

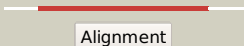

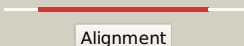







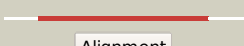











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3035_(-)_3395390_3396472
Date	Thu Aug 8 16:20:20 BST 2019
Unique Job ID	81c6eb17ea2f0197

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4pk1A_	 Alignment		100.0	18	PDB header: protein binding Chain: A: PDB Molecule: chimera protein of outer membrane protein assembly factors PDBTitle: structure of bamb fused to a bama potra domain fragment
2	c1yiqA_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: quinohemoprotein alcohol dehydrogenase; PDBTitle: molecular cloning and structural analysis of2 quinohemoprotein alcohol dehydrogenase adhiig from3 pseudomonas putida hk5. compariison to the other4 quinohemoprotein alcohol dehydrogenase adhiib found in the5 same microorganism.
3	c4cvcA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of quinone-dependent alcohol dehydrogenase from2 pseudogluconobacter saccharoketogenenes with zinc in the active site
4	c1kb0A_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: quinohemoprotein alcohol dehydrogenase; PDBTitle: crystal structure of quinohemoprotein alcohol dehydrogenase from2 comamonas testosteroni
5	c1kv9A_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: type ii quinohemoprotein alcohol dehydrogenase; PDBTitle: structure at 1.9 a resolution of a quinohemoprotein alcohol2 dehydrogenase from pseudomonas putida hk5
6	d1kb0a2	 Alignment		100.0	17	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
7	d2ad6a1	 Alignment		100.0	16	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
8	d1kv9a2	 Alignment		100.0	15	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
9	d1w6sa_	 Alignment		100.0	16	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
10	d1flga_	 Alignment		100.0	17	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
11	c4maeB_	 Alignment		100.0	12	PDB header: oxidoreductase Chain: B: PDB Molecule: methanol dehydrogenase; PDBTitle: methanol dehydrogenase from methylacidiphilum fumariolicum solv

12	c6damA_	Alignment		100.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: lanthanide-dependent methanol dehydrogenase xoxf; PDBTitle: crystal structure of lanthanide-dependent methanol dehydrogenase xoxf2 from methylomicrobium buryatense 5g
13	d1lrwa_	Alignment		100.0	14	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
14	c4mh1A_	Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: sorbose dehydrogenase; PDBTitle: crystal structure and functional studies of quinoprotein l-sorbose2 dehydrogenase from ketogulonigenium vulgare y25
15	c3p1A_	Alignment		100.0	17	PDB header: protein binding Chain: A: PDB Molecule: lipoprotein yfgl; PDBTitle: crystal structure of escherichia coli bamb, a lipoprotein component of2 the beta-barrel assembly machinery complex, native crystals.
16	c4hdjA_	Alignment		100.0	14	PDB header: protein binding Chain: A: PDB Molecule: outer membrane protein assembly factor bamb; PDBTitle: crystal structure of bamb from pseudomonas aeruginosa
17	c4immA_	Alignment		99.9	15	PDB header: chaperone Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfgl; PDBTitle: the crystal structure of bamb from moraxella catarrhalis
18	c3q54A_	Alignment		99.9	19	PDB header: lipid binding protein Chain: A: PDB Molecule: outer membrane assembly lipoprotein yfgl; PDBTitle: crystal structure of escherichia coli bamb
19	c5juyB_	Alignment		99.9	13	PDB header: apoptosis Chain: B: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: active human apoptosome with procaspase-9
20	c6nd4O_	Alignment		99.9	12	PDB header: ribosome Chain: Q: PDB Molecule: utp12; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
21	c5i2tA_	Alignment	not modelled	99.9	13	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
22	c3iytG_	Alignment	not modelled	99.9	10	PDB header: apoptosis Chain: G: PDB Molecule: apoptotic protease-activating factor 1; PDBTitle: structure of an apoptosome-procaspase-9 card complex
23	c6nd4O_	Alignment	not modelled	99.9	13	PDB header: ribosome Chain: O: PDB Molecule: utp1; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
24	c3hxA_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrrolo-quinoline quinone; PDBTitle: crystal structure of pyrrolo-quinoline quinone (pqq_dh) from2 methanococcus maripaludis, northeast structural genomics consortium3 target mrr86
25	c6nd4T_	Alignment	not modelled	99.9	17	PDB header: ribosome Chain: T: PDB Molecule: utp21; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
26	c6rteB_	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome c; PDBTitle: dihydro-heme d1 dehydrogenase nirn in complex with dhe
27	c5n1aB_	Alignment	not modelled	99.9	12	PDB header: translation Chain: B: PDB Molecule: utp4; PDBTitle: crystal structure of utp4 from chaetomium thermophilum
28	c3dm0A_	Alignment	not modelled	99.9	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 PDB header: signaling protein

