
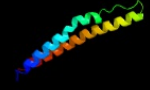
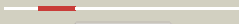






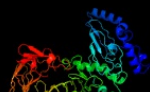



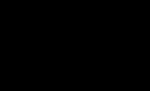





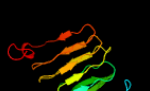

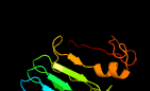
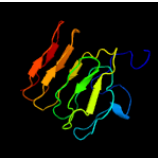
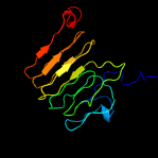
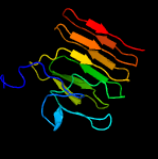
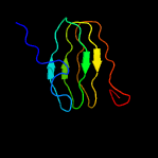
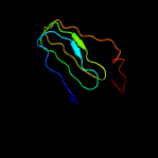






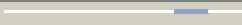
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2615c_(PE_PGRS45)_2943610_2944995
Date	Wed Aug 7 12:50:26 BST 2019
Unique Job ID	47de9da78376d218

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		99.8	42	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	26	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	26	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
4	c1k7gA_	 Alignment		99.4	11	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
5	c2zj6A_	 Alignment		99.3	15	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
6	c1ygvA_	 Alignment		99.3	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
7	c1y0fB_	 Alignment		99.2	23	PDB header: structural protein/contractile protein Chain: B: PDB Molecule: collagen i alpha 1; PDBTitle: the structure of collagen type i. single type i collagen2 molecule
8	c3hqvB_	 Alignment		99.2	24	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
9	c2qubG_	 Alignment		99.1	12	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
10	d1kapp1	 Alignment		98.6	20	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
11	c1satA_	 Alignment		98.5	22	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	d1g9ka1	Alignment		98.3	20	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
13	d1k7ia1	Alignment		98.2	22	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
14	d1sata1	Alignment		97.9	20	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
15	c2ml3A_	Alignment		97.9	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
16	c2ml2A_	Alignment		97.6	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		97.6	25	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
18	c1om8A_	Alignment		97.5	25	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
19	c1jiwP_	Alignment		97.5	20	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
20	c3bogB_	Alignment		95.9	39	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
21	c3bogA_	Alignment	not modelled	95.9	39	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
22	c2pneA_	Alignment	not modelled	95.8	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
23	c3boiB_	Alignment	not modelled	95.8	39	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
24	c3boiA_	Alignment	not modelled	95.8	39	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
25	c5cxIA_	Alignment	not modelled	95.6	28	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	95.5	12	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	87.6	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
28	c1nayC_	Alignment	not modelled	87.4	24	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure

29	c5ctdA_	 Alignment	not modelled	84.9	26	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	c5ctiC_	 Alignment	not modelled	84.2	26	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)
31	c4g1qA_	 Alignment	not modelled	34.6	20	PDB header: cell adhesion Chain: A: PDB Molecule: adhesin/invasin tibia autotransporter; PDBTitle: crystal structure of tibia-catalyzed hyper-glycosylated tibia55-3502 fragment
32	c5juhA_	 Alignment	not modelled	28.0	26	PDB header: cell adhesion Chain: A: PDB Molecule: antifreeze protein; PDBTitle: crystal structure of c-terminal domain (rv) of mpafp