

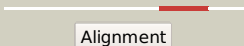



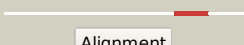




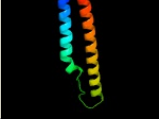

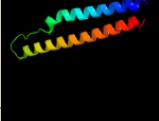
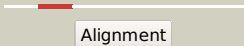

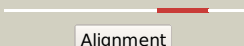




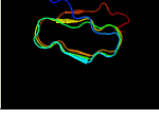
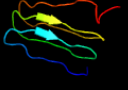



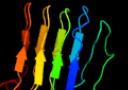
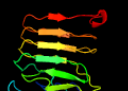

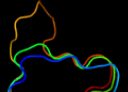


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0279c_(PE_PGRS4)_336560_339073
 Date Tue Jul 23 14:50:34 BST 2019
 Unique Job ID 097baddcbd984358

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qubG	 Alignment		99.0	17	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
2	c2zj6A	 Alignment		98.7	16	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
3	d1kapp1	 Alignment		98.4	13	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
4	d1k7ia1	 Alignment		98.1	16	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
5	c1ygvA	 Alignment		98.1	25	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
6	c2g38A	 Alignment		98.1	30	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
7	d2g38a1	 Alignment		98.1	30	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
8	c5xfxA	 Alignment		98.0	51	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp85 from m.2 tuberculosis
9	c1k7qA	 Alignment		98.0	15	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
10	d1g9ka1	 Alignment		98.0	15	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
11	c2ml2A	 Alignment		97.9	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

12	c2agmA	Alignment		97.7	15	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
13	c1jiwP	Alignment		97.7	14	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
14	c2ml3A	Alignment		97.7	10	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
15	c1satA	Alignment		97.7	13	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	c1om8A	Alignment		97.5	18	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
17	d1sata1	Alignment		97.5	13	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralyisin-like metalloprotease, C-terminal domain
18	c5cxlA	Alignment		96.8	18	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
19	c3p4qD	Alignment		95.6	10	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
20	c3hqvB	Alignment		91.6	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
21	c1y0fB	Alignment	not modelled	90.8	24	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
22	c4q1qA	Alignment	not modelled	67.5	16	PDB header: cell adhesion Chain: A: PDB Molecule: adhesin/invasin tiba autotransporter; PDBTitle: crystal structure of tbc-catalyzed hyper-glycosylated tiba55-3502 fragment
23	c5juhA	Alignment	not modelled	57.8	17	PDB header: cell adhesion Chain: A: PDB Molecule: antifreeze protein; PDBTitle: crystal structure of c-terminal domain (rv) of mpafp
24	c3bogA	Alignment	not modelled	13.4	33	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
25	c3bogB	Alignment	not modelled	13.4	33	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
26	c3boiB	Alignment	not modelled	13.0	33	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
27	c3boiA	Alignment	not modelled	13.0	33	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
28	c2pneA	Alignment	not modelled	13.0	33	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
						PDB header: structural protein Chain: B: PDB Molecule: collagen alpha-2(i) chain,collagen alpha-

29	c5ctdB_	Alignment	not modelled	8.6	29	2(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
30	c5ctdA_	Alignment	not modelled	8.4	33	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