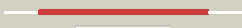
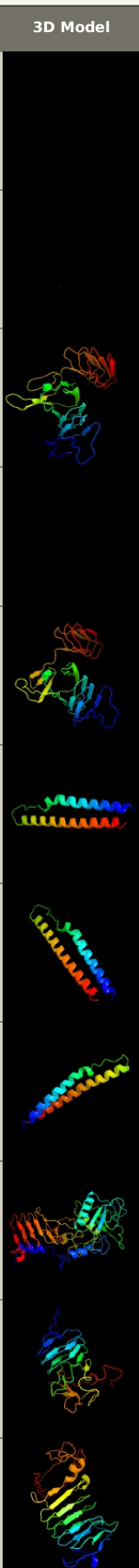




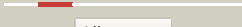
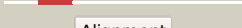
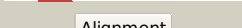
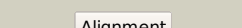
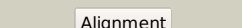
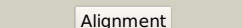
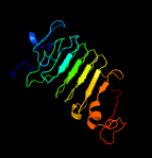

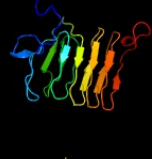
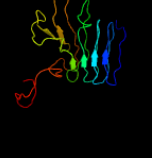
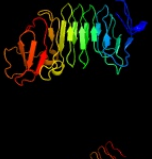
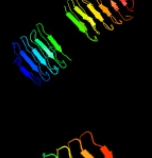

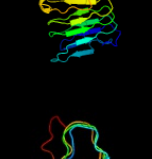
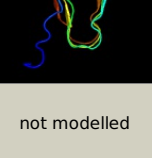


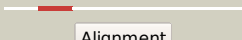



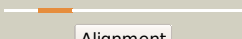
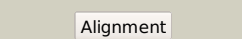
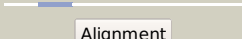
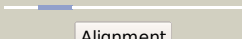


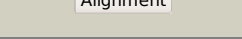
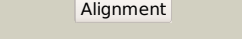
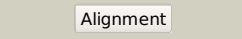
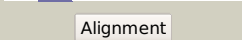
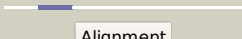
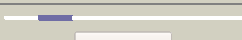


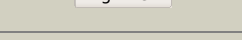
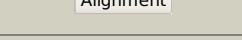
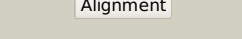
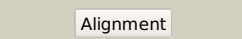

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3507_(PE_PGR553)_3926748_3930893
Date	Fri Aug 9 18:20:18 BST 2019
Unique Job ID	caab75955f65a044

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ygvA_	 Alignment		100.0	26	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 refinement
2	c1y0fB_	 Alignment		99.9	27	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
3	c2qubG_	 Alignment		99.8	17	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
4	c3hqvB_	 Alignment		99.8	25	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	c2zj6A_	 Alignment		99.8	23	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
6	d2g38a1	 Alignment		99.8	36	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
7	c2g38A_	 Alignment		99.8	36	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
8	c5xfsA_	 Alignment		99.8	46	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
9	c1k7qA_	 Alignment		99.7	16	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtcc from erwinia chrysanthemi: e189a mutant
10	c2ml3A_	 Alignment		99.5	15	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
11	c1satA_	 Alignment		99.5	20	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens

12	d1sata1	Alignment		99.5	16	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
13	d1g9ka1	Alignment		99.3	21	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
14	d1kapp1	Alignment		99.3	29	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
15	c2agmA_	Alignment		99.2	18	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
16	c1om8A_	Alignment		99.1	21	PDB header: hydrolase Chain: A: PDB Molecule: serralysin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
17	c3p4gD_	Alignment		99.1	17	PDB header: antifreeze protein Chain: D: PDB Molecule: antifreeze protein; PDBTitle: x-ray crystal structure of a hyperactive, ca2+-dependent, beta-helical2 antifreeze protein from an antarctic bacterium
18	d1k7ia1	Alignment		98.9	18	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
19	c1jiwP_	Alignment		98.8	21	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
20	c2ml2A_	Alignment		98.7	24	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r2 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
21	c4q1qA_	Alignment	not modelled	98.6	22	PDB header: cell adhesion Chain: A: PDB Molecule: adhesin/invasin tiba autotransporter; PDBTitle: crystal structure of tibi-catalyzed hyper-glycosylated tiba55-3502 fragment
22	c5cxIA_	Alignment	not modelled	98.1	26	PDB header: toxin Chain: A: PDB Molecule: bifunctional hemolysin/adenylate cyclase; PDBTitle: crystal structure of rtx domain block v of adenylate cyclase toxin2 from bordetella pertussis
23	c3bogB_	Alignment	not modelled	98.0	37	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
24	c3bogA_	Alignment	not modelled	98.0	37	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
25	c2pneA_	Alignment	not modelled	97.6	39	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
26	c3boiB_	Alignment	not modelled	97.6	39	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
27	c3boiA_	Alignment	not modelled	97.6	39	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
28	c1nayC_	Alignment	not modelled	95.8	21	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
29	c5juhA_	Alignment	not modelled	94.8	22	PDB header: cell adhesion Chain: A: PDB Molecule: antifreeze protein;

