

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3244c_(lpqB)_3623156_3624907
Date	Thu Aug 8 16:20:44 BST 2019
Unique Job ID	34ccdf3470364000

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6nd4H_	Alignment		99.9	11	PDB header: ribosome Chain: H: PDB Molecule: utp17; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
2	c5n1aB_	Alignment		99.9	14	PDB header: translation Chain: B: PDB Molecule: utp4; PDBTitle: crystal structure of utp4 from chaetomium thermophilum
3	c4yczA_	Alignment		99.9	10	PDB header: structural protein Chain: A: PDB Molecule: fusion protein of sec13 and nup145c; PDBTitle: y-complex hub (nup85-nup120-nup145c-sec13 complex) from m. thermophila2 (a.k.a. t. heterothallica)
4	c5a1vK_	Alignment		99.9	11	PDB header: transport protein Chain: K: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copi coat linkage i
5	c5a5uB_	Alignment		99.9	10	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: structure of mammalian eif3 in the context of the 43s preinitiation2 complex
6	c3dm0A_	Alignment		99.8	12	PDB header: sugar binding protein,signaling protein Chain: A: PDB Molecule: maltose-binding periplasmic protein fused with rack1; PDBTitle: maltose binding protein fusion with rack1 from a. thaliana
7	c3wj9A_	Alignment		99.8	10	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 2a; PDBTitle: crystal structure of the eukaryotic initiation factor
8	c5juyB_	Alignment		99.8	13	PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
9	c3jroA_	Alignment		99.8	10	PDB header: transport protein, structural protein Chain: A: PDB Molecule: fusion protein of protein transport protein sec13 and PDBTitle: nup84-nup145c-sec13 edge element of the npc lattice
10	c6qk7A_	Alignment		99.8	12	PDB header: translation Chain: A: PDB Molecule: elongator complex protein 1; PDBTitle: elongator catalytic subcomplex elp123 lobe
11	c5tzsT_	Alignment		99.8	10	PDB header: translation Chain: T: PDB Molecule: utp21; PDBTitle: architecture of the yeast small subunit processome

12	c4uerb_	Alignment		99.8	12	PDB header: translation Chain: B: PDB Molecule: us2; PDBTitle: 40s-eif1-eif1a-eif3-eif3j translation initiation complex from2 lachnaceae kluyveri
13	c6nd4Q_	Alignment		99.8	10	PDB header: ribosome Chain: Q: PDB Molecule: utp12; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
14	d1tl2a_	Alignment		99.8	9	Fold: 5-bladed beta-propeller Superfamily: Tachylectin-2 Family: Tachylectin-2
15	c6em5m_	Alignment		99.8	9	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l14-a; PDBTitle: state d architectural model (nsa1-tap flag-ytm1) - visualizing the2 assembly pathway of nucleolar pre-60s ribosomes
16	c6nd4O_	Alignment		99.7	14	PDB header: ribosome Chain: O: PDB Molecule: utp1; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
17	c5n4aA_	Alignment		99.7	10	PDB header: transport protein Chain: A: PDB Molecule: intraflagellar transport protein 80; PDBTitle: crystal structure of chlamydomonas ift80
18	c6nd4T_	Alignment		99.7	9	PDB header: ribosome Chain: T: PDB Molecule: utp21; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
19	c6nd4W_	Alignment		99.7	10	PDB header: ribosome Chain: W: PDB Molecule: utp7; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
20	c6chgD_	Alignment		99.7	13	PDB header: transferase Chain: D: PDB Molecule: klla0a08800p; PDBTitle: crystal structure of the yeast compass catalytic module
21	c3iytG_	Alignment	not modelled	99.7	12	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
22	c5f30B_	Alignment	not modelled	99.7	9	PDB header: oxidoreductase Chain: B: PDB Molecule: thiocyanate dehydrogenase; PDBTitle: thiocyanate dehydrogenase from thioalkalivibrio paradoxus
23	c2ymuA_	Alignment	not modelled	99.7	29	PDB header: unknown function Chain: A: PDB Molecule: wd-40 repeat protein; PDBTitle: structure of a highly repetitive propeller structure
24	c1nr0A_	Alignment	not modelled	99.7	11	PDB header: structural protein Chain: A: PDB Molecule: actin interacting protein 1; PDBTitle: two seven-bladed beta-propeller domains revealed by the2 structure of a c. elegans homologue of yeast actin3 interacting protein 1 (aip1).
