alignment	not modelled	75.8	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
27	c1k6fA_	Alignment	not modelled	75.3	48	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen triple helix; **PDBTitle:** crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
28	c1k6fB_	Alignment	not modelled	75.3	48	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen triple helix; **PDBTitle:** crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
						PDB header:structural protein

29	c1k6fC_	Alignment	not modelled	75.3	48	**Chain:** C: **PDB Molecule:**collagen triple helix; **PDBTitle:** crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
30	c1k6fF_	Alignment	not modelled	75.3	48	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen triple helix; **PDBTitle:** crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
31	c1k6fD_	Alignment	not modelled	75.3	48	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**collagen triple helix; **PDBTitle:** crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
32	c1k6fE_	Alignment	not modelled	75.3	48	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**collagen triple helix; **PDBTitle:** crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
33	c3ah9F_	Alignment	not modelled	70.3	54	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)9 at 1.1 a resolution
34	c3ah9D_	Alignment	not modelled	69.6	59	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)9 at 1.1 a resolution
35	c3ah9C_	Alignment	not modelled	67.7	54	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)9 at 1.1 a resolution
36	c3ah9E_	Alignment	not modelled	67.7	54	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)9 at 1.1 a resolution
37	c3ah9B_	Alignment	not modelled	67.7	54	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)9 at 1.1 a resolution
38	c3ah9A_	Alignment	not modelled	67.3	57	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)9 at 1.1 a resolution
39	c2cuoE_	Alignment	not modelled	64.0	50	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
40	c2cuoB_	Alignment	not modelled	64.0	50	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
41	c2cuoD_	Alignment	not modelled	64.0	50	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
42	c2cuoA_	Alignment	not modelled	64.0	50	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen model peptide (pro-pro-gly)9; **PDBTitle:** collagen model peptide (pro-pro-gly)9
43	c3a0mF_	Alignment	not modelled	63.4	54	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen-like peptide; **PDBTitle:** structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
44	c6nb3B_	Alignment	not modelled	61.7	19	**PDB header:**virus **Chain:** B: **PDB Molecule:**spike glycoprotein; **PDBTitle:** mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
45	c5x5fC_	Alignment	not modelled	58.1	19	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**s protein; **PDBTitle:** prefusion structure of mers-cov spike glycoprotein, conformation 2
46	c5xfsB_	Alignment	not modelled	56.5	24	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**ppe family protein ppe15; **PDBTitle:** crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
47	c4lwsB_	Alignment	not modelled	41.8	12	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
48	c3a0aE_	Alignment	not modelled	38.1	62	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**collagen-like peptide; **PDBTitle:** structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
49	c3a0aA_	Alignment	not modelled	33.1	62	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen-like peptide; **PDBTitle:** structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
50	c4rglA_	Alignment	not modelled	32.4	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**filamentation induced by camp protein fic; **PDBTitle:** crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution
51	d1lghb_	Alignment	not modelled	28.8	39	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
52	c3admC_	Alignment	not modelled	27.4	50	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
53	d1wa8b1	Alignment	not modelled	27.4	16	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
54	c5x5bB_	Alignment	not modelled	27.3	19	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**spike glycoprotein; **PDBTitle:** prefusion structure of sars-cov spike glycoprotein, conformation 2
55	c2d3fB_	Alignment	not modelled	27.1	57	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-

