




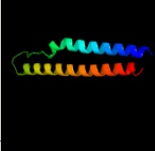


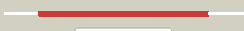


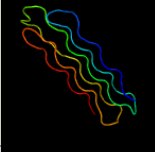

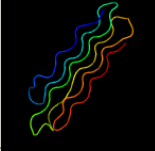

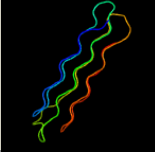

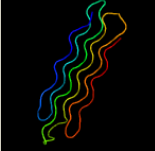




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0297_(PE_PGRS5)_361334_363109
 Date Tue Jul 23 14:50:36 BST 2019
 Unique Job ID e9220aa05836aa40

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ygvA_	 Alignment		99.9	27	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
2	c5xfsA_	 Alignment		99.9	49	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
3	c2g38A_	 Alignment		99.9	34	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	d2g38a1	 Alignment		99.9	34	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
5	c3hqvB_	 Alignment		99.8	26	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		99.8	26	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		98.3	36	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		98.3	36	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		98.3	37	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		98.3	37	PDB header: antifreeze protein Chain: B: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
11	c3boiA_	 Alignment		98.3	37	PDB header: antifreeze protein Chain: A: PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate

12	c1k7qA_	Alignment		97.6	12	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
13	c2ml3A_	Alignment		97.5	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
14	c2ml2A_	Alignment		97.1	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
15	d1k7ia1	Alignment		97.0	21	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
16	c2zj6A_	Alignment		96.9	22	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
17	d1kapp1	Alignment		96.8	19	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
18	c2agmA_	Alignment		96.6	17	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
19	c1jiwP_	Alignment		96.4	20	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
20	c1satA_	Alignment		96.4	17	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2 marcescens
21	c1om8A_	Alignment	not modelled	96.0	24	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
22	c5ctdA_	Alignment	not modelled	96.0	40	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
23	c5ctdB_	Alignment	not modelled	95.8	27	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
24	c1nayC_	Alignment	not modelled	95.8	21	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
25	c2qubG_	Alignment	not modelled	95.7	25	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
26	c5ctiC_	Alignment	not modelled	95.5	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)
27	c5cxlA_	Alignment	not modelled	94.4	23	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	91.7	23	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
29	d1sata1	Alignment	not modelled	88.3	18	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
30	c3p4gD_	Alignment	not modelled	87.6	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
31	c2klwA_	Alignment	not modelled	85.5	40	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
32	c1k6fB_	Alignment	not modelled	57.6	38	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
33	c1k6fF_	Alignment	not modelled	57.6	38	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
34	c1k6fA_	Alignment	not modelled	57.6	38	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
35	c1k6fD_	Alignment	not modelled	57.6	38	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
36	c1k6fC_	Alignment	not modelled	57.6	38	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
37	c1k6fE_	Alignment	not modelled	57.6	38	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
38	c2cuoF_	Alignment	not modelled	36.7	38	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
39	c2cuoC_	Alignment	not modelled	36.7	38	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
40	c3ah9D_	Alignment	not modelled	27.0	41	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
41	c3ah9F_	Alignment	not modelled	24.0	38	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
42	c3ah9A_	Alignment	not modelled	23.4	39	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
43	c3ah9B_	Alignment	not modelled	19.7	38	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
44	c3ah9E_	Alignment	not modelled	19.7	38	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
45	c3ah9C_	Alignment	not modelled	19.7	38	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
46	c5juhA_	Alignment	not modelled	18.4	22	PDB header: cell adhesion Chain: A: PDB Molecule: antifreeze protein; PDBTitle: crystal structure of c-terminal domain (rv) of mpafp
47	c3a0mF_	Alignment	not modelled	16.5	38	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
48	c2cuoA_	Alignment	not modelled	14.6	36	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
49	c2cuoB_	Alignment	not modelled	14.6	36	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
50	c2cuoE_	Alignment	not modelled	14.6	36	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
51	c2cuoD_	Alignment	not modelled	14.6	36	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
52	d1cvra2	Alignment	not modelled	8.4	0	Fold: Caspase-like Superfamily: Caspase-like Family: Gingipain R (RgpB), N-terminal domain
53	c4q1qA_	Alignment	not modelled	6.9	13	PDB header: cell adhesion Chain: A: PDB Molecule: adhesin/invasin tibia autotransporter; PDBTitle: crystal structure of tbc-catalyzed hyper-glycosylated tiba55-3502 fragment
54	c3lxB_	Alignment	not modelled	5.9	22	PDB header: chaperone Chain: B: PDB Molecule: nascent polypeptide-associated complex subunit alpha;

						PDBTitle: human nac dimerization domain PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: gingipain r; PDBTitle: crystal structure of the arg specific cysteine proteinase gingipain r2 (rgpb)
55	c1cvrA_	Alignment	not modelled	5.7	0	
56	c3abnA_	Alignment	not modelled	5.6	44	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 a
57	c2d3fE_	Alignment	not modelled	5.2	40	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
58	c1x1kB_	Alignment	not modelled	5.2	40	PDB header: structural protein Chain: B: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
59	c2d3fF_	Alignment	not modelled	5.2	40	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
60	c1x1kD_	Alignment	not modelled	5.2	40	PDB header: structural protein Chain: D: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
61	c2d3fD_	Alignment	not modelled	5.2	40	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4-pro-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-pro-hyp-gly-(pro-pro-gly)4
62	c1x1kA_	Alignment	not modelled	5.2	40	PDB header: structural protein Chain: A: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4
63	c1x1kC_	Alignment	not modelled	5.2	40	PDB header: structural protein Chain: C: PDB Molecule: host-guest peptide (pro-pro-gly)4-(pro-allohyp- PDBTitle: host-guest peptide (pro-pro-gly)4-(pro-allohyp-gly)-(pro-2 pro-gly)4