






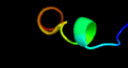



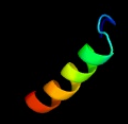

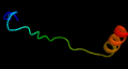

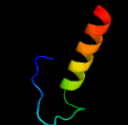



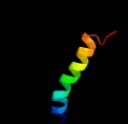

























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3335c (-)_3721902_3722771
Date	Thu Aug 8 16:20:54 BST 2019
Unique Job ID	902463cd788db15c

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2r6gf1	 Alignment		51.3	16	Fold: MalF N-terminal region-like Superfamily: MalF N-terminal region-like Family: MalF N-terminal region-like
2	c5mb9C_	 Alignment		19.8	31	PDB header: chaperone Chain: C: PDB Molecule: putative ribosome associated protein; PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair
3	c2qksA_	 Alignment		19.4	13	PDB header: metal transport Chain: A: PDB Molecule: kir3.1-prokaryotic kir channel chimera; PDBTitle: crystal structure of a kir3.1-prokaryotic kir channel chimera
4	c5mb9D_	 Alignment		18.5	31	PDB header: chaperone Chain: D: PDB Molecule: putative ribosome associated protein; PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair
5	c1xl6B_	 Alignment		15.6	8	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
6	d1aila_	 Alignment		10.1	38	Fold: S15/NS1 RNA-binding domain Superfamily: S15/NS1 RNA-binding domain Family: N-terminal, RNA-binding domain of nonstructural protein NS1
7	c4atbC_	 Alignment		9.5	29	PDB header: immune system Chain: C: PDB Molecule: interleukin enhancer-binding factor 2; PDBTitle: crystal structure of the nf90-nf45 dimerisation domain2 complex with ctp
8	c5ec0A_	 Alignment		9.1	35	PDB header: structural protein Chain: A: PDB Molecule: alp7a; PDBTitle: crystal structure of actin-like protein alp7a
9	d2h9da1	 Alignment		9.0	19	Fold: Chorismate mutase II Superfamily: Chorismate mutase II Family: Dimeric chorismate mutase
10	c5lnkW_	 Alignment		8.8	15	PDB header: oxidoreductase Chain: W: PDB Molecule: mitochondrial complex i, sgdh subunit; PDBTitle: entire ovine respiratory complex i
11	c4o9lA_	 Alignment		8.8	29	PDB header: antiviral protein Chain: A: PDB Molecule: mitochondrial antiviral signaling protein (mavs); PDBTitle: crystal structure of horse mavs card domain mutant e26r

12	c6cfwD_	Alignment		8.6	11	PDB header: membrane protein Chain: D: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
13	c1w8xP_	Alignment		8.6	12	PDB header: virus Chain: P: PDB Molecule: protein p16; PDBTitle: structural analysis of prd1
14	c1p0lA_	Alignment		8.3	14	PDB header: ribosome Chain: A: PDB Molecule: 19-mer peptide from 50s ribosomal protein l1; PDBTitle: hp (2-20) substitution gln to trp modification in sds-d252 micelles
15	c5lnk2_	Alignment		7.9	22	PDB header: oxidoreductase Chain: 2: PDB Molecule: mitochondrial complex i, 24 kda subunit; PDBTitle: entire ovine respiratory complex i
16	c4z3pA_	Alignment		7.8	13	PDB header: transport protein Chain: A: PDB Molecule: putative drug/sodium antiporter; PDBTitle: mate transporter clbm in complex with rb+
17	c2m6xC_	Alignment		7.7	23	PDB header: membrane protein Chain: C: PDB Molecule: p7; PDBTitle: structure of the p7 channel of hepatitis c virus, genotype 5a
18	c4iu8A_	Alignment		7.5	4	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)
19	c3p5nA_	Alignment		7.4	4	PDB header: transport protein Chain: A: PDB Molecule: riboflavin uptake protein; PDBTitle: structure and mechanism of the s component of a bacterial ecf2 transporter
20	c5kq4C_	Alignment		7.1	25	PDB header: hydrolase Chain: C: PDB Molecule: proline-rich nuclear receptor coactivator 2; PDBTitle: crystal structure of s. pombe dcp1/dcp2 in complex with h. sapiens2 pnrc2 and synthetic cap analog
21	c2f8xM_	Alignment	not modelled	7.1	56	PDB header: transcription/dna Chain: M: PDB Molecule: mastermind-like protein 1; PDBTitle: crystal structure of activated notch, csl and mam1 on hes-12 promoter dna sequence
22	d2hwna1	Alignment	not modelled	7.1	15	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
23	c2kpmA_	Alignment	not modelled	7.1	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of uncharacterized protein from gene2 locus ne0665 of nitrosomonas europaea. northeast structural3 genomics target ner103a
24	c3ixzB_	Alignment	not modelled	7.1	5	PDB header: hydrolase Chain: B: PDB Molecule: potassium-transporting atpase subunit beta; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
25	c2l16A_	Alignment	not modelled	6.9	14	PDB header: protein transport Chain: A: PDB Molecule: sec-independent protein translocase protein tatad; PDBTitle: solution structure of bacillus subtilis tatad protein in dpc micelles
26	d1vk3a4	Alignment	not modelled	6.8	10	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
27	c4rp9A_	Alignment	not modelled	6.8	12	PDB header: membrane protein Chain: A: PDB Molecule: ascorbate-specific permease iic component ulaa; PDBTitle: bacterial vitamin c transporter ulaa/sgat in c2 form

