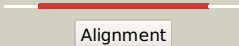
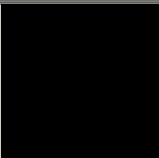

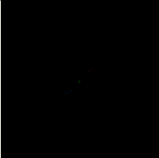
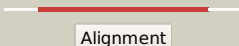

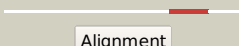
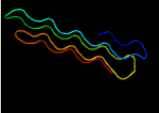
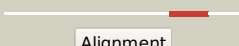

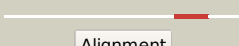

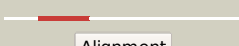

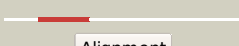


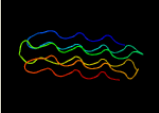

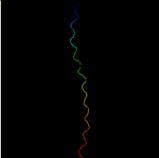

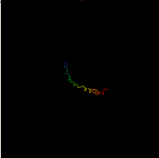

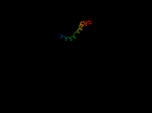
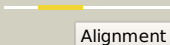
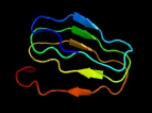
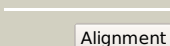
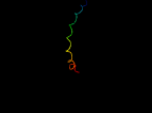



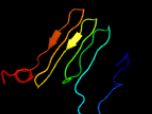
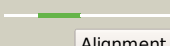
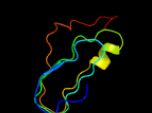
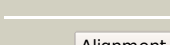

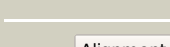
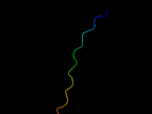
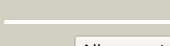
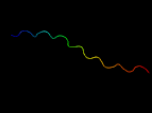
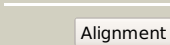

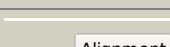
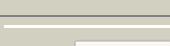

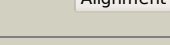
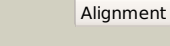

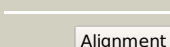


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3344c\_(PE\_PGRS49)\_3737155\_3738171  
 Date Thu Aug 8 16:20:55 BST 2019  
 Unique Job ID fcd258018eaf1748

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3hqvB_</a>	 Alignment		99.2	28	<b>PDB header:</b> structural protein, contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-2(i) chain; <b>PDBTitle:</b> low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
2	<a href="#">c1ygvA_</a>	 Alignment		98.7	26	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen i alpha 1; <b>PDBTitle:</b> the structure of collagen type i. single type i collagen2 molecule: rigid refinement
3	<a href="#">c1y0fB_</a>	 Alignment		98.4	27	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen i alpha 2; <b>PDBTitle:</b> the structure of collagen type i. single type i collagen2 molecule
4	<a href="#">c3bogB_</a>	 Alignment		97.7	33	<b>PDB header:</b> antifreeze protein <b>Chain:</b> B: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein quasi-racemate
5	<a href="#">c3bogA_</a>	 Alignment		97.7	33	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein quasi-racemate
6	<a href="#">c1nayC_</a>	 Alignment		96.6	36	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> gpp-foldon:x-ray structure
7	<a href="#">c2pneA_</a>	 Alignment		96.4	30	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> crystal structure of the snow flea antifreeze protein
8	<a href="#">c3boiA_</a>	 Alignment		96.4	30	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein racemate
9	<a href="#">c3boiB_</a>	 Alignment		96.4	30	<b>PDB header:</b> antifreeze protein <b>Chain:</b> B: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein racemate
10	<a href="#">c5ctiC_</a>	 Alignment		96.2	29	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen alpha-1(i) chain, collagen alpha-3(ix) chain; <b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
11	<a href="#">c5ctdA_</a>	 Alignment		96.1	25	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(i) chain, collagen alpha-1(ix) chain; <b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen

12	<a href="#">c5ctdB_</a>	 Alignment		96.0	28	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-2(i) chain, collagen alpha-2(ix) chain; <b>PDBTitle:</b> crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
13	<a href="#">c2ml2A_</a>	 Alignment		77.6	30	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 6; <b>PDBTitle:</b> solution structure of alge6r2 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
14	<a href="#">c2klwA_</a>	 Alignment		74.1	32	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> (pkg)10; <b>PDBTitle:</b> solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions
15	<a href="#">c2ml3A_</a>	 Alignment		68.3	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 6; <b>PDBTitle:</b> solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
16	<a href="#">c1k7qA_</a>	 Alignment		58.6	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted protease c; <b>PDBTitle:</b> prtC from erwinia chrysanthemi: e189a mutant
17	<a href="#">c2agmA_</a>	 Alignment		51.0	26	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 4; <b>PDBTitle:</b> solution structure of the r-module from alge4
18	<a href="#">c2cuoC_</a>	 Alignment		39.0	30	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
19	<a href="#">c2cuoF_</a>	 Alignment		39.0	30	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
20	<a href="#">c2cuoA_</a>	 Alignment		36.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
21	<a href="#">c2cuoB_</a>	 Alignment	not modelled	36.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
22	<a href="#">c2cuoD_</a>	 Alignment	not modelled	36.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
23	<a href="#">c2cuoE_</a>	 Alignment	not modelled	36.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
24	<a href="#">c3ah9D_</a>	 Alignment	not modelled	33.3	30	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
25	<a href="#">c1k6fE_</a>	 Alignment	not modelled	32.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
26	<a href="#">c1k6fA_</a>	 Alignment	not modelled	32.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
27	<a href="#">c1k6fD_</a>	 Alignment	not modelled	32.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
28	<a href="#">c1k6fF_</a>	 Alignment	not modelled	32.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
		 Alignment				<b>PDB header:</b> structural protein

29	<a href="#">c1k6fC_</a>	Alignment	not modelled	32.2	31	<b>Chain:</b> C: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
30	<a href="#">c1k6fB_</a>	Alignment	not modelled	32.2	31	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
31	<a href="#">d1k7ia1</a>	Alignment	not modelled	30.5	25	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
32	<a href="#">c3ah9F_</a>	Alignment	not modelled	29.8	28	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
33	<a href="#">c3ah9A_</a>	Alignment	not modelled	26.2	30	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
34	<a href="#">c3ah9B_</a>	Alignment	not modelled	21.3	29	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
35	<a href="#">c3ah9E_</a>	Alignment	not modelled	21.3	29	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
36	<a href="#">c3ah9C_</a>	Alignment	not modelled	21.3	29	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
37	<a href="#">d1kapp1</a>	Alignment	not modelled	21.1	28	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
38	<a href="#">c3a0mF_</a>	Alignment	not modelled	13.8	33	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
39	<a href="#">c1jiwP_</a>	Alignment	not modelled	13.4	20	<b>PDB header:</b> hydrolase/hyrolase inhibitor <b>Chain:</b> P: <b>PDB Molecule:</b> alkaline metalloproteinase; <b>PDBTitle:</b> crystal structure of the apr-aprin complex
40	<a href="#">c1om8A_</a>	Alignment	not modelled	12.5	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serralysin; <b>PDBTitle:</b> crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
41	<a href="#">c1satA_</a>	Alignment	not modelled	10.0	28	<b>PDB header:</b> hydrolase (serine protease) <b>Chain:</b> A: <b>PDB Molecule:</b> serratia protease; <b>PDBTitle:</b> crystal structure of the 50 kda metallo protease from s.2 marcescens
42	<a href="#">c5cx1A_</a>	Alignment	not modelled	8.0	25	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional hemolysin/adenylate cyclase; <b>PDBTitle:</b> crystal structure of rtx domain block v of adenylate cyclase toxin2 from bordetella pertussis