25	d1ospo_	Alignment	not modelled	99.7	9	Fold: open-sided beta-meander Superfamily: Outer surface protein Family: Outer surface protein
26	c2oajA_	Alignment	not modelled	99.7	14	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: protein sn1; PDBTitle: crystal structure of sro7 from s. cerevisiae
27	c4u1fA_	Alignment	not modelled	99.7	11	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: crystal structure of middle domain of eukaryotic translation2 initiation factor eif3b
28	c6nd4S_	Alignment	not modelled	99.7	12	PDB header: ribosome Chain: S: PDB Molecule: utp18; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit

29	c1gq1B	Alignment	not modelled	99.7	10	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome cd1 nitrite reductase; PDBTitle: cytochrome cd1 nitrite reductase, y25s mutant, oxidised form
30	c4o9dA	Alignment	not modelled	99.7	21	PDB header: gene regulation Chain: A: PDB Molecule: rik1-associated factor 1; PDBTitle: structure of dos1 propeller
31	c1pi6A	Alignment	not modelled	99.7	11	PDB header: protein binding Chain: A: PDB Molecule: actin interacting protein 1; PDBTitle: yeast actin interacting protein 1 (aip1), orthorhombic crystal form
32	c5cvoD	Alignment	not modelled	99.7	11	PDB header: hydrolase/protein binding Chain: D: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
33	c4wjsA	Alignment	not modelled	99.6	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: rsa4; PDBTitle: crystal structure of rsa4 from chaetomium thermophilum
34	c4bzkA	Alignment	not modelled	99.6	13	PDB header: protein transport Chain: A: PDB Molecule: protein transport protein sec31; PDBTitle: the structure of the copii coat assembled on membranes
35	c4e54B	Alignment	not modelled	99.6	11	PDB header: dna binding protein/dna Chain: B: PDB Molecule: dna damage-binding protein 2; PDBTitle: damaged dna induced uv-damaged dna-binding protein (uv-ddb)2 dimerization and its roles in chromatinized dna repair
36	c6cb1s	Alignment	not modelled	99.6	13	PDB header: ribosome Chain: S: PDB Molecule: 60s ribosomal protein l20-a; PDBTitle: yeast nucleolar pre-60s ribosomal subunit (state 3)
37	c6n8sA	Alignment	not modelled	99.6	12	PDB header: lipid binding protein Chain: A: PDB Molecule: lethal(2) giant larvae protein homolog 2; PDBTitle: crystal structure of the human cell polarity protein lethal giant2 larvae 2 (lg2). apkc phosphorylated, crystal form 3.
38	c3bwsA	Alignment	not modelled	99.6	11	PDB header: unknown function Chain: A: PDB Molecule: protein lp49; PDBTitle: crystal structure of the leptospiral antigen lp49
39	c5dfzB	Alignment	not modelled	99.6	8	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase vps15; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
40	c4wjuB	Alignment	not modelled	99.6	21	PDB header: biosynthetic protein Chain: B: PDB Molecule: ribosome assembly protein 4; PDBTitle: crystal structure of rsa4 from saccharomyces cerevisiae
41	c5cvoA	Alignment	not modelled	99.6	11	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
42	c5a1vL	Alignment	not modelled	99.6	11	PDB header: transport protein Chain: L: PDB Molecule: coatomer subunit beta; PDBTitle: the structure of the copii coat linkage i