						PDBTitle: crystal structure of c-terminal domain (rv) of mpafp
30	c5ctdB	 Alignment	not modelled	94.5	30	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 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
31	c5ctdA	 Alignment	not modelled	94.5	31	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 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
32	c5ctiC	 Alignment	not modelled	94.4	38	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 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
33	c2mu3A	 Alignment	not modelled	89.7	22	PDB header: structural protein Chain: A: PDB Molecule: aciniform spidroin 1; PDBTitle: spider wrapping silk fibre architecture arising from its modular2 soluble protein precursor
34	c2klwA	 Alignment	not modelled	83.2	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
35	c3a19D	 Alignment	not modelled	34.7	40	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
36	c2cuoC	 Alignment	not modelled	22.3	37	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
37	c2cuoF	 Alignment	not modelled	22.3	37	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
38	c2d3hC	 Alignment	not modelled	20.6	39	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
39	c3a19A	 Alignment	not modelled	20.6	39	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
40	c1k6fC	 Alignment	not modelled	19.7	34	PDB header: structural protein Chain: C: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
41	c1k6fB	 Alignment	not modelled	19.7	34	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
42	c1k6fD	 Alignment	not modelled	19.7	34	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
43	c1k6fF	 Alignment	not modelled	19.7	34	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
44	c1k6fE	 Alignment	not modelled	19.7	34	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
45	c1k6fA	 Alignment	not modelled	19.7	34	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
46	c3a0mF	 Alignment	not modelled	18.7	35	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
47	c3ah9F	 Alignment	not modelled	17.1	33	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
48	c3a19B	 Alignment	not modelled	16.7	41	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
49	c2d3hB	 Alignment	not modelled	16.7	41	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
50	c2d3hA	 Alignment	not modelled	16.7	41	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
51	c3a19C	 Alignment	not modelled	16.3	38	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
52	c3a19E	 Alignment	not modelled	16.3	38	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
						PDB header: structural protein

53	c3a08D	Alignment	not modelled	16.2	38	Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
54	c3a19F	Alignment	not modelled	16.2	38	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
55	c2d3hD	Alignment	not modelled	16.2	38	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
56	c3ah9D	Alignment	not modelled	16.1	36	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
57	c2d3hE	Alignment	not modelled	16.0	39	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
58	c3ah9A	Alignment	not modelled	15.0	33	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
59	c3ah9C	Alignment	not modelled	12.1	35	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
60	c3ah9E	Alignment	not modelled	12.1	35	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
61	c3ah9B	Alignment	not modelled	12.1	35	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
62	c2cuoE	Alignment	not modelled	10.4	35	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
63	c2cuoB	Alignment	not modelled	10.4	35	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
64	c2cuoA	Alignment	not modelled	10.4	35	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
65	c2cuoD	Alignment	not modelled	10.4	35	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
66	c2d3fE	Alignment	not modelled	8.7	42	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
67	c1x1kA	Alignment	not modelled	8.7	42	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
68	c1x1kD	Alignment	not modelled	8.7	42	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
69	c2d3fF	Alignment	not modelled	8.7	42	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
70	c1x1kB	Alignment	not modelled	8.7	42	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
71	c1x1kC	Alignment	not modelled	8.7	42	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
72	c2d3fD	Alignment	not modelled	8.7	42	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
73	c3abnA	Alignment	not modelled	8.6	40	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
74	c3admC	Alignment	not modelled	8.5	40	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
75	c3admA	Alignment	not modelled	8.5	40	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
76	c3admF	Alignment	not modelled	8.5	40	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
77	c3admB	Alignment	not modelled	8.5	40	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide;

77	c3a0mB_	Alignment	not modelled	8.5	40	PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4 PDB header: structural protein
78	c3admE_	Alignment	not modelled	8.5	40	Chain: E; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
79	c3a08C_	Alignment	not modelled	8.2	38	PDB header: structural protein Chain: C; PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
80	c2lyiA_	Alignment	not modelled	8.0	21	PDB header: structural protein Chain: A; PDB Molecule: protein (entity); PDBTitle: repetitive domain (rp) of aciniform spidroin 1 from nephila2 antipodiana
81	c3a08F_	Alignment	not modelled	7.4	36	PDB header: structural protein Chain: F; PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
82	c2d3hF_	Alignment	not modelled	7.2	35	PDB header: structural protein Chain: F; 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
83	c3a08E_	Alignment	not modelled	7.0	36	PDB header: structural protein Chain: E; PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
84	c3a08B_	Alignment	not modelled	6.9	38	PDB header: structural protein Chain: B; PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
85	c3a08A_	Alignment	not modelled	6.9	38	PDB header: structural protein Chain: A; PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
86	c3a0mC_	Alignment	not modelled	6.5	40	PDB header: structural protein Chain: C; PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
87	c6gwxA_	Alignment	not modelled	5.9	32	PDB header: structural protein Chain: A; PDB Molecule: optimised ppa-tyr; PDBTitle: stabilising and understanding a miniprotein by rational design.
88	c6bjcT_	Alignment	not modelled	5.5	50	PDB header: cell cycle Chain: T; PDB Molecule: targeting protein for xklp2; PDBTitle: tpx2_mini decorated gmppcp-microtubule
89	c6bjcP_	Alignment	not modelled	5.5	50	PDB header: cell cycle Chain: P; PDB Molecule: targeting protein for xklp2; PDBTitle: tpx2_mini decorated gmppcp-microtubule
90	c3a1hA_	Alignment	not modelled	5.5	45	PDB header: structural protein Chain: A; PDB Molecule: collagen-like peptide; PDBTitle: crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
91	c3a0aA_	Alignment	not modelled	5.5	45	PDB header: structural protein Chain: A; PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
92	c3a0mE_	Alignment	not modelled	5.2	39	PDB header: structural protein Chain: E; PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
93	c1x1kF_	Alignment	not modelled	5.1	33	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