


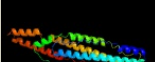

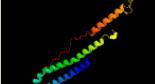

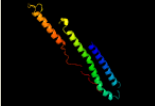

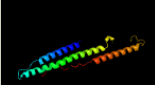





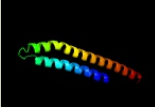



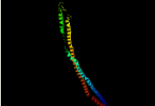

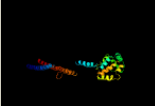
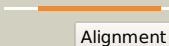

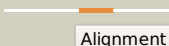


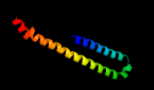


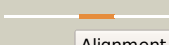

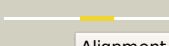

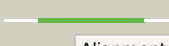
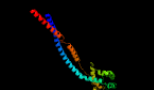

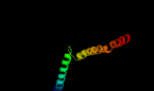

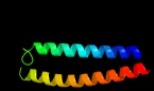
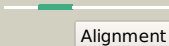
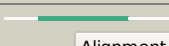
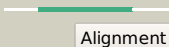
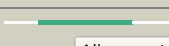
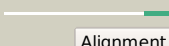
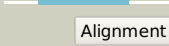
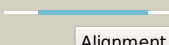
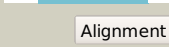



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3881c_(-)_4360721_4362103
Date	Sat Aug 10 22:05:06 BST 2019
Unique Job ID	34ccb3ee15016fac

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4wj2A_	 Alignment		100.0	27	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
2	c4xy3A_	 Alignment		100.0	98	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
3	c2g38B_	 Alignment		99.0	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	d2g38b1	 Alignment		99.0	15	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
5	c5xfsB_	 Alignment		98.9	21	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp5 from m.2 tuberculosis
6	c3gvmA_	 Alignment		95.6	17	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
7	c2vs0B_	 Alignment		95.1	15	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
8	c3zbhC_	 Alignment		94.9	17	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
9	c4iogD_	 Alignment		94.5	15	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
10	c6ogdB_	 Alignment		90.6	12	PDB header: toxin Chain: B: PDB Molecule: toxin subunit yena2; PDBTitle: cryo-em structure of yentca in its prepre state
11	c3vkhA_	 Alignment		90.5	10	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of a functional full-length dynein motor domain

12	c4cgkA_	 Alignment		88.1	7	PDB header: cell cycle Chain: A: PDB Molecule: secreted 45 kda protein; PDBTitle: crystal structure of the essential protein pcsb from streptococcus pneumoniae
13	d1wa8a1	 Alignment		83.7	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4lwsA_	 Alignment		82.5	16	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
15	c4lwsB_	 Alignment		82.3	15	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
16	d1wa8b1	 Alignment		82.0	10	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
17	c2kg7B_	 Alignment		77.8	15	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
18	c4rh7A_	 Alignment		59.3	11	PDB header: motor protein Chain: A: PDB Molecule: green fluorescent protein/cytoplasmic dynein 2 heavy chain PDBTitle: crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
19	c3ibpA_	 Alignment		58.9	13	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein mukb; PDBTitle: the crystal structure of the dimerization domain of escherichia coli2 structural maintenance of chromosomes protein mukb
20	c4i0xj_	 Alignment		55.0	13	PDB header: structural genomics, unknown function Chain: J: PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
21	d2p90a1	 Alignment	not modelled	46.4	9	Fold: Phosphorylase/hydrolase-like Superfamily: Cgl1923-like Family: Cgl1923-like
22	c5voxb_	 Alignment	not modelled	46.2	6	PDB header: hydrolase Chain: B: PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
23	c3vkgA_	 Alignment	not modelled	46.0	10	PDB header: motor protein Chain: A: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
24	c3vkgB_	 Alignment	not modelled	44.7	12	PDB header: motor protein Chain: B: PDB Molecule: dynein heavy chain, cytoplasmic; PDBTitle: x-ray structure of an mtbd truncation mutant of dynein motor domain
25	c4nl6C_	 Alignment	not modelled	41.2	11	PDB header: splicing Chain: C: PDB Molecule: survival motor neuron protein; PDBTitle: structure of the full-length form of the protein smn found in healthy2 patients
26	c6gy8B_	 Alignment	not modelled	38.4	16	PDB header: toxin Chain: B: PDB Molecule: xaxa; PDBTitle: crystal structure of xaxa from xenorhabdus nematophila
27	c5jxpA_	 Alignment	not modelled	33.5	10	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
28	c1vw2H_	 Alignment	not modelled	31.5	16	PDB header: toxin Chain: H: PDB Molecule: tcda1; PDBTitle: crystal structure of tcda1
		 Alignment				PDB header: protein binding