43	c2w8bB	Alignment	not modelled	99.6	15	PDB header: protein transport/membrane protein Chain: B: PDB Molecule: protein tolb; PDBTitle: crystal structure of processed tolb in complex with pal
44	c2ivzD	Alignment	not modelled	99.6	14	PDB header: protein transport/hydrolase Chain: D: PDB Molecule: protein tolb; PDBTitle: structure of tolb in complex with a peptide of the colicin2 e9 t-domain
45	c5cvlA	Alignment	not modelled	99.6	12	PDB header: protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48 (uaf-1), residues 2-580
46	c5nzvC	Alignment	not modelled	99.6	11	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit beta'; PDBTitle: the structure of the copii coat linkage iv
47	c5a1uC	Alignment	not modelled	99.6	10	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copii coat triad
48	d1fwxa2	Alignment	not modelled	99.6	11	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
49	c5wbiA	Alignment	not modelled	99.6	9	PDB header: protein binding Chain: A: PDB Molecule: regulatory-associated protein of tor 1; PDBTitle: crystal structure of the arabidopsis thaliana raptor
50	c4nsxA	Alignment	not modelled	99.6	9	PDB header: protein binding Chain: A: PDB Molecule: u3 small nucleolar rna-associated protein 21; PDBTitle: crystal structure of the utp21 tandem wd domain
51	c2j04B	Alignment	not modelled	99.6	12	PDB header: transcription Chain: B: PDB Molecule: ydr362cp; PDBTitle: the tau60-tau91 subcomplex of yeast transcription factor iiic
52	c6f3tD	Alignment	not modelled	99.6	12	PDB header: transcription Chain: D: PDB Molecule: transcription initiation factor tfiid subunit 5; PDBTitle: crystal structure of the human taf5-taf6-taf9 complex
53	c6iczw	Alignment	not modelled	99.6	13	PDB header: splicing Chain: W: PDB Molecule: pre-mrna-processing factor 17; PDBTitle: cryo-em structure of a human post-catalytic spliceosome (p complex) at2 3.0 angstrom
54	c2w18A	Alignment	not modelled	99.6	8	PDB header: nuclear protein Chain: A: PDB Molecule: partner and localizer of brca2; PDBTitle: crystal structure of the c-terminal wd40 domain of human2 palb2
55	c5i2tA	Alignment	not modelled	99.6	11	PDB header: biosynthetic protein Chain: A: PDB Molecule: periodic tryptophan protein 2; PDBTitle: domain characterization of the wd protein pwp2 and their relevance in2 ribosome biogenesis

56	c4xfvA_	Alignment	not modelled	99.6	10	PDB header: translation Chain: A; PDB Molecule: elongator complex protein 2; PDBTitle: crystal structure of elp2
57	c3lrvA_	Alignment	not modelled	99.6	9	PDB header: splicing Chain: A; PDB Molecule: pre-mrna-splicing factor 19; PDBTitle: the prp19 wd40 domain contains a conserved protein interaction region2 essential for its function.
58	c4noxA_	Alignment	not modelled	99.6	10	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: structure of the nine-bladed beta-propeller of eif3b
59	d1xfda1	Alignment	not modelled	99.6	11	Fold: 8-bladed beta-propeller Superfamily: DPP6 N-terminal domain-like Family: DPP6 N-terminal domain-like
60	c3j65q_	Alignment	not modelled	99.6	20	PDB header: ribosome Chain: Q; PDB Molecule: 60s ribosomal protein l18; PDBTitle: arx1 pre-60s particle. this entry contains the r-proteins and2 biogenesis factors.
