


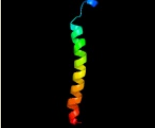

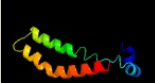



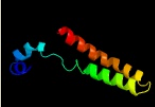

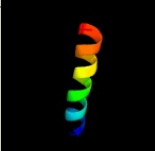

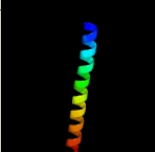

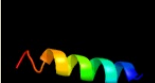



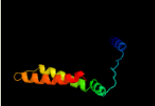








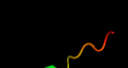

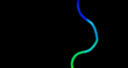


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2206 (-) _2470630_2471340
Date	Mon Aug 5 13:25:33 BST 2019
Unique Job ID	17c62bd4601a06db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6adqP_	 Alignment		62.8	14	PDB header: electron transport Chain: P; PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
2	c2mfrA_	 Alignment		52.6	16	PDB header: transferase Chain: A; PDB Molecule: insulin receptor; PDBTitle: solution structure of the transmembrane domain of the insulin receptor2 in micelles
3	c4hkrB_	 Alignment		34.9	18	PDB header: transport protein Chain: B; PDB Molecule: calcium release-activated calcium channel protein 1; PDBTitle: calcium release-activated calcium (crac) channel orai
4	c3k07A_	 Alignment		31.7	20	PDB header: transport protein Chain: A; PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa
5	c4hkrA_	 Alignment		30.9	18	PDB header: transport protein Chain: A; PDB Molecule: calcium release-activated calcium channel protein 1; PDBTitle: calcium release-activated calcium (crac) channel orai
6	c2mg2A_	 Alignment		29.7	15	PDB header: viral protein Chain: A; PDB Molecule: transmembrane protein gp41; PDBTitle: nmr assignment and structure of a peptide derived from the membrane2 proximal external region of hiv-1 gp41 in the presence of 3 hexafluoroisopropanol
7	c6agfB_	 Alignment		23.5	12	PDB header: membrane protein Chain: B; PDB Molecule: sodium channel subunit beta-1; PDBTitle: structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1
8	c5sv1Y_	 Alignment		23.5	21	PDB header: transport protein Chain: Y; PDB Molecule: biopolymer transport protein exbd; PDBTitle: structure of the exbb/exbd complex from e. coli at ph 4.5
9	c6d79A_	 Alignment		22.7	20	PDB header: transport protein Chain: A; PDB Molecule: sulfate transporter cysz; PDBTitle: structure of cysz, a sulfate permease from pseudomonas fragi
10	c5x0mA_	 Alignment		22.3	12	PDB header: membrane protein Chain: A; PDB Molecule: sodium channel protein; PDBTitle: structure of a eukaryotic voltage-gated sodium channel at near atomic2 resolution
11	c5sv1Z_	 Alignment		21.7	21	PDB header: transport protein Chain: Z; PDB Molecule: biopolymer transport protein exbd; PDBTitle: structure of the exbb/exbd complex from e. coli at ph 4.5

