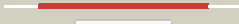
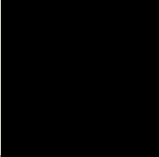


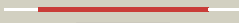




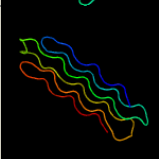

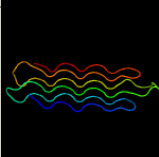

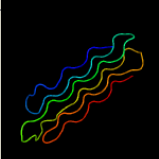

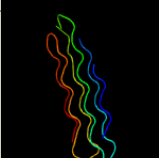

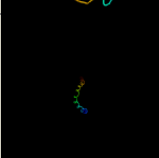

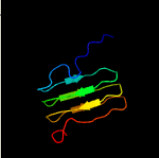

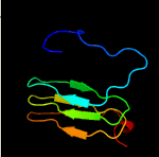

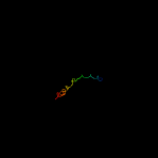

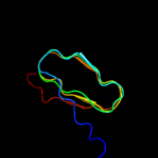
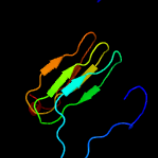

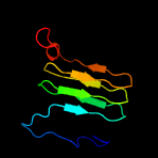
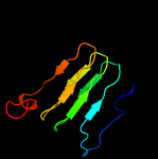



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0833_(PE_PGRS13)_925364_927613
Date	Fri Jul 26 01:50:42 BST 2019
Unique Job ID	0c1277b4a26c86a7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ygvA_	 Alignment		100.0	29	PDB header: structural protein/contractile protein Chain: A: PDB Molecule: collagen i alpha 1; PDBTitle: the structure of collagen type i. single type i collagen2 molecule: rigid refinement
2	c1y0fB_	 Alignment		99.8	29	PDB header: structural protein/contractile protein Chain: B: PDB Molecule: collagen i alpha 2; PDBTitle: the structure of collagen type i. single type i collagen2 molecule
3	c3hqvB_	 Alignment		99.8	27	PDB header: structural protein, contractile protein Chain: B: PDB Molecule: collagen alpha-2(i) chain; PDBTitle: low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
4	c2pneA_	 Alignment		97.9	36	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
5	c3boiB_	 Alignment		97.9	36	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
6	c3boiA_	 Alignment		97.9	36	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
7	c3bogA_	 Alignment		97.9	38	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
8	c3bogB_	 Alignment		97.9	38	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
9	c5ctdB_	 Alignment		96.4	28	PDB header: structural protein Chain: B: PDB Molecule: collagen alpha-2(i) chain, collagen alpha-2(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
10	c2ml3A_	 Alignment		96.2	24	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
11	c1k7qA_	 Alignment		96.1	25	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant

12	c5ctiC_	Alignment		95.8	37	PDB header: structural protein Chain: C: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-3(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
13	c5ctdA_	Alignment		95.8	37	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-1(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
14	c1nayC_	Alignment		95.7	24	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
15	c2ml2A_	Alignment		95.5	23	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r2 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
16	d1k7ia1	Alignment		95.2	25	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
17	c2agmA_	Alignment		95.0	23	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
18	c1jiwP_	Alignment		94.9	22	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloprotease; PDBTitle: crystal structure of the apr-aprin complex
19	d1kapp1	Alignment		94.1	22	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
20	c2zj6A_	Alignment		93.8	18	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
21	c1satA_	Alignment	not modelled	92.3	23	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens
22	c1om8A_	Alignment	not modelled	91.8	23	PDB header: hydrolase Chain: A: PDB Molecule: serralysin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
23	c5cx1A_	Alignment	not modelled	87.3	23	PDB header: toxin Chain: A: PDB Molecule: bifunctional hemolysin/adenylate cyclase; PDBTitle: crystal structure of rtx domain block v of adenylate cyclase toxin2 from bordetella pertussis
24	c2qubG_	Alignment	not modelled	76.7	15	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
25	d1g9ka1	Alignment	not modelled	70.9	11	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
26	d1sata1	Alignment	not modelled	67.9	15	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
27	c3p4qD_	Alignment	not modelled	56.4	9	PDB header: antifreeze protein Chain: D: PDB Molecule: antifreeze protein; PDBTitle: x-ray crystal structure of a hyperactive, ca2+-dependent, beta-helical2 antifreeze protein from an antarctic bacterium
28	c2klwA_	Alignment	not modelled	51.2	33	PDB header: de novo protein Chain: A: PDB Molecule: (pkg)10; PDBTitle: solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions