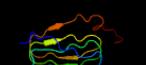
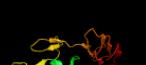
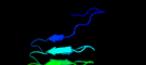


# Phyre<sup>2</sup>

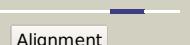
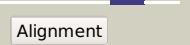
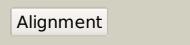
Email	mdejesus@rockefeller.edu
Description	RVBD1468c_(PE_PGRS29)_1655615_1656727
Date	Fri Aug 2 13:30:04 BST 2019
Unique Job ID	0a71b1523089ffa4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	clygvA_			99.7	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
2	c3hqvB_			99.5	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 ii collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
3	c2g38A_			99.4	30	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein; <b>PDBTitle:</b> a pe/ppe protein complex from mycobacterium tuberculosis
4	d2g38a1			99.4	30	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE
5	c5xfsA_			99.4	49	<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-ppe15 in complex with espf5 from m.2 tuberculosis
6	c1y0fB_			99.2	22	<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
7	c3bogB_			97.5	38	<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	c3bogA_			97.5	38	<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	c2pneA_			97.3	36	<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
10	c3boiB_			97.3	36	<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
11	c3boiA_			97.3	36	<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

12	<a href="#">c5ctdB</a>	Alignment		95.9	34	<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="#">c5ctiC</a>	Alignment		95.7	34	<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)
14	<a href="#">c5ctdA</a>	Alignment		95.6	37	<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
15	<a href="#">c2mi2A</a>	Alignment		95.3	9	<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
16	<a href="#">c2zj6A</a>	Alignment		94.7	14	<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
17	<a href="#">c2mi3A</a>	Alignment		94.5	13	<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
18	<a href="#">c2qubG</a>	Alignment		94.1	12	<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
19	<a href="#">c1k7qA</a>	Alignment		93.8	6	<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
20	<a href="#">c1satA</a>	Alignment		92.9	11	<b>PDB header:</b> hydrolase (serine protease) <b>Chain:</b> A; <b>PDB Molecule:</b> serratio protease; <b>PDBTitle:</b> crystal structure of the 50 kda metallo protease from s.2 marcescens
21	<a href="#">c1nayC</a>	Alignment	not modelled	92.6	27	<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
22	<a href="#">c1jiwP</a>	Alignment	not modelled	92.4	17	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> P; <b>PDB Molecule:</b> alkaline metalloproteinase; <b>PDBTitle:</b> crystal structure of the apr-aprin complex
23	<a href="#">d1k7ia1</a>	Alignment	not modelled	91.1	10	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
24	<a href="#">d1kapp1</a>	Alignment	not modelled	90.6	17	<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="#">c2agmA</a>	Alignment	not modelled	90.5	16	<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
26	<a href="#">c1om8A</a>	Alignment	not modelled	90.1	17	<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
27	<a href="#">c2klwA</a>	Alignment	not modelled	78.4	30	<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
28	<a href="#">c3p4gD</a>	Alignment	not modelled	69.3	16	<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
						<b>PDB header:</b> toxin