12	c4j8cA_	Alignment		19.4	33	PDB header: chaperone Chain: A: PDB Molecule: hsc70-interacting protein; PDBTitle: crystal structure of the dimerization domain of hsc70-interacting2 protein
13	c4j8cB_	Alignment		19.4	33	PDB header: chaperone Chain: B: PDB Molecule: hsc70-interacting protein; PDBTitle: crystal structure of the dimerization domain of hsc70-interacting2 protein
14	d2g1da1	Alignment		18.1	30	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: Ribosomal protein S24e
15	d2ffta1	Alignment		17.7	29	Fold: Intrinsically disordered proteins Superfamily: TSP9-like Family: TSP9-like
16	c5xsyB_	Alignment		17.3	10	PDB header: membrane protein Chain: B: PDB Molecule: voltage-gated sodium channel beta subunit 1; PDBTitle: structure of the nav1.4-beta1 complex from electric eel
17	c4qtnB_	Alignment		16.2	7	PDB header: transport protein Chain: B: PDB Molecule: nicotinamide riboside transporter pnuC; PDBTitle: crystal structure of the vitamin b3 transporter pnuC
18	d2v1pa1	Alignment		16.2	36	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Beta-eliminating lyases
19	c3izbU_	Alignment		15.9	15	PDB header: ribosome Chain: U: PDB Molecule: 40s ribosomal protein s24; PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
20	d2v94a1	Alignment		15.8	38	Fold: Ribosomal proteins S24e, L23 and L15e Superfamily: Ribosomal proteins S24e, L23 and L15e Family: Ribosomal protein S24e
21	c3iz6U_	Alignment	not modelled	15.2	22	PDB header: ribosome Chain: U: PDB Molecule: 40s ribosomal protein s24 (s24e); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
22	c6d73B_	Alignment	not modelled	15.1	14	PDB header: transport protein Chain: B: PDB Molecule: transient receptor potential cation channel, subfamily m; PDBTitle: cryo-em structure of the zebrafish trpm2 channel in the presence of 2 ca2+
23	c2zxeA_	Alignment	not modelled	14.9	16	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: na, k-atpase alpha subunit; PDBTitle: crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
24	d1oqwa_	Alignment	not modelled	14.5	28	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
25	c2mg3A_	Alignment	not modelled	14.5	20	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein gp41; PDBTitle: nmr assignment and structure of a peptide derived from the membrane2 proximal external region of hiv-1 gp41 in the presence of 3 dodecylphosphocholine micelles
26	c5zful_	Alignment	not modelled	14.4	29	PDB header: transport protein Chain: I: PDB Molecule: 22-mer peptide from biopolymer transport protein exbd; PDBTitle: structure of the exbb/exbd hexameric complex (exbb6exbd3tm)
27	c5zfvF_	Alignment	not modelled	14.4	29	PDB header: transport protein Chain: F: PDB Molecule: 22-mer peptide from biopolymer transport protein exbd; PDBTitle: structure of the exbb/exbd pentameric complex (exbb5exbd1tm)
						PDB header: transport protein

