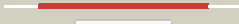
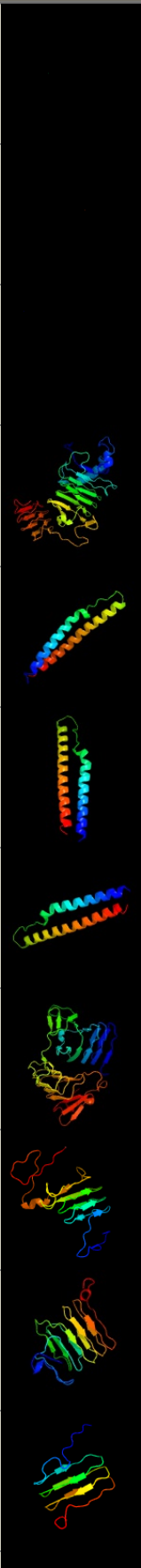

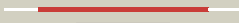








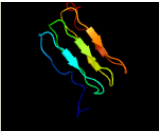


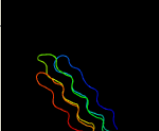
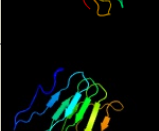

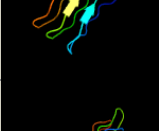
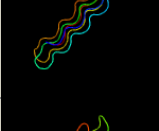







# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD1091\_(PE\_PGR522)\_1216474\_1219035  
 Date Wed Jul 31 22:05:17 BST 2019  
 Unique Job ID e9cd489d3732a1c7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ygvA_</a>	 Alignment		100.0	24	<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		99.8	27	<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	26	<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="#">c2qubG_</a>	 Alignment		99.1	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
5	<a href="#">c5xfxA_</a>	 Alignment		99.1	54	<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 esp95 from m.2 tuberculosis
6	<a href="#">c2g38A_</a>	 Alignment		99.1	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/pepe protein complex from mycobacterium tuberculosis
7	<a href="#">d2g38a1</a>	 Alignment		99.1	30	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE
8	<a href="#">c2zj6A_</a>	 Alignment		99.0	13	<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
9	<a href="#">c1k7qA_</a>	 Alignment		98.6	18	<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
10	<a href="#">d1kapp1</a>	 Alignment		98.3	16	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
11	<a href="#">c2ml3A_</a>	 Alignment		98.2	19	<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

12	<a href="#">c2ml2A_</a>	Alignment		98.0	21	<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
13	<a href="#">d1k7ia1</a>	Alignment		98.0	24	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
14	<a href="#">c3bogB_</a>	Alignment		97.9	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
15	<a href="#">c3bogA_</a>	Alignment		97.9	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
16	<a href="#">c1satA_</a>	Alignment		97.9	18	<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
17	<a href="#">c2agmA_</a>	Alignment		97.8	29	<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="#">c2pneA_</a>	Alignment		97.8	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> crystal structure of the snow flea antifreeze protein
19	<a href="#">c3boiB_</a>	Alignment		97.7	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 racemate
20	<a href="#">c3boiA_</a>	Alignment		97.7	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 racemate
21	<a href="#">c1jiwP_</a>	Alignment	not modelled	97.7	26	<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
22	<a href="#">d1sata1</a>	Alignment	not modelled	97.6	11	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
23	<a href="#">c1om8A_</a>	Alignment	not modelled	97.6	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
24	<a href="#">d1g9ka1</a>	Alignment	not modelled	97.5	11	<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	96.9	27	<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 adenylyate cyclase toxin2 from bordetella pertussis
26	<a href="#">c3p4gD_</a>	Alignment	not modelled	96.0	15	<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
27	<a href="#">c1nayC_</a>	Alignment	not modelled	92.3	22	<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
28	<a href="#">c5ctdB_</a>	Alignment	not modelled	89.4	26	<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 <b>PDB header:</b> cell adhesion

29	<a href="#">c4q1qA_</a>	 Alignment	not modelled	88.8	13	<b>Chain:</b> A; <b>PDB Molecule:</b> adhesin/invasin tiba autotransporter; <b>PDBTitle:</b> crystal structure of tbc-catalyzed hyper-glycosylated tiba55-3502 fragment
30	<a href="#">c5ctiC_</a>	 Alignment	not modelled	87.0	33	<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)
31	<a href="#">c5ctdA_</a>	 Alignment	not modelled	86.0	32	<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
32	<a href="#">c5juhA_</a>	 Alignment	not modelled	57.0	11	<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