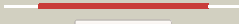
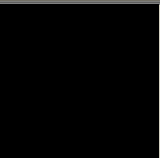

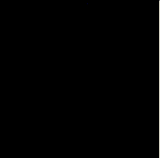
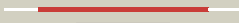
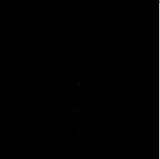

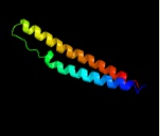

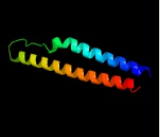

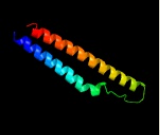



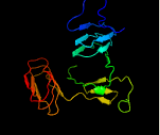



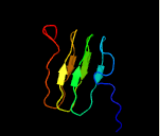







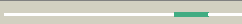



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1759c_(wag22)_1989840_1992584
Date	Fri Aug 2 13:30:36 BST 2019
Unique Job ID	b1a2aa6d132d579a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ygvA_	 Alignment		99.7	26	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	c3hqvB_	 Alignment		98.9	26	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
3	c1y0fB_	 Alignment		98.8	25	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
4	c5xfxA_	 Alignment		97.9	50	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
5	c2g38A_	 Alignment		97.8	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/pepe protein complex from mycobacterium tuberculosis
6	d2g38a1	 Alignment		97.8	31	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
7	c2qubG_	 Alignment		97.7	18	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
8	c2zj6A_	 Alignment		97.7	22	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
9	c1k7qA_	 Alignment		97.2	18	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
10	c2ml3A_	 Alignment		96.8	18	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	d1kapp1	 Alignment		96.8	15	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain

12	c1jiwP_	Alignment		96.7	19	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
13	d1k7ia1	Alignment		96.6	18	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralyisin-like metalloprotease, C-terminal domain
14	c1om8A_	Alignment		96.5	20	PDB header: hydrolase Chain: A: PDB Molecule: serralyisin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
15	c1satA_	Alignment		96.4	18	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens
16	c2ml2A_	Alignment		96.4	18	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
17	c2agmA_	Alignment		95.9	19	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
18	d1sata1	Alignment		95.8	14	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralyisin-like metalloprotease, C-terminal domain
19	c3bogB_	Alignment		95.7	37	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
20	c3bogA_	Alignment		95.7	37	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
21	d1g9ka1	Alignment	not modelled	95.3	18	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralyisin-like metalloprotease, C-terminal domain
22	c3boiA_	Alignment	not modelled	95.2	37	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
23	c3boiB_	Alignment	not modelled	95.2	37	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
24	c2pneA_	Alignment	not modelled	95.2	37	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
25	c5cxIA_	Alignment	not modelled	92.7	26	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
26	c3p4gD_	Alignment	not modelled	91.2	13	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
27	c5ctiC_	Alignment	not modelled	82.8	28	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)
28	c5ctdB_	Alignment	not modelled	81.9	27	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 hetero-

						trimerization2 domain with a guest fragment a2a1a1 of type i collagen
29	c5ctdA_	 Alignment	not modelled	80.0	27	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
30	c1nayC_	 Alignment	not modelled	78.4	24	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
31	c5juhA_	 Alignment	not modelled	48.4	22	PDB header: cell adhesion Chain: A: PDB Molecule: antifreeze protein; PDBTitle: crystal structure of c-terminal domain (rv) of mpafp
32	c4q1qA_	 Alignment	not modelled	43.9	13	PDB header: cell adhesion Chain: A: PDB Molecule: adhesin/invasin tibia autotransporter; PDBTitle: crystal structure of tbc-catalyzed hyper-glycosylated tiba55-3502 fragment
33	c2klwA_	 Alignment	not modelled	10.1	27	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
34	c4pkcC_	 Alignment	not modelled	6.4	25	PDB header: lyase Chain: C: PDB Molecule: tutf; PDBTitle: benzylsuccinate alpha-gamma complex
35	c5m0jH_	 Alignment	not modelled	6.1	40	PDB header: rna binding protein Chain: H: PDB Molecule: swi5-dependent ho expression protein 2, swi5-dependent ho PDBTitle: crystal structure of the cytoplasmic complex with she2p, she3p, and 2 the ash1 mrna e3-localization element