28	c5zfuH_	Alignment	not modelled	14.4	29	Chain: H: PDB Molecule: 22-mer peptide from biopolymer transport protein exbd; PDBTitle: structure of the exbb/exbd hexameric complex (exbb6exbd3tm)
29	c5zfuG_	Alignment	not modelled	14.4	29	PDB header: transport protein Chain: G: PDB Molecule: 22-mer peptide from biopolymer transport protein exbd; PDBTitle: structure of the exbb/exbd hexameric complex (exbb6exbd3tm)
30	c6hwhb_	Alignment	not modelled	14.3	17	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
31	c5v2sA_	Alignment	not modelled	14.2	23	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein b; PDBTitle: crystal structure of glycoprotein b from herpes simplex virus type i
32	c2ndjA_	Alignment	not modelled	13.7	26	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e member 3; PDBTitle: structural basis for kcne3 and estrogen modulation of the kcnq12 channel
33	c2mmuA_	Alignment	not modelled	13.7	17	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein crga; PDBTitle: structure of crga, a cell division structural and regulatory protein2 from mycobacterium tuberculosis, in lipid bilayers
34	c4kt0F_	Alignment	not modelled	13.5	35	PDB header: electron transport Chain: F: PDB Molecule: photosystem i subunit iii; PDBTitle: crystal structure of a virus like photosystem i from the2 cyanobacterium synechocystis pcc 6803
35	c2na6B_	Alignment	not modelled	13.4	18	PDB header: apoptosis Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
36	c2na6A_	Alignment	not modelled	13.4	18	PDB header: apoptosis Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
37	c2na6C_	Alignment	not modelled	13.4	18	PDB header: apoptosis Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
38	c4ye7A_	Alignment	not modelled	13.3	33	PDB header: viral protein Chain: A: PDB Molecule: orf22 similar to xcv orf19; PDBTitle: n-terminal domain of orf22, a cydia pomonella granulovirus envelope2 protein
39	d1neea1	Alignment	not modelled	13.1	21	Fold: Ribosome binding domain-like Superfamily: Translation initiation factor 2 beta, aIF2beta, N-terminal domain Family: Translation initiation factor 2 beta, aIF2beta, N-terminal domain
40	c2kglA_	Alignment	not modelled	12.9	32	PDB header: chaperone Chain: A: PDB Molecule: mesoderm development candidate 2; PDBTitle: nmr solution structure of mesd
41	c6d6tE_	Alignment	not modelled	12.6	7	PDB header: transport protein Chain: E: PDB Molecule: human gaba-a receptor subunit gamma-2; PDBTitle: human gaba-a receptor alpha1-beta2-gamma2 subtype in complex with gaba2 and flumazenil, conformation b
42	c5gapG_	Alignment	not modelled	12.4	15	PDB header: transcription Chain: G: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: body region of the u4/u6.u5 tri-snrnp
43	c4xtrG_	Alignment	not modelled	12.2	21	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: pep12p; PDBTitle: structure of get3 bound to the transmembrane domain of pep12
44	c3icoA_	Alignment	not modelled	12.0	23	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of 6-phosphogluconolactonase from mycobacterium2 tuberculosis
45	d1jb0f_	Alignment	not modelled	11.8	35	Fold: Single transmembrane helix Superfamily: Subunit III of photosystem I reaction centre, PsaF Family: Subunit III of photosystem I reaction centre, PsaF
46	c3cssA_	Alignment	not modelled	11.8	19	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of 6-phosphogluconolactonase from leishmania2 guyanensis
47	c5zx5D_	Alignment	not modelled	11.8	14	PDB header: transferase Chain: D: PDB Molecule: transient receptor potential cation channel subfamily m PDBTitle: 3.3 angstrom structure of mouse trpm7 with edta
48	c1ijjA_	Alignment	not modelled	11.3	21	PDB header: signaling protein Chain: A: PDB Molecule: erbB-2 receptor protein-tyrosine kinase; PDBTitle: solution structure of the neu/erbB-2 membrane spanning2 segment
49	c5hvdA_	Alignment	not modelled	11.3	17	PDB header: transport protein Chain: A: PDB Molecule: ion transport protein; PDBTitle: full length open-form sodium channel navms i218c
50	c4qndA_	Alignment	not modelled	11.3	20	PDB header: membrane protein Chain: A: PDB Molecule: chemical transport protein; PDBTitle: crystal structure of a semisweet
51	c3sokB_	Alignment	not modelled	11.2	24	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
						PDB header: cell adhesion, structural protein, elect