61	c5k1bB_	Alignment	not modelled	99.6	12	PDB header: protein binding/hydrolase Chain: B; PDB Molecule: wd repeat-containing protein 48; PDBTitle: crystal structure of the uaf1/usp12 complex in f222 space group
62	c2aq5A_	Alignment	not modelled	99.6	14	PDB header: structural protein Chain: A; PDB Molecule: coronin-1a; PDBTitle: crystal structure of murine coronin-1
63	c5ch2A_	Alignment	not modelled	99.6	10	PDB header: transferase Chain: A; PDB Molecule: putative polycomb protein eed; PDBTitle: crystal structure of an active polycomb repressive complex 2 in the2 basal state
64	c1n6dE_	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: E; PDB Molecule: tricorn protease; PDBTitle: tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
65	c4yhca_	Alignment	not modelled	99.5	7	PDB header: structural protein Chain: A; PDB Molecule: sterol regulatory element-binding protein cleavage- PDBTitle: crystal structure of the wd40 domain of scap from fission yeast
66	c1k32E_	Alignment	not modelled	99.5	13	PDB header: hydrolase Chain: E; PDB Molecule: tricorn protease; PDBTitle: crystal structure of the tricorn protease
67	c6mzcG_	Alignment	not modelled	99.5	14	PDB header: transcription Chain: G; PDB Molecule: transcription initiation factor tfiid subunit 5; PDBTitle: human tfiid bc core
68	c6rteB_	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome c; PDBTitle: dihydro-heme d1 dehydrogenase nirn in complex with dhe
69	c6nd4N_	Alignment	not modelled	99.5	9	PDB header: ribosome Chain: N; PDB Molecule: utp4; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
70	c4ozuA_	Alignment	not modelled	99.5	12	PDB header: structural protein Chain: A; PDB Molecule: coronin; PDBTitle: crystal structure of wd40 domain from toxoplasma gondii coronin
71	c4h5jB_	Alignment	not modelled	99.5	10	PDB header: protein transport Chain: B; PDB Molecule: guanine nucleotide-exchange factor sec12; PDBTitle: crystal structure of the guanine nucleotide exchange factor sec12 (p642 form)
72	c3mkqA_	Alignment	not modelled	99.5	10	PDB header: transport protein Chain: A; PDB Molecule: coatome beta'-subunit; PDBTitle: crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat
73	c6gzbD_	Alignment	not modelled	99.5	18	PDB header: structural protein Chain: D; PDB Molecule: spore germination protein germ; PDBTitle: tandem germn domains of the sporulation protein germ from bacillus2 subtilis
74	c3jcmB_	Alignment	not modelled	99.5	19	PDB header: transcription Chain: B; PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp4; PDBTitle: cryo-em structure of the spliceosomal u4/u6.u5 tri-snrnp
75	d1k32a3	Alignment	not modelled	99.5	9	Fold: 7-bladed beta-propeller Superfamily: Tricorn protease domain 2 Family: Tricorn protease domain 2
76	c6fqIA_	Alignment	not modelled	99.5	10	PDB header: rna binding protein Chain: A; PDB Molecule: e3 ubiquitin-protein ligase trim71; PDBTitle: crystal structure of danio rerio lin41 filamin-nhl domains in complex2 with mab-10 3'utr 13mer rna
77	d1gxra_	Alignment	not modelled	99.5	12	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like Family: WD40-repeat
78	c6e29C_	Alignment	not modelled	99.5	18	PDB header: protein binding Chain: C; PDB Molecule: swd1-like protein; PDBTitle: crystal structure of myceliophtheria_thermophila cps50 (swd1) beta-2 propeller domain
79	c3acpA_	Alignment	not modelled	99.5	10	PDB header: chaperone Chain: A; PDB Molecule: wd repeat-containing protein ygl004c; PDBTitle: crystal structure of yeast rpn14, a chaperone of the 19s regulatory2 particle of the proteasome
80	c6bx3B_	Alignment	not modelled	99.5	13	PDB header: gene regulation/transferase Chain: B; PDB Molecule: compass component swd1; PDBTitle: structure of histone h3k4 methyltransferase
81	c6nd4L_	Alignment	not modelled	99.5	11	PDB header: ribosome Chain: L; PDB Molecule: utp5; PDBTitle: conformational switches control early maturation of the

					eukaryotic2 small ribosomal subunit PDB header: hydrolase Chain: B: PDB Molecule: periplasmic gluconolactonase, ppgl; PDBTitle: the structure of pseudomonas aeruginosa periplasmic gluconolactonase,2 ppgl