29	c4yzsB_	Alignment	not modelled	99.9	18	Chain: B; PDB Molecule: eukaryotic translation initiation factor 2-alpha kinase 3; PDBTitle: crystal structures reveal transient perk luminal domain2 tetramerization in er stress signaling
30	c4nsxA_	Alignment	not modelled	99.8	10	PDB header: protein binding Chain: A; PDB Molecule: u3 small nucleolar rna-associated protein 21; PDBTitle: crystal structure of the utp21 tandem wd domain
31	c5a5uB_	Alignment	not modelled	99.8	13	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
32	c5a1vK_	Alignment	not modelled	99.8	10	PDB header: transport protein Chain: K; PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copi coat linkage i
33	c5dfzB_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: B; PDB Molecule: serine/threonine-protein kinase vps15; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
34	c5tzsT_	Alignment	not modelled	99.8	15	PDB header: translation Chain: T; PDB Molecule: utp21; PDBTitle: architecture of the yeast small subunit processome
35	d1jmxB_	Alignment	not modelled	99.8	13	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
36	c4o9dA_	Alignment	not modelled	99.8	9	PDB header: gene regulation Chain: A; PDB Molecule: rik1-associated factor 1; PDBTitle: structure of dos1 propeller
37	c2w18A_	Alignment	not modelled	99.8	9	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
38	c2ymuA_	Alignment	not modelled	99.8	12	PDB header: unknown function Chain: A; PDB Molecule: wd-40 repeat protein; PDBTitle: structure of a highly repetitive propeller structure
39	c3no2A_	Alignment	not modelled	99.8	14	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein of unknown function (baccac_01654) from2 bacteroides caccae at 1.35 a resolution
40	c3wj9A_	Alignment	not modelled	99.8	9	PDB header: translation Chain: A; PDB Molecule: eukaryotic translation initiation factor 2a; PDBTitle: crystal structure of the eukaryotic initiation factor
41	c4wjuB_	Alignment	not modelled	99.8	10	PDB header: biosynthetic protein Chain: B; PDB Molecule: ribosome assembly protein 4; PDBTitle: crystal structure of rsa4 from saccharomyces cerevisiae
42	c1nr0A_	Alignment	not modelled	99.8	14	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).
43	c3bwsA_	Alignment	not modelled	99.8	16	PDB header: unknown function Chain: A; PDB Molecule: protein lp49; PDBTitle: crystal structure of the leptospiral antigen lp49
44	c4wjsA_	Alignment	not modelled	99.8	11	PDB header: biosynthetic protein Chain: A; PDB Molecule: rsa4; PDBTitle: crystal structure of rsa4 from chaetomium thermophilum
45	c1gq1B_	Alignment	not modelled	99.8	10	PDB header: oxidoreductase Chain: B; PDB Molecule: cytochrome cd1 nitrite reductase; PDBTitle: cytochrome cd1 nitrite reductase, y25s mutant, oxidised form
46	c1pi6A_	Alignment	not modelled	99.8	12	PDB header: protein binding Chain: A; PDB Molecule: actin interacting protein 1; PDBTitle: yeast actin interacting protein 1 (aip1), orthorhombic crystal form
47	c5cvlA_	Alignment	not modelled	99.8	10	PDB header: protein binding Chain: A; PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48 (uaf-1), residues 2-580
48	c5thaA_	Alignment	not modelled	99.8	15	PDB header: rna binding protein Chain: A; PDB Molecule: gem-associated protein 5; PDBTitle: gemin5 wd40 repeats in complex with a guanosyl moiety
49	c6em5m_	Alignment	not modelled	99.8	10	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
50	c6chgD_	Alignment	not modelled	99.8	12	PDB header: transferase Chain: D; PDB Molecule: klla0a08800p; PDBTitle: crystal structure of the yeast compass catalytic module
51	c5k1bB_	Alignment	not modelled	99.8	9	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
52	c6cb1s_	Alignment	not modelled	99.8	13	PDB header: ribosome Chain: S; PDB Molecule: 60s ribosomal protein l20-a; PDBTitle: yeast nucleolar pre-60s ribosomal subunit (state 3)
53	c5wbiA_	Alignment	not modelled	99.8	15	PDB header: protein binding Chain: A; PDB Molecule: regulatory-associated protein of tor 1; PDBTitle: crystal structure of the arabidopsis thaliana raptor
54	c3j65q_	Alignment	not modelled	99.8	10	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. PDB header: ribosome