52	c2m7gA_	Alignment	not modelled	10.9	25	Chain: A: PDB Molecule: geopilin domain 1 protein; PDBTitle: structure of the type iva major pilin from the electrically conductive2 bacterial nanowires of geobacter sulfurreducens
53	d1mna_	Alignment	not modelled	10.9	36	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: DNA-binding domain from NDT80
54	c2euzA_	Alignment	not modelled	10.9	36	PDB header: cell cycle/dna Chain: A: PDB Molecule: ndt80 protein; PDBTitle: structure of a ndt80-dna complex (mse mutant mc5t)
55	d1q90d_	Alignment	not modelled	10.8	25	Fold: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Superfamily: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) Family: a domain/subunit of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
56	c6drkD_	Alignment	not modelled	10.8	14	PDB header: transport protein Chain: D: PDB Molecule: transient receptor potential cation channel, subfamily m, PDBTitle: structure of trpm2 ion channel receptor by single particle electron2 cryo-microscopy, apo state
57	c6m97A_	Alignment	not modelled	10.8	14	PDB header: transport protein Chain: A: PDB Molecule: chimera protein of high affinity copper uptake protein 1 PDBTitle: crystal structure of the high-affinity copper transporter ctr1
58	c3u5cY_	Alignment	not modelled	10.7	11	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24-a; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
59	c3j3aY_	Alignment	not modelled	10.5	22	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24; PDBTitle: structure of the human 40s ribosomal proteins
60	c3j60Y_	Alignment	not modelled	10.3	22	PDB header: ribosome Chain: Y: PDB Molecule: 40s ribosomal protein s24e; PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
61	c6gwsE_	Alignment	not modelled	10.3	100	PDB header: replication Chain: E: PDB Molecule: pcna-associated factor; PDBTitle: crystal structure of human pcna in complex with three p15 peptides
62	c6gwsD_	Alignment	not modelled	10.3	100	PDB header: replication Chain: D: PDB Molecule: pcna-associated factor; PDBTitle: crystal structure of human pcna in complex with three p15 peptides
63	c5xxuY_	Alignment	not modelled	10.2	11	PDB header: ribosome Chain: Y: PDB Molecule: ribosomal protein es24; PDBTitle: small subunit of toxoplasma gondii ribosome
64	c4y3uB_	Alignment	not modelled	10.2	32	PDB header: membrane protein Chain: B: PDB Molecule: cardiac phospholamban; PDBTitle: the structure of phospholamban bound to the calcium pump serca1a
65	c4mt1A_	Alignment	not modelled	9.9	12	PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump
66	c2xzmP_	Alignment	not modelled	9.8	22	PDB header: ribosome Chain: P: PDB Molecule: rps24e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
67	c2ezdA_	Alignment	not modelled	9.5	100	PDB header: dna binding protein/dna Chain: A: PDB Molecule: high mobility group protein hmg-i/hmg-y; PDBTitle: solution structure of a complex of the second dna binding2 domain of human hmg-i(y) bound to dna dodecamer containing3 the prdii site of the interferon-beta promoter, nmr,4 minimized average structure
68	c4d2gD_	Alignment	not modelled	9.5	100	PDB header: transcription Chain: D: PDB Molecule: p15; PDBTitle: crystal structure of human pcna in complex with p15 peptide
69	c4d2gE_	Alignment	not modelled	9.5	100	PDB header: transcription Chain: E: PDB Molecule: p15; PDBTitle: crystal structure of human pcna in complex with p15 peptide
70	c5zx9A_	Alignment	not modelled	9.5	25	PDB header: protein binding Chain: A: PDB Molecule: alanine and proline-rich secreted protein apa; PDBTitle: crystal structure of a protein from mycobacterium
71	c1oy8A_	Alignment	not modelled	9.4	12	PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump
72	d2f6mb1	Alignment	not modelled	9.4	27	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
73	d1v74b_	Alignment	not modelled	9.3	7	Fold: Four-helical up-and-down bundle Superfamily: Colicin D immunity protein Family: Colicin D immunity protein
74	c2n2aA_	Alignment	not modelled	9.3	17	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: spatial structure of her2/erbb2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
75	c1xl6B_	Alignment	not modelled	9.2	14	PDB header: metal transport Chain: B: PDB Molecule: inward rectifier potassium channel; PDBTitle: intermediate gating structure 2 of the inwardly rectifying k+ channel2 kirbac3.1
						Fold: Ribosomal proteins S24e, L23 and L15e

76	diywx1	Alignment	not modelled	9.1	20	Superfamily: Ribosomal proteins S24e, L23 and L15e Family: Ribosomal protein S24e
77	c4gn0D	Alignment	not modelled	9.0	19	PDB header: signaling protein Chain: D: PDB Molecule: hamp domain of af1503; PDBTitle: de novo phasing of a hamp-complex using an improved arcimboldo method
78	c6fddC	Alignment	not modelled	9.0	12	PDB header: structural protein Chain: C: PDB Molecule: whirlin; PDBTitle: crystal structure of the hhd2 domain of whirlin
79	c2ezeA	Alignment	not modelled	8.9	100	PDB header: dna binding protein/dna Chain: A: PDB Molecule: high mobility group protein hmg-i/hmg-y; PDBTitle: solution structure of a complex of the second dna binding2 domain of human hmg-i(y) bound to dna dodecamer containing3 the prdii site of the interferon-beta promoter, nmr, 354 structures
80	c6ehtE	Alignment	not modelled	8.9	100	PDB header: dna binding protein Chain: E: PDB Molecule: pcna-associated factor; PDBTitle: modulation of pcna sliding surface by p15paf suggests a suppressive2 mechanism for cisplatin-induced dna lesion bypass by pol eta3 holoenzyme
81	c5ghwP	Alignment	not modelled	8.8	17	PDB header: immune system Chain: P: PDB Molecule: endogenous retrovirus group k member 8 env polyprotein; PDBTitle: crystal structure of broad neutralizing antibody 10e8 with long2 epitope bound
82	c3jcmK	Alignment	not modelled	8.8	15	PDB header: transcription Chain: K: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: cryo-em structure of the spliceosomal u4/u6.u5 tri-snrnp
83	c2cazB	Alignment	not modelled	8.7	27	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein vps28; PDBTitle: escrt-i core
84	d2cazb1	Alignment	not modelled	8.7	27	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS28 N-terminal domain
85	c6agfA	Alignment	not modelled	8.7	12	PDB header: membrane protein Chain: A: PDB Molecule: sodium channel protein type 4 subunit alpha; PDBTitle: structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1
86	c6ehtD	Alignment	not modelled	8.5	100	PDB header: dna binding protein Chain: D: PDB Molecule: pcna-associated factor; PDBTitle: modulation of pcna sliding surface by p15paf suggests a suppressive2 mechanism for cisplatin-induced dna lesion bypass by pol eta3 holoenzyme
87	c5tbfB	Alignment	not modelled	8.4	44	PDB header: translation Chain: B: PDB Molecule: translation elongation factor; PDBTitle: crystal structure of semet derivatives of domain2 and domain 3 of rctb
88	c6fosF	Alignment	not modelled	8.3	25	PDB header: photosynthesis Chain: F: PDB Molecule: photosystem i reaction center subunit ii; PDBTitle: cyanidioschyzon merolae photosystem i
89	c5ir6C	Alignment	not modelled	8.0	24	PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
90	c3eamB	Alignment	not modelled	7.8	11	PDB header: membrane protein, transport protein Chain: B: PDB Molecule: glr4197 protein; PDBTitle: an open-pore structure of a bacterial pentameric ligand-2 gated ion channel
91	c5ubfB	Alignment	not modelled	7.8	44	PDB header: dna binding protein Chain: B: PDB Molecule: rctb replication initiator protein; PDBTitle: crystal structure of the rctb domains 2-3, rctb-155-483
92	c4pguA	Alignment	not modelled	7.6	11	PDB header: membrane protein Chain: A: PDB Molecule: uncharacterized protein yetj; PDBTitle: crystal structure of yetj from bacillus subtilis at ph 7 by soaking
93	c4zyaA	Alignment	not modelled	7.5	63	PDB header: ligase Chain: A: PDB Molecule: asparagine--trna ligase, cytoplasmic; PDBTitle: the n-terminal extension domain of human asparaginyl-trna synthetase
94	c2l6wB	Alignment	not modelled	7.4	22	PDB header: membrane protein Chain: B: PDB Molecule: beta-type platelet-derived growth factor receptor; PDBTitle: pdgfr beta-tm
95	c6c9aB	Alignment	not modelled	7.4	19	PDB header: membrane protein Chain: B: PDB Molecule: two pore calcium channel protein 1; PDBTitle: cryo-em structure of mouse tpc1 channel in the ptdins(3,5)p2-bound2 state
96	c5doqC	Alignment	not modelled	7.2	26	PDB header: oxidoreductase Chain: C: PDB Molecule: putative membrane protein; PDBTitle: the structure of bd oxidase from geobacillus thermodenitrificans
97	c2k21A	Alignment	not modelled	7.2	11	PDB header: membrane protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily e PDBTitle: nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
98	c5xyiY	Alignment	not modelled	7.2	38	PDB header: ribosome Chain: Y: PDB Molecule: ribosomal protein s24e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
99	c5m73D	Alignment	not modelled	7.1	44	PDB header: rna binding protein Chain: D: PDB Molecule: signal recognition particle subunit srp72; PDBTitle: structure of the human srp s domain with srp72 rna-binding domain