

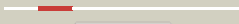
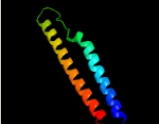

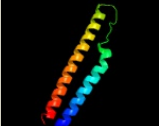




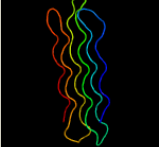

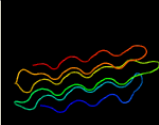

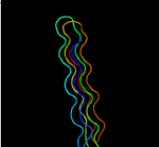

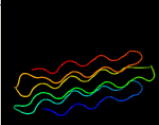

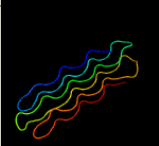
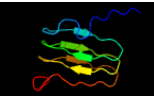
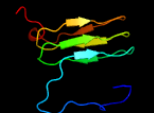
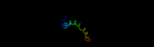
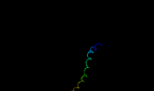



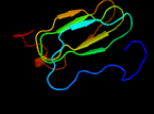



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1768_(PE_PGRS31)_2000621_2002477
 Date Fri Aug 2 13:30:37 BST 2019
 Unique Job ID d6abcd9c760e8639

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		99.8	51	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
2	c2g38A_	 Alignment		99.8	34	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38a1	 Alignment		99.8	34	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
4	c1ygvA_	 Alignment		99.7	23	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
5	c1y0fB_	 Alignment		99.4	28	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
6	c3hqvB_	 Alignment		99.0	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
7	c3bogB_	 Alignment		96.0	38	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
8	c3bogA_	 Alignment		96.0	38	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
9	c2pneA_	 Alignment		95.9	39	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
10	c3boiA_	 Alignment		95.9	39	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
11	c3boiB_	 Alignment		95.9	39	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate

12	c2ml3A_	Alignment		92.7	19	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	c1k7qA_	Alignment		88.9	19	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
14	c5ctdB_	Alignment		87.4	29	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
15	c5ctiC_	Alignment		85.8	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)
16	c5ctdA_	Alignment		85.8	29	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
17	c2ml2A_	Alignment		85.8	20	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
18	c2qubG_	Alignment		84.7	16	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
19	d1k7ia1	Alignment		84.7	18	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
20	c2agmA_	Alignment		84.1	18	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
21	c1nayC_	Alignment	not modelled	83.5	25	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
22	d1kapp1	Alignment	not modelled	82.2	19	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
23	c2zj6A_	Alignment	not modelled	82.1	14	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
24	c1jiwP_	Alignment	not modelled	78.7	19	PDB header: hydrolase/hydrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
25	c1satA_	Alignment	not modelled	73.2	23	PDB header: hydrolase Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens
26	c1om8A_	Alignment	not modelled	71.3	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
27	c5cxIA_	Alignment	not modelled	56.4	25	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
28	d1g9ka1	Alignment	not modelled	17.8	16	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
29	d1sata1	Alignment	not modelled	11.0	16	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain

30	c3p4gD_	Alignment	not modelled	8.4	21	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
31	c6irwA_	Alignment	not modelled	8.4	40	PDB header: transferase Chain: A: PDB Molecule: phosphorylated ctd-interacting factor 1; PDBTitle: crystal structure of the human cap-specific adenosine2 methyltransferase bound to sah