29	c3ojaB	Alignment	not modelled	27.8	6	Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of Irim1/apl1c complex
30	c3ghgl	Alignment	not modelled	27.5	5	PDB header: blood clotting Chain: I: PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of human fibrinogen
31	c1x1kF	Alignment	not modelled	27.4	22	PDB header: structural protein Chain: F: 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
32	c1gw4A	Alignment	not modelled	26.7	41	PDB header: high density lipoproteins Chain: A: PDB Molecule: apoa-i; PDBTitle: the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
33	c3a19E	Alignment	not modelled	24.8	25	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
34	c3a19C	Alignment	not modelled	24.8	25	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
35	c3g67A	Alignment	not modelled	24.6	11	PDB header: signaling protein Chain: A: PDB Molecule: methyl-accepting chemotaxis protein; PDBTitle: crystal structure of a soluble chemoreceptor from thermotoga2 maritima
36	c3a08B	Alignment	not modelled	22.4	25	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
37	c3a08A	Alignment	not modelled	22.4	25	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
38	d2q22a1	Alignment	not modelled	22.0	7	Fold: Ava3019-like Superfamily: Ava3019-like Family: Ava3019-like
39	c3a19D	Alignment	not modelled	21.8	21	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
40	c2d3hE	Alignment	not modelled	21.7	26	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
41	c3a19F	Alignment	not modelled	19.5	22	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
42	c3a08D	Alignment	not modelled	19.5	22	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
43	c2d3hD	Alignment	not modelled	19.5	22	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
44	c3a08E	Alignment	not modelled	19.4	27	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
45	c3ls1A	Alignment	not modelled	19.1	12	PDB header: photosynthesis Chain: A: PDB Molecule: ssl1638 protein; PDBTitle: crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
46	c1bg1A	Alignment	not modelled	18.6	9	PDB header: transcription/dna Chain: A: PDB Molecule: protein (transcription factor stat3b); PDBTitle: transcription factor stat3b/dna complex
47	d1k78a1	Alignment	not modelled	17.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
48	c2d3hA	Alignment	not modelled	16.8	23	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
49	c3a19B	Alignment	not modelled	16.8	23	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
50	c2d3hB	Alignment	not modelled	16.8	23	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
51	c2cuoC	Alignment	not modelled	16.5	22	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
52	c2cuoF	Alignment	not modelled	16.5	22	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
53	c1y4cA	Alignment	not modelled	16.5	11	PDB header: de novo protein Chain: A: PDB Molecule: maltose binding protein fused with designed PDBTitle: designed helical protein fusion mbp

54	d2gtsa1	Alignment	not modelled	15.5	12	Fold: Ferritin-like Superfamily: HP0062-like Family: HP0062-like
55	c3n4xB	Alignment	not modelled	15.3	17	PDB header: replication Chain: B: PDB Molecule: monopolin complex subunit csm1; PDBTitle: structure of csm1 full-length
56	c4wvmB	Alignment	not modelled	15.3	10	PDB header: toxin Chain: B: PDB Molecule: stonustoxin subunit beta; PDBTitle: stonustoxin structure
57	c3a19A	Alignment	not modelled	14.0	23	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4_h monoclinic, twinned crystal
58	c2d3hC	Alignment	not modelled	14.0	23	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
59	c5dolB	Alignment	not modelled	13.8	12	PDB header: replication Chain: B: PDB Molecule: initiation-control protein yaba; PDBTitle: crystal structure of yaba amino-terminal domain from bacillus subtilis
60	c5gasN	Alignment	not modelled	13.5	9	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
61	c3a7oB	Alignment	not modelled	13.2	18	PDB header: protein transport Chain: B: PDB Molecule: autophagy protein 16; PDBTitle: the crystal structure of the coiled-coil domain of2 saccharomyces cerevisiae atg16
62	c2w6bA	Alignment	not modelled	13.2	21	PDB header: signaling protein Chain: A: PDB Molecule: rho guanine nucleotide exchange factor 7; PDBTitle: crystal structure of the trimeric beta-pix coiled-coil2 domain
63	c1degF	Alignment	not modelled	13.1	7	PDB header: blood clotting Chain: F: PDB Molecule: fibrinogen (gamma chain); PDBTitle: the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
64	c3ah9C	Alignment	not modelled	12.9	24	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
65	c3ah9B	Alignment	not modelled	12.9	24	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
66	c3ah9E	Alignment	not modelled	12.9	24	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
67	c2d3hF	Alignment	not modelled	12.5	27	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptides (pro-pro-gly)4-hyp-hyp- PDBTitle: crystal structures of collagen model peptides (pro-pro-gly)2 4-hyp-hyp-gly-(pro-pro-gly)4
68	c3tnuA	Alignment	not modelled	11.0	3	PDB header: cytosolic protein Chain: A: PDB Molecule: keratin, type i cytoskeletal 14; PDBTitle: heterocomplex of coil 2b domains of human intermediate filament2 proteins, keratin 5 (krt5) and keratin 14 (krt14)
69	c1uc5M	Alignment	not modelled	10.9	27	PDB header: lyase Chain: M: PDB Molecule: diol dehydrase gamma subunit; PDBTitle: structure of diol dehydratase complexed with (r)-1,2-2 propanediol
70	d1eexg	Alignment	not modelled	10.9	27	Fold: Open three-helical up-and-down bundle Superfamily: Diol dehydratase, gamma subunit Family: Diol dehydratase, gamma subunit
71	d1iwpg	Alignment	not modelled	10.9	20	Fold: Open three-helical up-and-down bundle Superfamily: Diol dehydratase, gamma subunit Family: Diol dehydratase, gamma subunit
72	c5jxfA	Alignment	not modelled	10.7	6	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDBTitle: crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
73	c2cuoD	Alignment	not modelled	10.5	23	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
74	c2cuoB	Alignment	not modelled	10.5	23	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
75	c2cuoE	Alignment	not modelled	10.5	23	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
76	c2cuoA	Alignment	not modelled	10.5	23	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
77	c3a08F	Alignment	not modelled	10.4	29	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
78	c5eofB	Alignment	not modelled	10.2	6	PDB header: protein binding/transferase Chain: B: PDB Molecule: optineurin; PDBTitle: crystal structure of optn ntd and tbk1 ctd complex
79	c3cwgA	Alignment	not modelled	10.0	13	PDB header: transcription Chain: A: PDB Molecule: signal transducer and activator of transcription PDBTitle: unphosphorylated mouse stat3 core fragment
						Fold: DNA/RNA-binding 3-helical bundle

80	d6paxa1	Alignment	not modelled	9.5	15	Superfamily: Homeodomain-like Family: Paired domain
81	c5ew5C_	Alignment	not modelled	9.3	11	PDB header: hydrolase Chain: C: PDB Molecule: colicin-e9; PDBTitle: crystal structure of colicin e9 in complex with its immunity protein2 im9
82	c6g7oA_	Alignment	not modelled	8.9	12	PDB header: membrane protein Chain: A: PDB Molecule: alkaline ceramidase 3,soluble cytochrome b562; PDBTitle: crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 angstrom resolution
83	c4hwfB_	Alignment	not modelled	8.7	16	PDB header: apoptosis Chain: B: PDB Molecule: bag family molecular chaperone regulator 3; PDBTitle: crystal structure of atbag3
84	c1ny9A_	Alignment	not modelled	8.7	19	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator tipa-s; PDBTitle: antibiotic binding domain of a tipa-class multidrug2 resistance transcriptional regulator
85	d1ny9a_	Alignment	not modelled	8.7	19	Fold: Antibiotic binding domain of TipA-like multidrug resistance regulators Superfamily: Antibiotic binding domain of TipA-like multidrug resistance regulators Family: Antibiotic binding domain of TipA-like multidrug resistance regulators
86	c1yuzB_	Alignment	not modelled	8.6	10	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
87	c3a08C_	Alignment	not modelled	8.5	24	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-oog-(ppg)4, monoclinic, twinned crystal
88	c3a1hF_	Alignment	not modelled	8.3	18	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure analysis of the collagen-like peptide, (ppg)4-otg-2 (ppg)4
89	c3ah9F_	Alignment	not modelled	8.1	21	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
90	c6o7ua_	Alignment	not modelled	8.0	10	PDB header: membrane protein Chain: A: PDB Molecule: PDBTitle: saccharomyces cerevisiae v-atpase stv1-vo
91	c5xuaB_	Alignment	not modelled	7.6	7	PDB header: signaling protein Chain: B: PDB Molecule: methyl-accepting chemotaxis sensory transducer; PDBTitle: the ligand-free dimer of chemoreceptor mcp2201 ligand binding domain
92	c1ei3C_	Alignment	not modelled	7.4	10	PDB header: blood clotting Chain: C: PDB Molecule: fibrinogen; PDBTitle: crystal structure of native chicken fibrinogen
93	d2oeqa1	Alignment	not modelled	7.3	13	Fold: YheA-like Superfamily: YheA/YmcA-like Family: YheA-like
94	c6cfzC_	Alignment	not modelled	7.2	17	PDB header: nuclear protein Chain: C: PDB Molecule: dad2; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
95	c3lnrA_	Alignment	not modelled	7.2	11	PDB header: signaling protein Chain: A: PDB Molecule: aerotaxis transducer aer2; PDBTitle: crystal structure of poly-hamp domains from the p. aeruginosa soluble2 receptor aer2
96	c1x1kD_	Alignment	not modelled	7.1	31	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
97	c1x1kA_	Alignment	not modelled	7.1	31	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
98	c2d3fD_	Alignment	not modelled	7.1	31	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
99	c2d3fE_	Alignment	not modelled	7.1	31	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