


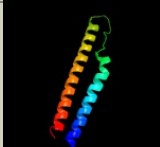

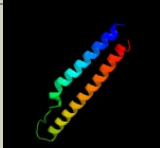




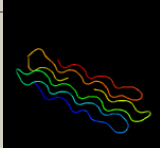

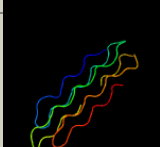

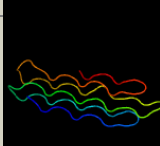

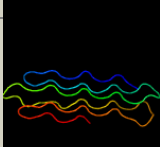

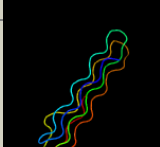
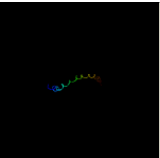
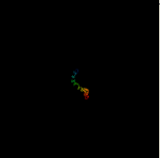
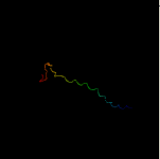
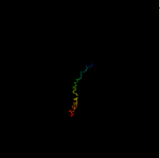
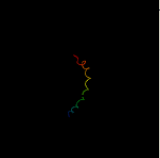
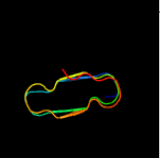
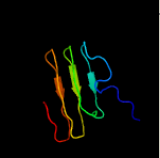
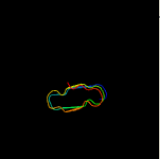
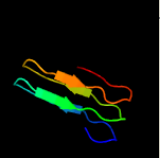


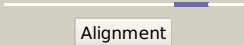
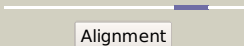
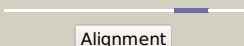

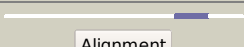
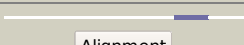
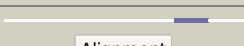
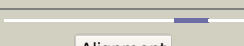
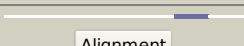

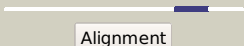
Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2741_(PE_PGRS47)_3053924_3055501
 Date Wed Aug 7 12:50:39 BST 2019
 Unique Job ID a455c87e1c7a39a2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		100.0	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
2	d2g38a1	 Alignment		100.0	30	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c2g38A_	 Alignment		100.0	30	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: pe family protein; PDBTitle: a pe/pppe protein complex from mycobacterium tuberculosis
4	c1ygvA_	 Alignment		99.3	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
5	c3hqvB_	 Alignment		99.3	27	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
6	c1y0fB_	 Alignment		98.8	30	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
7	c3bogB_	 Alignment		97.0	33	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		97.0	33	PDB header: antifreeze protein Chain: A; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
9	c3boiB_	 Alignment		95.6	29	PDB header: antifreeze protein Chain: B; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
10	c3boiA_	 Alignment		95.6	29	PDB header: antifreeze protein Chain: A; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
11	c2pneA_	 Alignment		95.6	29	PDB header: antifreeze protein Chain: A; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein

12	c5ctiC_	Alignment		94.4	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)
13	c5ctdB_	Alignment		94.1	26	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
14	c1nayC_	Alignment		93.7	21	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
15	c5ctdA_	Alignment		93.7	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
16	c2klwA_	Alignment		79.2	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
17	c1jiwP_	Alignment		74.3	24	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
18	c2ml3A_	Alignment		72.7	22	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
19	d1kapp1	Alignment		67.0	24	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
20	c2zj6A_	Alignment		62.5	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
21	d1k7ia1	Alignment	not modelled	58.9	24	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
22	c2ml2A_	Alignment	not modelled	58.2	19	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
23	c1k7qA_	Alignment	not modelled	56.6	25	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
24	c2agmA_	Alignment	not modelled	53.7	20	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
25	c1om8A_	Alignment	not modelled	52.4	27	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
26	c1satA_	Alignment	not modelled	46.0	27	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens
27	c5cxIA_	Alignment	not modelled	19.0	21	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	c3p4gD_	Alignment	not modelled	17.9	20	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

29	c2qubG_	 Alignment	not modelled	14.6	25	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
30	c1k6fE_	 Alignment	not modelled	13.1	28	PDB header: structural protein Chain: E: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
31	c1k6fD_	 Alignment	not modelled	13.1	28	PDB header: structural protein Chain: D: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
32	c1k6fA_	 Alignment	not modelled	13.1	28	PDB header: structural protein Chain: A: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
33	c1k6fB_	 Alignment	not modelled	13.1	28	PDB header: structural protein Chain: B: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
34	c1k6fF_	 Alignment	not modelled	13.1	28	PDB header: structural protein Chain: F: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
35	c1k6fC_	 Alignment	not modelled	13.1	28	PDB header: structural protein Chain: C: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model [(pro-pro-gly)2 10]3
36	c2cuoC_	 Alignment	not modelled	11.2	30	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
37	c2cuoF_	 Alignment	not modelled	11.2	30	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
38	c3ah9D_	 Alignment	not modelled	5.2	32	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
39	c3ah9A_	 Alignment	not modelled	5.1	29	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution