






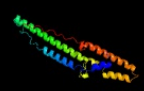

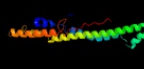



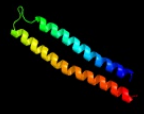

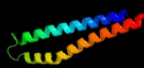





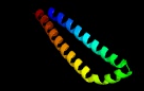


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1918c_(PPE35)_2167656_2170619
Date	Fri Aug 2 13:30:53 BST 2019
Unique Job ID	79273149c191ed22

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	49	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38B_	 Alignment		100.0	30	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	30	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	16	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		97.5	15	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.2	8	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	 Alignment		97.1	14	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
8	c3gvmA_	 Alignment		96.9	11	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	c3zbhC_	 Alignment		96.7	14	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		96.4	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsA_	 Alignment		85.8	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsB_	Alignment		85.4	8	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		84.7	18	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	d1ui5a2	Alignment		73.9	28	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
15	c2kg7B_	Alignment		69.9	19	PDB header: unknown function Chain: B; PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	c4i0xA_	Alignment		67.0	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	c3jywF_	Alignment		47.8	39	PDB header: ribosome Chain: F; PDB Molecule: 60s ribosomal protein l7(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
18	c2vsnB_	Alignment		44.5	11	PDB header: transferase Chain: B; PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of3 intracellular glycosylation
19	c3pe3D_	Alignment		42.8	14	PDB header: transferase Chain: D; PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
20	c5djsA_	Alignment		40.6	18	PDB header: transferase Chain: A; PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcna2 transferase mutant - k341m
21	c4i0xJ_	Alignment	not modelled	34.8	18	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
22	c1bkvA_	Alignment	not modelled	23.4	50	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
23	c5frgA_	Alignment	not modelled	22.5	63	PDB header: protein binding Chain: A; PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
24	c1bkvB_	Alignment	not modelled	22.0	50	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
25	c1bkvC_	Alignment	not modelled	22.0	50	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
26	d3cx5d1	Alignment	not modelled	21.1	28	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
27	d1ppid1	Alignment	not modelled	20.9	25	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
28	c2kg7A_	Alignment	not modelled	18.9	38	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein esxg (pe family protein); PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
						Fold: Aminoacid dehydrogenase-like, N-terminal domain

29	d1luaa2	Alignment	not modelled	16.9	27	Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
30	c4b3yB	Alignment	not modelled	15.1	14	PDB header: transferase Chain: B: PDB Molecule: fatty acid synthase; PDBTitle: cryo-em structure of the mycobacterial fatty acid synthase
31	d1hi9a	Alignment	not modelled	14.5	25	Fold: Dipeptide transport protein Superfamily: Dipeptide transport protein Family: Dipeptide transport protein
32	c2ke4A	Alignment	not modelled	14.5	63	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
33	c3ahrA	Alignment	not modelled	13.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: ero1-like protein alpha; PDBTitle: inactive human ero1
34	d2a15a1	Alignment	not modelled	12.7	22	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
35	c3cwbQ	Alignment	not modelled	12.5	25	PDB header: oxidoreductase Chain: Q: PDB Molecule: mitochondrial cytochrome c1, heme protein; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
36	c3h6pB	Alignment	not modelled	12.0	34	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
37	c4yk2B	Alignment	not modelled	11.3	24	PDB header: protein binding Chain: B: PDB Molecule: bartonella effector protein (bep) substrate of virb t4ss; PDBTitle: crystal structure of the bid domain of bep9 from bartonella2 clarridgeiae
38	c1zrtD	Alignment	not modelled	11.3	44	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
39	d3cnxa1	Alignment	not modelled	11.1	16	Fold: Cystatin-like Superfamily: NTF2-like Family: SAV4671-like
40	c2kwuA	Alignment	not modelled	10.9	31	PDB header: protein binding/signaling protein Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
41	d1rp4a	Alignment	not modelled	10.9	23	Fold: ERO1-like Superfamily: ERO1-like Family: ERO1-like
42	c3fpjA	Alignment	not modelled	10.6	11	PDB header: biosynthetic protein, transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of e81q mutant of mtas in complex with s-2 adenosylmethionine
43	c5ucOB	Alignment	not modelled	10.5	80	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein cog5400; PDBTitle: crystal structure of beta-barrel-like, uncharacterized protein of2 cog5400 from brucella abortus
44	c4rqoB	Alignment	not modelled	10.5	32	PDB header: lyase Chain: B: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure of l-serine dehydratase from legionella pneumophila
45	c5ddwD	Alignment	not modelled	10.3	20	PDB header: transferase Chain: D: PDB Molecule: crmg; PDBTitle: crystal structure of aminotransferase crmg from actinoalloteichus sp.2 wh1-2216-6 in complex with the pmp external aldimine adduct with3 caerulomycin m
46	c2lyyB	Alignment	not modelled	10.2	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein nb7890a from shewanella sp
47	c1p84D	Alignment	not modelled	10.2	31	PDB header: oxidoreductase Chain: D: PDB Molecule: cytochrome c1, heme protein; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
48	c5lzkB	Alignment	not modelled	10.0	4	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
49	c2pheC	Alignment	not modelled	9.7	31	PDB header: transcription Chain: C: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to pc4
50	c2l5bA	Alignment	not modelled	9.5	56	PDB header: apoptosis Chain: A: PDB Molecule: activator of apoptosis harakiri; PDBTitle: solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles
51	c5jn6A	Alignment	not modelled	9.5	56	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the nmr solution structure of rpa3313
52	c1fqvK	Alignment	not modelled	9.2	30	PDB header: ligase Chain: K: PDB Molecule: skp2; PDBTitle: insights into scf ubiquitin ligases from the structure of2 the skp1-skp2 complex
53	c5ig0A	Alignment	not modelled	8.7	15	PDB header: transferase Chain: A: PDB Molecule: camk/camk2 protein kinase; PDBTitle: crystal structure of s. rosetta camkii hub
54	c3bkhA	Alignment	not modelled	8.4	18	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144 PDB header: oxidoreductase

55	c4y9iA_	Alignment	not modelled	8.3	33	Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
56	d1g03a_	Alignment	not modelled	8.2	20	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
57	c4k8nF_	Alignment	not modelled	8.2	21	PDB header: lipid transport Chain: F: PDB Molecule: glycolipid transfer protein domain-containing protein 1; PDBTitle: crystal structure of human ceramide-1-phosphate transfer protein2 (cptp) in complex with 18:1 ceramide-1-phosphate (18:1-c1p)
58	c3b5oA_	Alignment	not modelled	7.8	38	PDB header: oxidoreductase Chain: A: PDB Molecule: cadd-like protein of unknown function; PDBTitle: crystal structure of a cadd-like protein of unknown function2 (npun_f6505) from nostoc punctiforme pcc 73102 at 1.35 a resolution
59	c3h96B_	Alignment	not modelled	7.7	0	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
60	d1swxa_	Alignment	not modelled	7.6	28	Fold: Glycolipid transfer protein, GLTP Superfamily: Glycolipid transfer protein, GLTP Family: Glycolipid transfer protein, GLTP
61	d1xkna_	Alignment	not modelled	7.6	17	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
62	d1byra_	Alignment	not modelled	7.6	22	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Nuclease
63	c3j21Y_	Alignment	not modelled	7.6	31	PDB header: ribosome Chain: Y: PDB Molecule: 50s ribosomal protein l30p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
64	c2i3fA_	Alignment	not modelled	7.5	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: glycolipid transfer-like protein; PDBTitle: crystal structure of a glycolipid transfer-like protein from galdieria2 sulphuraria
65	c4urjA_	Alignment	not modelled	7.5	13	PDB header: unknown function Chain: A: PDB Molecule: protein fam83a; PDBTitle: crystal structure of human bj-tsa-9
66	c4i6jB_	Alignment	not modelled	7.5	22	PDB header: transcription Chain: B: PDB Molecule: f-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
67	c5kdiA_	Alignment	not modelled	7.4	12	PDB header: lipid transport Chain: A: PDB Molecule: pleckstrin homology domain-containing family a member 8; PDBTitle: how fapp2 selects simple glycosphingolipids using the gltp-fold
68	c3dfuB_	Alignment	not modelled	7.2	15	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized protein from 6-phosphogluconate PDBTitle: crystal structure of a putative rossmann-like dehydrogenase (cgl2689)2 from corynebacterium glutamicum at 2.07 a resolution
69	c5i4rA_	Alignment	not modelled	7.1	43	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
70	c3lhoA_	Alignment	not modelled	7.1	33	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative hydrolase (yp_751971.1) from shewanella2 frigidimarina ncimb 400 at 1.80 a resolution
71	c3j3bF_	Alignment	not modelled	7.0	31	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the human 60s ribosomal proteins
72	c4lrV_L_	Alignment	not modelled	6.9	40	PDB header: dna binding protein Chain: L: PDB Molecule: dna sulfur modification protein dnde; PDBTitle: crystal structure of dnde from escherichia coli b7a involved in dna2 phosphorothioation modification
73	c4fe1M_	Alignment	not modelled	6.9	50	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem i reaction center subunit xii; PDBTitle: improving the accuracy of macromolecular structure refinement at 7 a2 resolution
74	d1jb0m_	Alignment	not modelled	6.9	50	Fold: Single transmembrane helix Superfamily: Subunit XII of photosystem I reaction centre, PsaM Family: Subunit XII of photosystem I reaction centre, PsaM
75	c1jb0M_	Alignment	not modelled	6.9	50	PDB header: photosynthesis Chain: M: PDB Molecule: photosystem 1 reaction centre subunit xii; PDBTitle: crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
76	c3j39F_	Alignment	not modelled	6.8	31	PDB header: ribosome Chain: F: PDB Molecule: 60s ribosomal protein l7; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
77	c2lkqA_	Alignment	not modelled	6.8	56	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
78	c6ajrA_	Alignment	not modelled	6.8	18	PDB header: dna binding protein Chain: A: PDB Molecule: uracil dna glycosylase superfamily protein; PDBTitle: complex form of uracil dna glycosylase x and uracil
79	c3i5tB_	Alignment	not modelled	6.7	17	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase prk07036 from