28	c1cdIG_	 Alignment	not modelled	6.7	29	PDB header: calcium-binding protein Chain: G; PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
29	c1cdIF_	 Alignment	not modelled	6.7	29	PDB header: calcium-binding protein Chain: F; PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
30	c1cdIE_	 Alignment	not modelled	6.7	29	PDB header: calcium-binding protein Chain: E; PDB Molecule: calcium/calmodulin-dependent protein kinase type PDBTitle: target enzyme recognition by calmodulin: 2.4 angstroms2 structure of a calmodulin-peptide complex
31	d1rh1a1	 Alignment	not modelled	6.7	18	Fold: Cloacin translocation domain Superfamily: Cloacin translocation domain Family: Cloacin translocation domain
32	c1rh1A_	 Alignment	not modelled	6.6	18	PDB header: antibiotic Chain: A; PDB Molecule: colicin b; PDBTitle: crystal structure of the cytotoxic bacterial protein2 colicin b at 2.5 a resolution
33	c2ht2B_	 Alignment	not modelled	6.5	9	PDB header: membrane protein Chain: B; PDB Molecule: h(+)/cl(-) exchange transporter clca; PDBTitle: structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
34	c2o5gB_	 Alignment	not modelled	6.3	29	PDB header: metal binding protein Chain: B; PDB Molecule: smooth muscle myosin light chain kinase peptide; PDBTitle: calmodulin-smooth muscle light chain kinase peptide complex
35	c2lz1B_	 Alignment	not modelled	6.2	31	PDB header: membrane protein Chain: B; PDB Molecule: fibroblast growth factor receptor 3; PDBTitle: fgfr3tm
36	d2as0a1	 Alignment	not modelled	6.1	0	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical RNA methyltransferase domain (HRMD)
37	c6n10A_	 Alignment	not modelled	6.1	15	PDB header: lyase Chain: A; PDB Molecule: diphosphomevalonate decarboxylase mvd1, peroxisomal; PDBTitle: crystal structure of arabidopsis thaliana mevalonate 5-diphosphate2 decarboxylase 1 complexed with (r)-mvapp
38	d1r2aa_	 Alignment	not modelled	6.1	15	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
39	d2ca5a1	 Alignment	not modelled	6.0	14	Fold: Long alpha-hairpin Superfamily: MxiH-like Family: MxiH-like
40	c1hgza_	 Alignment	not modelled	6.0	21	PDB header: virus Chain: A; PDB Molecule: ph75 inovirus major coat protein; PDBTitle: filamentous bacteriophage ph75
41	c1qtxB_	 Alignment	not modelled	5.9	29	PDB header: signaling protein Chain: B; PDB Molecule: protein (rs20); PDBTitle: the 1.65 angstrom structure of calmodulin rs20 peptide2 complex
42	c5ojyA_	 Alignment	not modelled	5.9	14	PDB header: transcription Chain: A; PDB Molecule: tetr family transcription regulator; PDBTitle: co-complex structure of regulator protein 2 (pamr2) with pamamycin 6072 from streptomyces alboniger
43	c3f5tA_	 Alignment	not modelled	5.7	43	PDB header: viral protein Chain: A; PDB Molecule: nonstructural protein 1; PDBTitle: x-ray structure of h5n1 ns1
44	c6bhuA_	 Alignment	not modelled	5.5	7	PDB header: transport protein Chain: A; PDB Molecule: multidrug resistance-associated protein 1; PDBTitle: cryo-em structure of atp-bound, outward-facing bovine multidrug2 resistance protein 1 (mrp1)
45	c4od5C_	 Alignment	not modelled	5.4	14	PDB header: transferase Chain: C; PDB Molecule: 4-hydroxybenzoate octaprenyltransferase; PDBTitle: substrate-bound structure of a ubia homolog from aeropyrum pernix k1
46	c2v6ll_	 Alignment	not modelled	5.3	13	PDB header: protein transport Chain: I; PDB Molecule: mxih; PDBTitle: molecular model of a type iii secretion system needle
47	c4wxmD_	 Alignment	not modelled	5.3	40	PDB header: transcription regulator Chain: D; PDB Molecule: transcriptional regulator fleq; PDBTitle: fleq rec domain from pseudomonas aeruginosa pao1
48	c4fp9B_	 Alignment	not modelled	5.3	21	PDB header: transferase Chain: B; PDB Molecule: mterf4-nsun4 domain-containing protein 2; PDBTitle: human mterf4-nsun4 protein complex
49	d1e3ha5	Alignment	not modelled	5.2	15	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
50	c2hkeB_	Alignment	not modelled	5.2	10	PDB header: lyase Chain: B; PDB Molecule: diphosphomevalonate decarboxylase, putative; PDBTitle: mevalonate diphosphate decarboxylase from trypanosoma brucei
51	c1fi4A_	Alignment	not modelled	5.2	13	PDB header: lyase Chain: A; PDB Molecule: mevalonate 5-diphosphate decarboxylase; PDBTitle: the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
52	d1k1a	Alignment	not modelled	5.2	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response

52	v11q1a_	Alignment	not modelled	5.2	13	regulators Family: Spo0A
53	c3j9pD_	Alignment	not modelled	5.2	8	PDB header: transport protein Chain: D: PDB Molecule: maltose-binding periplasmic protein, transient receptor PDBTitle: structure of the trpa1 ion channel determined by electron cryo-2 microscopy
54	c5lc5m_	Alignment	not modelled	5.1	14	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4; PDBTitle: structure of mammalian respiratory complex i, class2