						gly)2 4-pro-hyp-gly-(pro-pro-gly)4
56	c2d3fC_	Alignment	not modelled	27.1	57	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
57	c1x1kE_	Alignment	not modelled	27.1	57	**PDB header:**structural protein **Chain:** E: **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
58	c2d3fA_	Alignment	not modelled	27.1	57	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
59	d1f0la3	Alignment	not modelled	26.4	28	**Fold:**Toxins' membrane translocation domains **Superfamily:**Diphtheria toxin, middle domain **Family:**Diphtheria toxin, middle domain
60	c1x1kB_	Alignment	not modelled	25.4	57	**PDB header:**structural protein **Chain:** B: **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
61	c1x1kC_	Alignment	not modelled	25.4	57	**PDB header:**structural protein **Chain:** C: **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
62	c1x1kD_	Alignment	not modelled	25.4	57	**PDB header:**structural protein **Chain:** D: **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
63	c2d3fD_	Alignment	not modelled	25.4	57	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
64	c2d3fF_	Alignment	not modelled	25.4	57	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
65	c2d3fE_	Alignment	not modelled	25.4	57	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**collagen model peptides (pro-pro-gly)4-pro-hyp- **PDBTitle:** crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
66	c1x1kA_	Alignment	not modelled	25.4	57	**PDB header:**structural protein **Chain:** A: **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
67	c6cs2A_	Alignment	not modelled	25.0	19	**PDB header:**viral protein/hydrolase **Chain:** A: **PDB Molecule:**spike glycoprotein,fibritin; **PDBTitle:** sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
68	c3s90D_	Alignment	not modelled	23.7	42	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**talin-1; **PDBTitle:** human vinculin head domain vh1 (residues 1-252) in complex with murine2 talin (vbs33; residues 1512-1546)
69	c3admB_	Alignment	not modelled	23.3	50	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
70	c3admF_	Alignment	not modelled	23.3	50	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
71	c3admA_	Alignment	not modelled	23.3	50	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
72	c3admE_	Alignment	not modelled	23.3	50	**PDB header:**structural protein **Chain:** E: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
73	c3nzzA_	Alignment	not modelled	22.9	34	**PDB header:**cell invasion **Chain:** A: **PDB Molecule:**cell invasion protein sipd; **PDBTitle:** crystal structure of the salmonella type iii secretion system tip2 protein sipd
74	c1wrgA_	Alignment	not modelled	21.7	30	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**light-harvesting protein b-880, beta chain; **PDBTitle:** light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
75	c6et5u_	Alignment	not modelled	21.3	22	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**light-harvesting protein b-1015 gamma chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
76	c5szsC_	Alignment	not modelled	19.9	17	**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
77	c2w0cR_	Alignment	not modelled	19.9	28	**PDB header:**virus **Chain:** R: **PDB Molecule:**protein p3; **PDBTitle:** x-ray structure of the entire lipid-containing bacteriophage pm2
78	c3abnA_	Alignment	not modelled	19.5	46	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a

79	c2c9kA_	Alignment	not modelled	19.4	19	**PDB header:**toxin **Chain:** A: **PDB Molecule:**pesticidal crystal protein cry4aa; **PDBTitle:** structure of the functional form of the mosquito-larvicidal2 cry4aa toxin from bacillus thuringiensis at 2.8 a3 resolution
80	c6cv0C_	Alignment	not modelled	18.8	18	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**spike glycoprotein; **PDBTitle:** cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
81	c3a08D_	Alignment	not modelled	18.4	43	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**collagen-like peptide; **PDBTitle:** structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
82	c3a19F_	Alignment	not modelled	18.4	43	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen-like peptide; **PDBTitle:** structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
83	c2d3hD_	Alignment	not modelled	18.4	43	**PDB header:**structural protein **Chain:** D: **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
84	d2g38b1	Alignment	not modelled	18.3	19	**Fold:**Ferritin-like **Superfamily:**PE/PPE dimer-like **Family:**PPE
85	c2g38B_	Alignment	not modelled	18.3	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ppe family protein; **PDBTitle:** a pe/ppe protein complex from mycobacterium tuberculosis
86	c3a19D_	Alignment	not modelled	17.5	42	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**collagen-like peptide; **PDBTitle:** structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
87	d1yaro1	Alignment	not modelled	17.3	19	**Fold:**Four-helical up-and-down bundle **Superfamily:**Proteasome activator **Family:**Proteasome activator
88	c3onjA_	Alignment	not modelled	16.6	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**t-snare vti1; **PDBTitle:** crystal structure of yeast vti1p_habc domain
89	c3a0aF_	Alignment	not modelled	16.6	63	**PDB header:**structural protein **Chain:** F: **PDB Molecule:**collagen-like peptide; **PDBTitle:** structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
90	c3a0aC_	Alignment	not modelled	15.8	57	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen-like peptide; **PDBTitle:** structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
91	c3a0mC_	Alignment	not modelled	14.5	48	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**collagen-like peptide; **PDBTitle:** structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
92	d1mbsa_	Alignment	not modelled	13.7	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
93	c1x1kF_	Alignment	not modelled	13.4	41	**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
94	c5xlrC_	Alignment	not modelled	13.2	19	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**spike glycoprotein; **PDBTitle:** structure of sars-cov spike glycoprotein
95	c3abnB_	Alignment	not modelled	12.9	55	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
96	c5i08A_	Alignment	not modelled	12.6	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**spike glycoprotein, envelope glycoprotein chimera; **PDBTitle:** prefusion structure of a human coronavirus spike protein
97	c3admD_	Alignment	not modelled	12.5	52	**PDB header:**structural protein **Chain:** D: **PDB Molecule:**collagen-like peptide; **PDBTitle:** crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
98	c3u8pB_	Alignment	not modelled	12.5	15	**PDB header:**fluorescent protein, electron transport **Chain:** B: **PDB Molecule:**cytochrome b562 integral fusion with enhanced green **PDBTitle:** cytochrome b562 integral fusion with egfp
99	c6nzkB_	Alignment	not modelled	12.3	14	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**spike surface glycoprotein; **PDBTitle:** structural basis for human coronavirus attachment to sialic acid2 receptors