
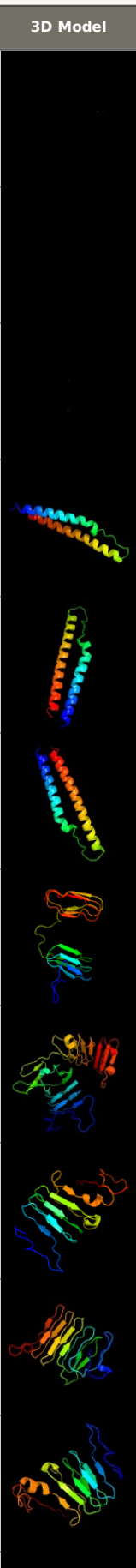
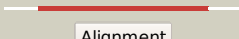
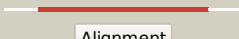








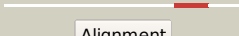
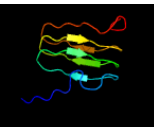
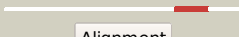


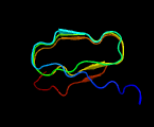

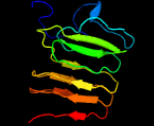



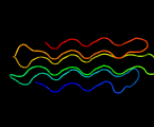

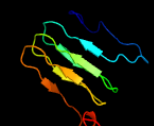
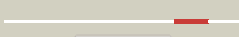



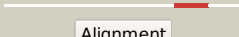
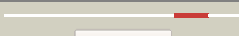
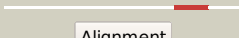
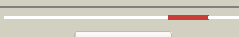
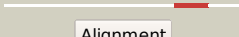







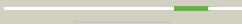

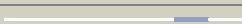

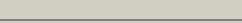
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3511_(PE_PGR55)_3939796_3941940
Date	Fri Aug 9 18:20:19 BST 2019
Unique Job ID	2c0f258c709c822c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ygvA_	 Alignment		100.0	31	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	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
3	c3hqvB_	 Alignment		99.8	25	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	c5xfA_	 Alignment		99.1	49	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
5	d2g38a1	 Alignment		99.1	29	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
6	c2g38A_	 Alignment		99.1	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
7	c2zj6A_	 Alignment		98.2	21	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
8	c2qubG_	 Alignment		98.1	14	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serrattia2 marcescens
9	c1k7qA_	 Alignment		98.0	16	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
10	d1kapp1	 Alignment		98.0	20	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
11	c1satA_	 Alignment		97.8	15	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens

12	c2ml3A_	 Alignment		97.5	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
13	d1k7ia1	 Alignment		97.4	18	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
14	c2ml2A_	 Alignment		97.3	17	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
15	d1g9ka1	 Alignment		97.2	18	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
16	c3bogB_	 Alignment		97.2	36	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
17	c3bogA_	 Alignment		97.2	36	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
18	c1jiwP_	 Alignment		97.1	18	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
19	c3boiB_	 Alignment		97.0	35	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
20	c3boiA_	 Alignment		97.0	35	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
21	c2pneA_	 Alignment	not modelled	97.0	35	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
22	c1om8A_	 Alignment	not modelled	97.0	17	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	c2agmA_	 Alignment	not modelled	96.8	15	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
24	d1sata1	 Alignment	not modelled	96.3	16	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
25	c5cxlA_	 Alignment	not modelled	95.0	22	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	91.9	7	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	c5ctdB_	 Alignment	not modelled	90.8	32	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
28	c5ctdA_	 Alignment	not modelled	89.9	32	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 hetero-

						trimerization2 domain with a guest fragment a2a1a1 of type i collagen
29	c5ctiC_	Alignment 	not modelled	89.5	30	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)
30	c1nayC_	Alignment 	not modelled	89.0	21	PDB header: structural protein Chain: C; PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
31	c5juhA_	Alignment 	not modelled	57.7	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	41.5	8	PDB header: cell adhesion Chain: A; PDB Molecule: adhesin/invasin tiba autotransporter; PDBTitle: crystal structure of tbc-catalyzed hyper-glycosylated tiba55-3502 fragment
33	c2klwA_	Alignment 	not modelled	22.0	30	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	c5gapG_	Alignment 	not modelled	13.7	54	PDB header: transcription Chain: G; PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: body region of the u4/u6.u5 tri-snrnp
35	c3jcmK_	Alignment 	not modelled	13.1	54	PDB header: transcription Chain: K; PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: cryo-em structure of the spliceosomal u4/u6.u5 tri-snrnp