29	<a href="#">c5cxIA</a>	Alignment	not modelled	68.9	13	<b>Chain: A: PDB Molecule:</b> bifunctional hemolysin/adenylate cyclase; <b>PDBTitle:</b> crystal structure of rtx domain block v of adenylate cyclase toxin2 from bordetella pertussis
30	<a href="#">d1g9ka1</a>	Alignment	not modelled	36.4	12	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralsin-like metalloprotease, C-terminal domain
31	<a href="#">c3a0mF</a>	Alignment	not modelled	32.0	40	<b>PDB header:</b> structural protein <b>Chain: F: PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
32	<a href="#">c1k6fB</a>	Alignment	not modelled	25.4	32	<b>PDB header:</b> structural protein <b>Chain: B: PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
33	<a href="#">c1k6fC</a>	Alignment	not modelled	25.4	32	<b>PDB header:</b> structural protein <b>Chain: C: PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
34	<a href="#">c1k6fF</a>	Alignment	not modelled	25.4	32	<b>PDB header:</b> structural protein <b>Chain: F: PDB Molecule:</b> collagen triple helix; <b>PDBTitle:</b> crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
35	<a href="#">c1k6fD</a>	Alignment	not modelled	25.4	32	<b>PDB header:</b> structural protein <b>Chain: D: 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="#">c1k6fE</a>	Alignment	not modelled	25.4	32	<b>PDB header:</b> structural protein <b>Chain: E: 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="#">c1k6fA</a>	Alignment	not modelled	25.4	32	<b>PDB header:</b> structural protein <b>Chain: A: 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="#">c2cuoC</a>	Alignment	not modelled	19.0	33	<b>PDB header:</b> structural protein <b>Chain: C: PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
39	<a href="#">c2cuoF</a>	Alignment	not modelled	19.0	33	<b>PDB header:</b> structural protein <b>Chain: F: PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
40	<a href="#">c4q1qA</a>	Alignment	not modelled	18.8	9	<b>PDB header:</b> cell adhesion <b>Chain: A: PDB Molecule:</b> adhesin/invasin tiba autotransporter; <b>PDBTitle:</b> crystal structure of tibc-catalyzed hyper-glycosylated tiba55-3502 fragment
41	<a href="#">c3ah9D</a>	Alignment	not modelled	17.1	33	<b>PDB header:</b> structural protein <b>Chain: D: PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
42	<a href="#">d1sata1</a>	Alignment	not modelled	14.9	9	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralsin-like metalloprotease, C-terminal domain
43	<a href="#">c3ah9F</a>	Alignment	not modelled	13.4	35	<b>PDB header:</b> structural protein <b>Chain: F: PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
44	<a href="#">c3ah9A</a>	Alignment	not modelled	12.9	33	<b>PDB header:</b> structural protein <b>Chain: A: PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
45	<a href="#">c3ah9E</a>	Alignment	not modelled	11.8	35	<b>PDB header:</b> structural protein <b>Chain: E: PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
46	<a href="#">c3ah9C</a>	Alignment	not modelled	11.8	35	<b>PDB header:</b> structural protein <b>Chain: C: PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
47	<a href="#">c3ah9B</a>	Alignment	not modelled	11.8	35	<b>PDB header:</b> structural protein <b>Chain: B: PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)9 at 1.1 a resolution
48	<a href="#">c5juhA</a>	Alignment	not modelled	9.9	14	<b>PDB header:</b> cell adhesion <b>Chain: A: PDB Molecule:</b> antifreeze protein; <b>PDBTitle:</b> crystal structure of c-terminal domain (rv) of mpafp
49	<a href="#">c2cuoA</a>	Alignment	not modelled	8.8	36	<b>PDB header:</b> structural protein <b>Chain: A: PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
50	<a href="#">c2cuoE</a>	Alignment	not modelled	8.8	36	<b>PDB header:</b> structural protein <b>Chain: E: PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
51	<a href="#">c2cuoB</a>	Alignment	not modelled	8.8	36	<b>PDB header:</b> structural protein <b>Chain: B: PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
52	<a href="#">c2cuoD</a>	Alignment	not modelled	8.8	36	<b>PDB header:</b> structural protein <b>Chain: D: PDB Molecule:</b> collagen model peptide (pro-pro-gly)9; <b>PDBTitle:</b> collagen model peptide (pro-pro-gly)9
53	<a href="#">c3admC</a>	Alignment	not modelled	8.3	42	<b>PDB header:</b> structural protein <b>Chain: C: PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-ser-gly-(pro-pro-gly)4
54	<a href="#">c3a0mC</a>	Alignment	not modelled	6.9	44	<b>PDB header:</b> structural protein <b>Chain: C: PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
55	<a href="#">c3abnA</a>	Alignment	not modelled	6.3	42	<b>PDB header:</b> structural protein <b>Chain: A: PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a

56	<a href="#">c3admB</a>		Alignment	not modelled	6.2	42	<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)4-hyp-ser-gly-(pro-pro-gly)4
57	<a href="#">c3admA</a>		Alignment	not modelled	6.2	42	<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)4-hyp-ser-gly-(pro-pro-gly)4
58	<a href="#">c3admF</a>		Alignment	not modelled	6.2	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)4-hyp-ser-gly-(pro-pro-gly)4