
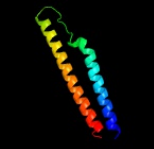

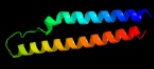
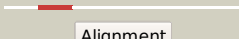

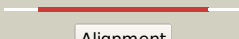
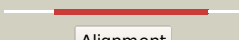












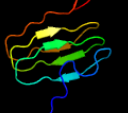

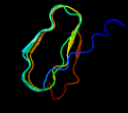

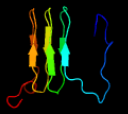



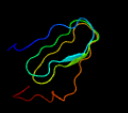

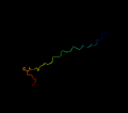

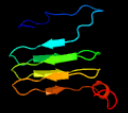

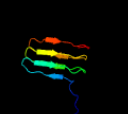











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1803c_(PE_PGRS32)_2044930_2046849
Date	Fri Aug 2 13:30:41 BST 2019
Unique Job ID	5436789c25772c32

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g38A_	 Alignment		100.0	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
2	d2g38a1	 Alignment		100.0	26	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c5xfsA_	 Alignment		100.0	47	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
4	c1ygvA_	 Alignment		99.2	28	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		98.8	23	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		98.5	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
7	c3bogB_	 Alignment		96.8	34	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		96.8	34	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		95.8	34	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	c3boiB_	 Alignment		95.8	34	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
11	c3boiA_	 Alignment		95.8	34	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate

12	c2ml3A_	 Alignment		94.4	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	c2ml2A_	 Alignment		93.2	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
14	c1k7qA_	 Alignment		92.5	19	PDB header: hydrolase Chain: A; PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
15	d1k7ia1	 Alignment		90.7	19	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
16	c2agmA_	 Alignment		90.3	18	PDB header: isomerase Chain: A; PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
17	c1nayC_	 Alignment		89.0	26	PDB header: structural protein Chain: C; PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
18	d1kapp1	 Alignment		88.2	18	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
19	c2zj6A_	 Alignment		85.7	22	PDB header: hydrolase Chain: A; PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
20	c2qubG_	 Alignment		85.1	18	PDB header: hydrolase Chain: G; PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
21	c1jiwP_	 Alignment	not modelled	84.8	18	PDB header: hydrolase/hyrolase inhibitor Chain: P; PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
22	c1satA_	 Alignment	not modelled	82.8	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
23	c1om8A_	 Alignment	not modelled	82.1	18	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
24	c5cx1A_	 Alignment	not modelled	75.9	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
25	c5ctdB_	 Alignment	not modelled	67.1	31	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
26	c5ctdA_	 Alignment	not modelled	65.8	36	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
27	c5ctiC_	 Alignment	not modelled	54.5	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)

28	d1g9ka1	Alignment	not modelled	45.9	16	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
29	c4wj2A	Alignment	not modelled	37.0	9	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
30	c3p4gD	Alignment	not modelled	35.6	16	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	c3ah9F	Alignment	not modelled	18.0	48	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
32	c2cuoD	Alignment	not modelled	15.8	46	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
33	c2cuoB	Alignment	not modelled	15.8	46	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
34	c2cuoA	Alignment	not modelled	15.8	46	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
35	c2cuoE	Alignment	not modelled	15.8	46	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
36	c2cuoC	Alignment	not modelled	14.6	46	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	14.6	46	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	14.4	43	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	c3ah9C	Alignment	not modelled	14.4	48	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
40	c3ah9B	Alignment	not modelled	14.4	48	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
41	c3ah9E	Alignment	not modelled	14.4	48	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
42	c3a0mF	Alignment	not modelled	13.5	48	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
43	c3fkeB	Alignment	not modelled	12.6	17	PDB header: rna binding protein Chain: B: PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of the ebola vp35 interferon inhibitory domain
44	c3ah9A	Alignment	not modelled	10.1	45	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
45	c2w0cR	Alignment	not modelled	8.2	25	PDB header: virus Chain: R: PDB Molecule: protein p3; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
46	d1sata1	Alignment	not modelled	7.1	17	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
47	c2klwA	Alignment	not modelled	6.3	37	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
48	d1f0la3	Alignment	not modelled	5.4	21	Fold: Toxins' membrane translocation domains Superfamily: Diphtheria toxin, middle domain Family: Diphtheria toxin, middle domain
49	c5juhA	Alignment	not modelled	5.1	17	PDB header: cell adhesion Chain: A: PDB Molecule: antifreeze protein; PDBTitle: crystal structure of c-terminal domain (rv) of mpafp