						rhodobacter2 sphaeroides kd131
80	c2mtyA_	Alignment	not modelled	6.7	29	PDB header: peptide binding Chain: A: PDB Molecule: starp antigen; PDBTitle: 3d structure determination of starp peptides implicated in p.2 falciparum invasion of hepatic cells
81	c2k2uB_	Alignment	not modelled	6.7	33	PDB header: transcription Chain: B: PDB Molecule: alpha trans-inducing protein; PDBTitle: nmr structure of the complex between tfb1 subunit of tfiih2 and the activation domain of vp16
82	c5kdmD_	Alignment	not modelled	6.6	36	PDB header: chaperone / dna binding protein Chain: D: PDB Molecule: major tegument protein; PDBTitle: crystal structure of ebv tegument protein bnrf1 in complex with2 histone chaperone daxx and histones h3.3-h4
83	d1c52a_	Alignment	not modelled	6.5	22	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
84	c1fs1A_	Alignment	not modelled	6.5	38	PDB header: ligase Chain: A: PDB Molecule: cyclin a/cdk2-associated p19; PDBTitle: insights into scf ubiquitin ligases from the structure of2 the skp1-skp2 complex
85	d1fs1a1	Alignment	not modelled	6.5	38	Fold: F-box domain Superfamily: F-box domain Family: F-box domain
86	c6ijoH_	Alignment	not modelled	6.5	14	PDB header: photosynthesis Chain: H: PDB Molecule: psah; PDBTitle: photosystem i of chlamydomonas reinhardtii
87	c4p3gC_	Alignment	not modelled	6.4	33	PDB header: rna binding protein Chain: C: PDB Molecule: signal recognition particle subunit srp68; PDBTitle: structure of the srp68-rbd from chaetomium thermophilum
88	c2iu1A_	Alignment	not modelled	6.3	28	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
89	c4jzaB_	Alignment	not modelled	6.3	53	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a legionella phosphoinositide phosphatase:2 insights into lipid metabolism in pathogen host interaction
90	c3r5zB_	Alignment	not modelled	6.3	17	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
91	d2g38a1	Alignment	not modelled	6.2	13	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
92	c2g38A_	Alignment	not modelled	6.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
93	c1t3mA_	Alignment	not modelled	6.0	9	PDB header: hydrolase Chain: A: PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
94	c3q3hA_	Alignment	not modelled	5.9	14	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
95	c4nl6C_	Alignment	not modelled	5.8	57	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
96	d2z0da1	Alignment	not modelled	5.8	37	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Autophagin-like
97	c3e4pB_	Alignment	not modelled	5.8	19	PDB header: transferase Chain: B: PDB Molecule: c4-dicarboxylate transport sensor protein dctb; PDBTitle: crystal structure of malonate occupied dctb
98	c2m0qA_	Alignment	not modelled	5.8	53	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 2; PDBTitle: solution nmr analysis of intact kcne2 in detergent micelles2 demonstrate a straight transmembrane helix
99	c2ch0A_	Alignment	not modelled	5.8	60	PDB header: nuclear protein Chain: A: PDB Molecule: inner nuclear membrane protein man1; PDBTitle: solution structure of the human man1 c-terminal domain (residues 655-2 775)