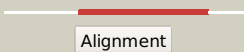

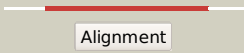

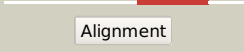


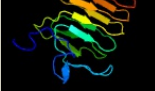


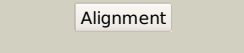
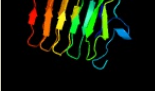
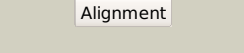



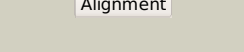

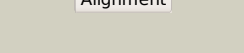
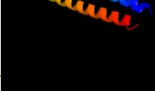
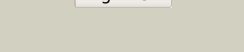


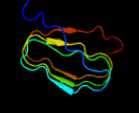


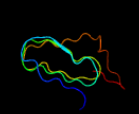
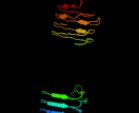
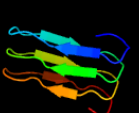


# Phyre2


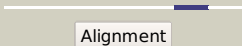


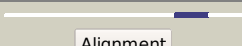
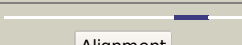
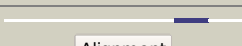
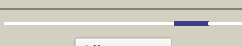

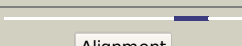
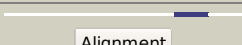



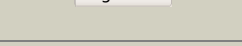
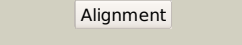

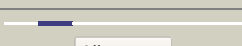
Email	mdejesus@rockefeller.edu
Description	RVBD3367_(PE_PGRS51)_3778739_3780514
Date	Fri Aug 9 18:20:03 BST 2019
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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1k7qA_</a>	 Alignment		99.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted protease c; <b>PDBTitle:</b> prt c from erwinia chrysanthemi: e189a mutant
2	<a href="#">c2zj6A_</a>	 Alignment		99.0	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
3	<a href="#">c2qubG_</a>	 Alignment		98.9	18	<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
4	<a href="#">d1kapp1</a>	 Alignment		98.6	20	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
5	<a href="#">d1g9ka1</a>	 Alignment		98.5	19	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
6	<a href="#">d1k7ia1</a>	 Alignment		98.4	18	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
7	<a href="#">d1sata1</a>	 Alignment		98.4	21	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
8	<a href="#">c1satA_</a>	 Alignment		98.3	16	<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
9	<a href="#">c5xfsA_</a>	 Alignment		98.3	51	<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 esp g5 from m.2 tuberculosis
10	<a href="#">c2g38A_</a>	 Alignment		98.2	34	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein; <b>PDBTitle:</b> a pe/pp e protein complex from mycobacterium tuberculosis
11	<a href="#">d2g38a1</a>	 Alignment		98.2	34	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE

12	<a href="#">c1jiwP</a>	Alignment		97.9	21	<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
13	<a href="#">c2ml2A</a>	Alignment		97.9	20	<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="#">c1om8A</a>	Alignment		97.9	23	<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
15	<a href="#">c2ml3A</a>	Alignment		97.8	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
16	<a href="#">c2agmA</a>	Alignment		97.8	21	<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
17	<a href="#">c3p4gD</a>	Alignment		97.5	24	<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
18	<a href="#">c5cxlA</a>	Alignment		96.8	23	<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
19	<a href="#">c1ygvA</a>	Alignment		96.4	21	<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
20	<a href="#">c3hqvB</a>	Alignment		95.0	25	<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
21	<a href="#">c4q1qA</a>	Alignment	not modelled	89.7	16	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> adhesin/invasin tiba autotransporter; <b>PDBTitle:</b> crystal structure of tibr-catalyzed hyper-glycosylated tiba55-3502 fragment
22	<a href="#">c5juhA</a>	Alignment	not modelled	84.1	22	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> antifreeze protein; <b>PDBTitle:</b> crystal structure of c-terminal domain (rv) of mpafp
23	<a href="#">c3boiB</a>	Alignment	not modelled	81.7	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 racemate
24	<a href="#">c3boiA</a>	Alignment	not modelled	81.7	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 racemate
25	<a href="#">c2pneA</a>	Alignment	not modelled	81.7	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> crystal structure of the snow flea antifreeze protein
26	<a href="#">c1y0fB</a>	Alignment	not modelled	75.6	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
27	<a href="#">c3bogB</a>	Alignment	not modelled	72.7	32	<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
28	<a href="#">c3bogA</a>	Alignment	not modelled	72.7	32	<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
						<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen alpha-1(i) chain,collagen alpha-

