
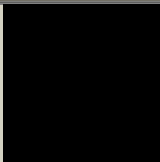

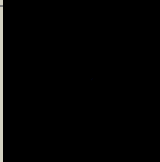

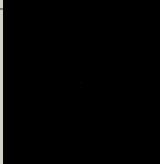

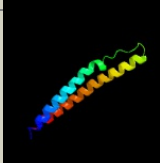

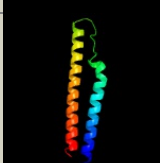

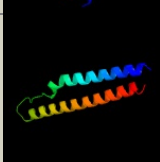

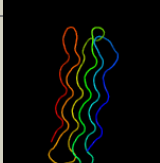

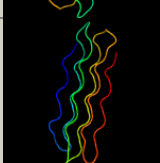

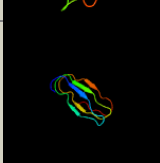

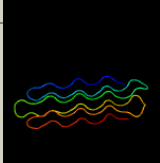

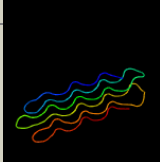



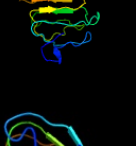
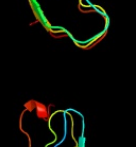
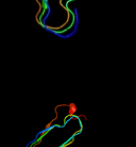
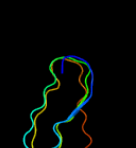

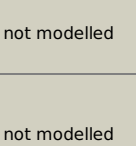


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1452c_(PE_PGRS28)_1636010_1638235
Date	Fri Aug 2 13:30:03 BST 2019
Unique Job ID	1f85e7450bbd0c24

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ygvA_</a>	 Alignment		99.9	32	<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
2	<a href="#">c3hqvB_</a>	 Alignment		99.9	22	<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
3	<a href="#">c1y0fB_</a>	 Alignment		99.8	25	<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="#">c5xfA_</a>	 Alignment		99.8	40	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein pe8; <b>PDBTitle:</b> crystal structure of pe8-ppp15 in complex with esp95 from m.2 tuberculosis
5	<a href="#">c2g38A_</a>	 Alignment		99.8	31	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein; <b>PDBTitle:</b> a pe/ppp protein complex from mycobacterium tuberculosis
6	<a href="#">d2g38a1</a>	 Alignment		99.8	31	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE
7	<a href="#">c3bogB_</a>	 Alignment		96.7	35	<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
8	<a href="#">c3bogA_</a>	 Alignment		96.7	35	<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
9	<a href="#">c2zj6A_</a>	 Alignment		96.6	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
10	<a href="#">c3boiA_</a>	 Alignment		96.4	34	<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
11	<a href="#">c3boiB_</a>	 Alignment		96.4	34	<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

12	<a href="#">c2pneA</a>	Alignment		96.4	34	<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
13	<a href="#">c2ml2A</a>	Alignment		96.2	31	<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="#">c2qubG</a>	Alignment		96.2	19	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> extracellular lipase; <b>PDBTitle:</b> crystal structure of extracellular lipase lipa from serratia2 marcescens
15	<a href="#">d1kapp1</a>	Alignment		96.1	16	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
16	<a href="#">c2ml3A</a>	Alignment		96.1	27	<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
17	<a href="#">c1k7qA</a>	Alignment		96.0	28	<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
18	<a href="#">d1k7ia1</a>	Alignment		95.4	28	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
19	<a href="#">c2agmA</a>	Alignment		95.3	24	<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
20	<a href="#">c1jiwP</a>	Alignment		94.9	22	<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
21	<a href="#">c1om8A</a>	Alignment	not modelled	93.5	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
22	<a href="#">c5ctdA</a>	Alignment	not modelled	93.3	38	<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
23	<a href="#">c5ctdB</a>	Alignment	not modelled	92.7	23	<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
24	<a href="#">d1g9ka1</a>	Alignment	not modelled	92.7	22	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
25	<a href="#">c5cxIA</a>	Alignment	not modelled	92.5	24	<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
26	<a href="#">d1sata1</a>	Alignment	not modelled	92.4	14	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
27	<a href="#">c1satA</a>	Alignment	not modelled	92.4	24	<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
						<b>PDB header:</b> structural protein

28	<a href="#">c1nayC_</a>	Alignment	not modelled	92.3	34	<b>Chain:</b> C; <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> gpp-foldon:x-ray structure
29	<a href="#">c5ctiC_</a>	Alignment	not modelled	91.9	21	<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)
30	<a href="#">c3p4gD_</a>	Alignment	not modelled	82.3	18	<b>PDB header:</b> antifreeze protein <b>Chain:</b> D; <b>PDB Molecule:</b> antifreeze protein; <b>PDBTitle:</b> x-ray crystal structure of a hyperactive, ca2+-dependent, beta-helical2 antifreeze protein from an antarctic bacterium
31	<a href="#">c2klwA_</a>	Alignment	not modelled	61.6	43	<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
32	<a href="#">c2cuoF_</a>	Alignment	not modelled	20.9	41	<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
33	<a href="#">c2cuoC_</a>	Alignment	not modelled	20.9	41	<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
34	<a href="#">c4q1qA_</a>	Alignment	not modelled	15.3	13	<b>PDB header:</b> cell adhesion <b>Chain:</b> A; <b>PDB Molecule:</b> adhesin/invasin tiba autotransporter; <b>PDBTitle:</b> crystal structure of tiba-catalyzed hyper-glycosylated tiba55-3502 fragment
35	<a href="#">c1k6fC_</a>	Alignment	not modelled	15.0	41	<b>PDB header:</b> structural protein <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
36	<a href="#">c1k6fA_</a>	Alignment	not modelled	15.0	41	<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
37	<a href="#">c1k6fD_</a>	Alignment	not modelled	15.0	41	<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
38	<a href="#">c1k6fF_</a>	Alignment	not modelled	15.0	41	<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
39	<a href="#">c1k6fB_</a>	Alignment	not modelled	15.0	41	<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
40	<a href="#">c1k6fE_</a>	Alignment	not modelled	15.0	41	<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
41	<a href="#">c3ah9D_</a>	Alignment	not modelled	13.3	50	<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
42	<a href="#">c3ah9F_</a>	Alignment	not modelled	12.1	42	<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
43	<a href="#">c3ah9E_</a>	Alignment	not modelled	12.0	40	<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
44	<a href="#">c3ah9C_</a>	Alignment	not modelled	12.0	40	<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
45	<a href="#">c3ah9B_</a>	Alignment	not modelled	12.0	40	<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
46	<a href="#">c2cuoA_</a>	Alignment	not modelled	11.3	38	<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
47	<a href="#">c2cuoD_</a>	Alignment	not modelled	11.3	38	<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
48	<a href="#">c2cuoB_</a>	Alignment	not modelled	11.3	38	<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
49	<a href="#">c2cuoE_</a>	Alignment	not modelled	11.3	38	<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
50	<a href="#">c3ah9A_</a>	Alignment	not modelled	10.9	38	<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
51	<a href="#">c3a0mF_</a>	Alignment	not modelled	9.9	42	<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
52	<a href="#">c3lkbB_</a>	Alignment	not modelled	6.5	33	<b>PDB header:</b> chaperone <b>Chain:</b> B; <b>PDB Molecule:</b> nascent polypeptide-associated complex subunit alpha; <b>PDBTitle:</b> human nac dimerization domain