82	c6igbB_	Alignment	not modelled	99.5	18
83	c3fgbB_	Alignment	not modelled	99.5	11
84	c3u4yA_	Alignment	not modelled	99.4	13
85	c6iyyA_	Alignment	not modelled	99.4	13
86	c2pm9A_	Alignment	not modelled	99.4	15
87	c3jb9U_	Alignment	not modelled	99.4	10
88	c6r5kA_	Alignment	not modelled	99.4	9
89	c5tf2A_	Alignment	not modelled	99.4	11
90	c5o9zL_	Alignment	not modelled	99.4	12
91	c5cxcA_	Alignment	not modelled	99.4	14
92	c3ei4D_	Alignment	not modelled	99.4	10
93	c6nd4J_	Alignment	not modelled	99.4	12
94	c6eojD_	Alignment	not modelled	99.4	12
95	c3jrpA_	Alignment	not modelled	99.4	15
96	d1erja_	Alignment	not modelled	99.4	13
97	c5jk7C_	Alignment	not modelled	99.4	9
98	c5ov3B_	Alignment	not modelled	99.4	17
99	c4ci8B_	Alignment	not modelled	99.4	12
100	c3pe7A_	Alignment	not modelled	99.4	11
101	c5a31R_	Alignment	not modelled	99.4	14
102	c3g4hB_	Alignment	not modelled	99.4	11
103	c5mzhB_	Alignment	not modelled	99.4	11
104	c5o9zF_	Alignment	not modelled	99.3	12
105	c2j57J_	Alignment	not modelled	99.3	10

106	c1r5mA	Alignment	not modelled	99.3	24	PDB header: transcription Chain: A: PDB Molecule: sir4-interacting protein sif2; PDBTitle: crystal structure of the c-terminal wd40 domain of sif2
107	c1nnoA	Alignment	not modelled	99.3	10	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: conformational changes occurring upon no binding in nitrite reductase2 from pseudomonas aeruginosa
108	c4ui9R	Alignment	not modelled	99.3	15	PDB header: cell cycle Chain: R: PDB Molecule: fizzy-related protein homolog; PDBTitle: atomic structure of the human anaphase-promoting complex
109	d2hqsa1	Alignment	not modelled	99.3	17	Fold: 6-bladed beta-propeller Superfamily: TolB, C-terminal domain Family: TolB, C-terminal domain
110	d1qksa2	Alignment	not modelled	99.3	7	Fold: 8-bladed beta-propeller Superfamily: C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase Family: C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase
111	c5c2vB	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: hydrazine synthase beta subunit; PDBTitle: kueneria stuttgartiensis hydrazine synthase
112	c2pbiB	Alignment	not modelled	99.3	12	PDB header: signaling protein Chain: B: PDB Molecule: guanine nucleotide-binding protein subunit beta 5; PDBTitle: the multifunctional nature of gbeta5/rgs9 revealed from its crystal2 structure
113	d2bgra1	Alignment	not modelled	99.3	12	Fold: 8-bladed beta-propeller Superfamily: DPP6 N-terminal domain-like Family: DPP6 N-terminal domain-like
114	c4nlmA	Alignment	not modelled	99.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lmo1340 protein; PDBTitle: 1.18 angstrom resolution crystal structure of uncharacterized protein2 lmo1340 from listeria monocytogenes egd-e
115	d1qnia2	Alignment	not modelled	99.3	8	Fold: 7-bladed beta-propeller Superfamily: Nitrous oxide reductase, N-terminal domain Family: Nitrous oxide reductase, N-terminal domain
116	c2vduB	Alignment	not modelled	99.3	13	PDB header: transferase Chain: B: PDB Molecule: trna (guanine-n(7)-)-methyltransferase- PDBTitle: structure of trm8-trm82, the yeast trna m7g methylation2 complex
117	c4a11B	Alignment	not modelled	99.3	14	PDB header: dna binding protein Chain: B: PDB Molecule: dna excision repair protein ercc-8; PDBTitle: structure of the hsddb1-hscsa complex
118	c5thaA	Alignment	not modelled	99.3	13	PDB header: rna binding protein Chain: A: PDB Molecule: gem-associated protein 5; PDBTitle: gemin5 wd40 repeats in complex with a guanosyl moiety
119	c3dwlH	Alignment	not modelled	99.3	7	PDB header: structural protein Chain: H: PDB Molecule: actin-related protein 2/3 complex subunit 1; PDBTitle: crystal structure of fission yeast arp2/3 complex lacking the arp22 subunit
120	c6hqaB	Alignment	not modelled	99.3	16	PDB header: transcription Chain: B: PDB Molecule: subunit (90 kda) of tfiid and saga complexes; PDBTitle: molecular structure of promoter-bound yeast tfiid