29	<a href="#">c5ctdA</a>	Alignment	not modelled	51.5	31	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
30	<a href="#">c1nayC</a>	Alignment	not modelled	47.9	21	<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
31	<a href="#">c5ctiC</a>	Alignment	not modelled	47.6	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)
32	<a href="#">c5ctdB</a>	Alignment	not modelled	45.2	33	<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
33	<a href="#">c3abnA</a>	Alignment	not modelled	18.6	46	<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-asp-gly-(pro-pro-gly)4 at 1.022 a
34	<a href="#">c3abnC</a>	Alignment	not modelled	15.0	45	<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)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
35	<a href="#">c3admC</a>	Alignment	not modelled	11.0	42	<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)4-hyp-ser-gly-(pro-pro-gly)4
36	<a href="#">c1x1kC</a>	Alignment	not modelled	10.1	42	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
37	<a href="#">c1x1kD</a>	Alignment	not modelled	10.1	42	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
38	<a href="#">c2d3fE</a>	Alignment	not modelled	10.1	42	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
39	<a href="#">c1x1kB</a>	Alignment	not modelled	10.1	42	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
40	<a href="#">c1x1kA</a>	Alignment	not modelled	10.1	42	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
41	<a href="#">c2d3fF</a>	Alignment	not modelled	10.1	42	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
42	<a href="#">c2d3fD</a>	Alignment	not modelled	10.1	42	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
43	<a href="#">c3abnB</a>	Alignment	not modelled	9.7	43	<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-asp-gly-(pro-pro-gly)4 at 1.022 a
44	<a href="#">c3admE</a>	Alignment	not modelled	9.6	42	<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)4-hyp-ser-gly-(pro-pro-gly)4
45	<a href="#">c3admA</a>	Alignment	not modelled	9.6	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
46	<a href="#">c3admB</a>	Alignment	not modelled	9.6	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
47	<a href="#">c3admF</a>	Alignment	not modelled	9.6	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
48	<a href="#">c3a0mC</a>	Alignment	not modelled	9.4	42	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
49	<a href="#">c3a1hB</a>	Alignment	not modelled	9.2	41	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
50	<a href="#">c3a1hA</a>	Alignment	not modelled	8.8	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
51	<a href="#">c3a0aE</a>	Alignment	not modelled	8.8	38	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal

52	<a href="#">c3a1hF_</a>	 Alignment	not modelled	8.7	41	<b>PDB header:</b> structural protein <b>Chain:</b> F: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
53	<a href="#">c3a0aC_</a>	 Alignment	not modelled	8.5	41	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
54	<a href="#">c3a0aB_</a>	 Alignment	not modelled	8.4	38	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
55	<a href="#">c3a1hC_</a>	 Alignment	not modelled	7.8	38	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
56	<a href="#">c3a1hD_</a>	 Alignment	not modelled	7.8	38	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
57	<a href="#">c3a1hE_</a>	 Alignment	not modelled	7.8	38	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
58	<a href="#">c3admD_</a>	 Alignment	not modelled	7.8	41	<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)4-hyp-ser-gly-(pro-pro-gly)4
59	<a href="#">c3a0aA_</a>	 Alignment	not modelled	7.6	38	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-opg-(ppg)4, monoclinic, twinned crystal
60	<a href="#">c6a0aA_</a>	 Alignment	not modelled	7.4	31	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
61	<a href="#">c6a0aC_</a>	 Alignment	not modelled	7.1	31	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
62	<a href="#">c6a0aB_</a>	 Alignment	not modelled	7.1	31	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen type iii peptide; <b>PDBTitle:</b> structure of a triple-helix region of human collagen type iii
63	<a href="#">d1w72l1</a>	 Alignment	not modelled	6.8	30	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> V set domains (antibody variable domain-like)
64	<a href="#">c2d3fC_</a>	 Alignment	not modelled	6.8	41	<b>PDB header:</b> structural protein <b>Chain:</b> C: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
65	<a href="#">c2d3fB_</a>	 Alignment	not modelled	6.8	41	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
66	<a href="#">c1x1kE_</a>	 Alignment	not modelled	6.8	41	<b>PDB header:</b> structural protein <b>Chain:</b> E: <b>PDB Molecule:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp- <b>PDBTitle:</b> host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
67	<a href="#">c2d3fA_</a>	 Alignment	not modelled	6.8	41	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen model peptides (pro-pro-gly)4-pro-hyp- <b>PDBTitle:</b> crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
68	<a href="#">c6irwA_</a>	 Alignment	not modelled	6.2	50	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphorylated ctd-interacting factor 1; <b>PDBTitle:</b> crystal structure of the human cap-specific adenosine2 methyltransferase bound to sah
69	<a href="#">c3a0mB_</a>	 Alignment	not modelled	5.7	41	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen-like peptide; <b>PDBTitle:</b> structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal