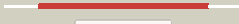
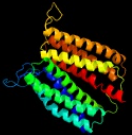
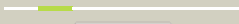
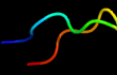



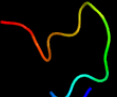







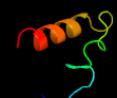







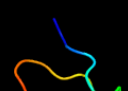







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1456c_(-)_1641499_1642431
Date	Fri Aug 2 13:30:03 BST 2019
Unique Job ID	ed8b55a665157508

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6iedA_	 Alignment		100.0	16	PDB header: membrane protein Chain: A: PDB Molecule: heme a synthase; PDBTitle: crystal structure of heme a synthase from bacillus subtilis
2	c1yp8A_	 Alignment		66.9	33	PDB header: cell cycle Chain: A: PDB Molecule: tricyclon a; PDBTitle: solution structure of the cyclotide tricyclon a
3	c5oc0A_	 Alignment		65.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: cytochrome b561; PDBTitle: structure of e. coli superoxide oxidase
4	c2wanA_	 Alignment		55.7	25	PDB header: hydrolase Chain: A: PDB Molecule: pullulanase; PDBTitle: pullulanase from bacillus acidopullulyticus
5	d1nekd_	 Alignment		55.1	16	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD)
6	c1wqbA_	 Alignment		51.7	50	PDB header: toxin Chain: A: PDB Molecule: aptotoxin vii; PDBTitle: three-dimensional solution structure of aptotoxin vii, from2 the venom of a trap-door spider
7	c3ghgD_	 Alignment		47.4	27	PDB header: blood clotting Chain: D: PDB Molecule: fibrinogen alpha chain; PDBTitle: crystal structure of human fibrinogen
8	c2cseW_	 Alignment		45.3	30	PDB header: virus Chain: W: PDB Molecule: major core protein lambda 1; PDBTitle: features of reovirus outer-capsid protein mu1 revealed by2 electron and image reconstruction of the virion at 7.0-a3 resolution
9	c1k48A_	 Alignment		43.9	56	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
10	c1jzA_	 Alignment		43.7	56	PDB header: plant protein Chain: A: PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
11	c3k1qC_	 Alignment		39.3	19	PDB header: PDB COMPND:

12	c3k1qB_	Alignment		39.0	19	PDB header: PDB COMPND:
13	c6fo2R_	Alignment		38.3	46	PDB header: membrane protein Chain: R: PDB Molecule: cytochrome b-c1 complex subunit rieske, mitochondrial; PDBTitle: cryoem structure of bovine cytochrome bc1 with no ligand bound
14	d1n1ua_	Alignment		35.4	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
15	c1n1uA_	Alignment		35.4	33	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
16	c2kukA_	Alignment		32.4	31	PDB header: antiviral protein Chain: A: PDB Molecule: leaf cyclotide 2; PDBTitle: solution structure of vhl-2
17	d1ma3a_	Alignment		32.1	13	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
18	c2a45J_	Alignment		29.2	27	PDB header: hydrolase/hydrolase inhibitor Chain: J: PDB Molecule: fibrinogen alpha chain; PDBTitle: crystal structure of the complex between thrombin and the central "e"2 region of fibrin
19	c4ttnA_	Alignment		28.1	63	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1
20	c3cwbC_	Alignment		27.9	16	PDB header: oxidoreductase Chain: C: PDB Molecule: cytochrome b; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
21	c2khaB_	Alignment	not modelled	27.9	63	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of linear kalata b1 (loop 6)
22	c4ttmA_	Alignment	not modelled	27.9	63	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: racemic structure of kalata b1 (kb1)
23	c1m1jA_	Alignment	not modelled	27.7	27	PDB header: blood clotting Chain: A: PDB Molecule: fibrinogen alpha subunit; PDBTitle: crystal structure of native chicken fibrinogen with two different2 bound ligands
24	c4ttoA_	Alignment	not modelled	27.3	63	PDB header: plant protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [v25a] kalata b1
25	c2f2iA_	Alignment	not modelled	27.1	29	PDB header: antimicrobial protein Chain: A: PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
26	d1pt4a_	Alignment	not modelled	26.8	43	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
27	d1ppic2	Alignment	not modelled	24.5	14	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
28	c6dhrA_	Alignment	not modelled	24.4	40	PDB header: plant protein Chain: A: PDB Molecule: rivi3; PDBTitle: nmr solution structure of rivi3
29	d2e74a1	Alignment	not modelled	24.3	14	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes

29	v2e79a1	Alignment	not modelled	24.3	14	Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
30	c1nb1A	Alignment	not modelled	23.8	36	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
31	d1nb1a	Alignment	not modelled	23.8	36	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
32	c1orxA	Alignment	not modelled	23.7	56	PDB header: antibiotic Chain: A: PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
33	c3e4hA	Alignment	not modelled	23.5	31	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: crystal structure of the cyclotide varv f
34	d1tafa	Alignment	not modelled	23.4	33	Fold: Histone-fold Superfamily: Histone-fold Family: TBP-associated factors, TAFs
35	d1efnb	Alignment	not modelled	23.4	50	Fold: Regulatory factor Nef Superfamily: Regulatory factor Nef Family: Regulatory factor Nef
36	c3ik5A	Alignment	not modelled	23.2	50	PDB header: viral protein/signaling protein Chain: A: PDB Molecule: protein nef; PDBTitle: sivmac239 nef in complex with tcr zeta itam 1 polypeptide (a63-r80)
37	c2xi1A	Alignment	not modelled	23.1	50	PDB header: viral protein Chain: A: PDB Molecule: nef; PDBTitle: crystal structure of the hiv-1 nef sequenced from a patient's sample
38	c4g7wB	Alignment	not modelled	23.0	57	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the n-terminal domain of the minor coat protein2 piiii from ctxphi
39	c2k7gA	Alignment	not modelled	22.8	50	PDB header: plant protein Chain: A: PDB Molecule: varv peptide f; PDBTitle: solution structure of varv f
40	d1mjta	Alignment	not modelled	22.7	18	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
41	c4g7xA	Alignment	not modelled	22.7	57	PDB header: protein binding/protein binding Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a complex between the ctxphi piiii n-terminal2 domain and the vibrio cholerae tola c-terminal domain
42	c3tb8A	Alignment	not modelled	21.6	50	PDB header: apoptosis Chain: A: PDB Molecule: protein nef; PDBTitle: crystal structure of full-length myristoylated hiv-1 nef
43	c3rbbA	Alignment	not modelled	21.2	50	PDB header: viral protein, protein binding Chain: A: PDB Molecule: protein nef; PDBTitle: hiv-1 nef protein in complex with engineered hck sh3 domain
44	d1umrc	Alignment	not modelled	20.9	57	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
45	c2eg9B	Alignment	not modelled	20.5	44	PDB header: hydrolase Chain: B: PDB Molecule: adp-ribosyl cyclase 1; PDBTitle: crystal structure of the truncated extracellular domain of2 mouse cd38
46	d1om4a	Alignment	not modelled	20.1	44	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
47	c1fooA	Alignment	not modelled	20.1	44	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase; PDBTitle: bovine endothelial nitric oxide synthase heme domain complexed with l-2 arg and no(h4b-free)
48	c2qjkM	Alignment	not modelled	19.8	18	PDB header: electron transport Chain: M: PDB Molecule: cytochrome b; PDBTitle: crystal structure analysis of mutant rhodobacter2 sphaeroides bc1 with stigmatellin and antimycin
49	d1q90b	Alignment	not modelled	19.7	13	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
50	d2nefa	Alignment	not modelled	19.1	50	Fold: Regulatory factor Nef Superfamily: Regulatory factor Nef Family: Regulatory factor Nef
51	d3e7ma1	Alignment	not modelled	19.0	44	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
52	c2mn1A	Alignment	not modelled	18.8	50	PDB header: unknown function Chain: A: PDB Molecule: kalata b1[w23ww]; PDBTitle: solution structure of kalata b1[w23ww]
53	c3aygA	Alignment	not modelled	18.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric oxide reductase; PDBTitle: crystal structure of nitric oxide reductase complex with hqno
54	d3e7ga1	Alignment	not modelled	18.4	48	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
55	c2gj0A	Alignment	not modelled	18.3	40	PDB header: plant protein Chain: A: PDB Molecule: cycloviolacin o14; PDBTitle: cycloviolacin o14
						Fold: Nitric oxide (NO) synthase oxygenase domain

56	d1m7va_	Alignment	not modelled	18.2	19	Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
57	c2lamA_	Alignment	not modelled	16.8	44	PDB header: antiviral protein Chain: A: PDB Molecule: cyclotide cter m; PDBTitle: three-dimensional structure of the cyclotide cter m
58	c3cx5N_	Alignment	not modelled	16.3	12	PDB header: oxidoreductase Chain: N: PDB Molecule: cytochrome b; PDBTitle: structure of complex iii with bound cytochrome c in reduced state and2 definition of a minimal core interface for electron transfer.
59	c2flqA_	Alignment	not modelled	16.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric oxide synthase; PDBTitle: crystal structure of nitric oxide synthase from geobacillus2 stearothermophilus (atcc 12980) complexed with l-arginine
60	d1kqfc_	Alignment	not modelled	16.1	10	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Formate dehydrogenase N, cytochrome (gamma) subunit
61	d1m9ma_	Alignment	not modelled	14.9	46	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
62	c1q01A_	Alignment	not modelled	14.1	71	PDB header: blood clotting Chain: A: PDB Molecule: lebetin 2 isoform alpha; PDBTitle: lebetin peptides, a new class of potent aggregation2 inhibitors
63	c3sbcG_	Alignment	not modelled	13.8	36	PDB header: oxidoreductase Chain: G: PDB Molecule: peroxiredoxin tsa1; PDBTitle: crystal structure of saccharomyces cerevisiae tsa1c47s mutant protein
64	c6cfzH_	Alignment	not modelled	13.3	40	PDB header: nuclear protein Chain: H: PDB Molecule: dam1; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
65	c6av8A_	Alignment	not modelled	13.3	64	PDB header: toxin Chain: A: PDB Molecule: u5-theraphotoxin-hs1b 1; PDBTitle: exploring cystine dense peptide space to open a unique molecular2 toolbox
66	c2lurA_	Alignment	not modelled	13.3	63	PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
67	d1q2oa_	Alignment	not modelled	13.2	46	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
68	d1atxa_	Alignment	not modelled	13.1	36	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
69	c2kncA_	Alignment	not modelled	13.1	18	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: platelet integrin alfaiiib-beta3 transmembrane-cytoplasmic2 heterocomplex
70	c3j6vU_	Alignment	not modelled	12.7	33	PDB header: ribosome Chain: U: PDB Molecule: 28s ribosomal protein s21, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
71	c2nx6A_	Alignment	not modelled	12.5	36	PDB header: structural protein Chain: A: PDB Molecule: nematocyst outer wall antigen; PDBTitle: structure of nowa cysteine rich domain 6
72	c5ir6A_	Alignment	not modelled	12.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: bd-type quinol oxidase subunit i; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
73	c6elhA_	Alignment	not modelled	12.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide reductase; PDBTitle: low resolution structure of neisseria meningitidis qnor
74	d1uhua_	Alignment	not modelled	12.3	28	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: MMLV matrix protein-like
75	c2jwmA_	Alignment	not modelled	12.3	36	PDB header: plant protein Chain: A: PDB Molecule: kalata-b7; PDBTitle: nmr spatial srtructure of ternary complex kalata b7/mn2+/dpc2 micelle
76	c1yk1E_	Alignment	not modelled	12.2	63	PDB header: hormone/growth factor receptor Chain: E: PDB Molecule: natriuretic peptides b; PDBTitle: structure of natriuretic peptide receptor-c complexed with brain2 natriuretic peptide
77	c2aapA_	Alignment	not modelled	11.9	64	PDB header: toxin Chain: A: PDB Molecule: jingzhaotoxin-vii; PDBTitle: solution structure of jingzhaotoxin-vii
78	c6g1cV_	Alignment	not modelled	11.7	25	PDB header: antitoxin Chain: V: PDB Molecule: antitoxin hicb; PDBTitle: crystal structure of the n-terminal domain of burkholderia2 pseudomallei antitoxin hicb
79	d1lpba2	Alignment	not modelled	11.5	33	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Colipase-like Family: Colipase-like
80	c6hqaF_	Alignment	not modelled	11.4	17	PDB header: transcription Chain: F: PDB Molecule: subunit (17 kda) of tfiid and saga complexes, involved in PDBTitle: molecular structure of promoter-bound yeast tfiid
81	c6mzIM_	Alignment	not modelled	11.4	29	PDB header: transcription Chain: M: PDB Molecule: transcription initiation factor tfiid subunit 9, taf9; PDBTitle: human tfiid canonical state
						Fold: Crambin-like

82	d1bhpa_	Alignment	not modelled	11.3	60	Superfamily: Crambin-like Family: Crambin-like
83	d1mn8a_	Alignment	not modelled	11.1	22	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: MMLV matrix protein-like
84	d1xpa2	Alignment	not modelled	10.9	29	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain
85	d1hhna_	Alignment	not modelled	10.9	13	Fold: P-domain of calnexin/calreticulin Superfamily: P-domain of calnexin/calreticulin Family: P-domain of calnexin/calreticulin
86	c2m9oA_	Alignment	not modelled	10.7	63	PDB header: plant protein Chain: A; PDB Molecule: kalata-b7; PDBTitle: solution structure of kalata b7
87	c1zuvA_	Alignment	not modelled	10.3	45	PDB header: antimicrobial protein Chain: A; PDB Molecule: amaranthus caudatus antimicrobial peptide 2; PDBTitle: 24 nmr structures of acamp2-like peptide with phenylalanine2 18 mutated to tryptophan
88	d1bcc3	Alignment	not modelled	10.1	18	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
89	c1h6wA_	Alignment	not modelled	9.8	24	PDB header: structural protein Chain: A; PDB Molecule: bacteriophage t4 short tail fibre; PDBTitle: crystal structure of a heat- and protease-stable fragment of the2 bacteriophage t4 short fibre
90	c5czoC_	Alignment	not modelled	9.7	7	PDB header: transferase Chain: C; PDB Molecule: monopolin complex subunit mam1; PDBTitle: structure of s. cerevisiae hrr25:mam1 complex, form 2
91	c2mvhA_	Alignment	not modelled	9.2	44	PDB header: protein binding Chain: A; PDB Molecule: stage v sporulation protein m; PDBTitle: structure determination of stage v sporulation protein m (spovm)
92	d1v4lb_	Alignment	not modelled	8.8	57	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
93	c5d5nA_	Alignment	not modelled	8.7	30	PDB header: viral protein Chain: A; PDB Molecule: virion egress protein ul34 homolog; PDBTitle: crystal structure of the human cytomegalovirus pul50-pul53 complex
94	c5hvcC_	Alignment	not modelled	8.7	15	PDB header: transferase Chain: C; PDB Molecule: small membrane a-kinase anchor protein; PDBTitle: crystal structure of smakap akb domain bound ria dimerization/docking2 (d/d) complex at 2.0 a resolution
95	d1c3ab_	Alignment	not modelled	8.5	57	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: C-type lectin domain
96	c2l8sA_	Alignment	not modelled	8.2	10	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
97	d2ef1a1	Alignment	not modelled	7.5	36	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: ADP ribosyl cyclase-like
98	c2mvjA_	Alignment	not modelled	7.4	44	PDB header: protein binding Chain: A; PDB Molecule: stage v sporulation protein m; PDBTitle: structure of stage v sporulation protein m (spovm) p9a mutant
99	c1yk0E_	Alignment	not modelled	7.4	83	PDB header: hormone/growth factor receptor Chain: E; PDB Molecule: atrial natriuretic factor; PDBTitle: structure of natriuretic peptide receptor-c complexed with atrial2 natriuretic peptide