55	c6nd4W_	Alignment	not modelled	99.8	11	Chain: W: PDB Molecule: utp7; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
56	c4uerb_	Alignment	not modelled	99.7	12	PDB header: translation Chain: B: PDB Molecule: us2; PDBTitle: 40s-eif1-eif1a-eif3-eif3j translation initiation complex from2 lachancea kluyveri
57	c4yhca_	Alignment	not modelled	99.7	9	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
58	c5v1dA_	Alignment	not modelled	99.7	16	PDB header: transferase/substrate Chain: A: PDB Molecule: eif2ak3 protein; PDBTitle: complex structure of the bovine perk luminal domain and its substrate2 peptide
59	c5sv7D_	Alignment	not modelled	99.7	18	PDB header: translation Chain: D: PDB Molecule: eukaryotic translation initiation factor 2-alpha kinase 3; PDBTitle: the crystal structure of a chaperone
60	c5cvoA_	Alignment	not modelled	99.7	9	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
61	c5f30B_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: thiocyanate dehydrogenase; PDBTitle: thiocyanate dehydrogenase from thioalkalivibrio paradoxus
62	c4e54B_	Alignment	not modelled	99.7	9	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
63	c5cvoD_	Alignment	not modelled	99.7	10	PDB header: hydrolase/protein binding Chain: D: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
64	c4u1fA_	Alignment	not modelled	99.7	12	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
65	c5mzhB_	Alignment	not modelled	99.7	12	PDB header: motor protein Chain: B: PDB Molecule: dynein assembly factor with wdr repeat domains 1; PDBTitle: crystal structure of oda16 from chlamydomonas reinhardtii
66	c2oaiA_	Alignment	not modelled	99.7	13	PDB header: endocytosis/exocytosis Chain: A: PDB Molecule: protein sni1; PDBTitle: crystal structure of sro7 from s. cerevisiae
67	c4ycza_	Alignment	not modelled	99.7	14	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)
68	c6iczW_	Alignment	not modelled	99.7	11	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
69	c4noxA_	Alignment	not modelled	99.7	11	PDB header: translation Chain: A: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: structure of the nine-bladed beta-propeller of eif3b
70	d1nxb2	Alignment	not modelled	99.7	9	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like Family: WD40-repeat
71	c6nd4U_	Alignment	not modelled	99.7	9	PDB header: ribosome Chain: U: PDB Molecule: sof1; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
72	c6e29C_	Alignment	not modelled	99.7	12	PDB header: protein binding Chain: C: PDB Molecule: swd1-like protein; PDBTitle: crystal structure of myceliophtheria_thermophila cps50 (swd1) beta-2 propeller domain
73	c5nnozB_	Alignment	not modelled	99.7	13	PDB header: transport protein Chain: B: PDB Molecule: dynein assembly factor with wdr repeat domains 1; PDBTitle: crystal structure of human oda16
74	c5n4aA_	Alignment	not modelled	99.7	16	PDB header: transport protein Chain: A: PDB Molecule: intraflagellar transport protein 80; PDBTitle: crystal structure of chlamydomonas ift80
75	c1nexD_	Alignment	not modelled	99.7	9	PDB header: ligase, cell cycle Chain: D: PDB Molecule: cdc4 protein; PDBTitle: crystal structure of scskp1-sccdc4-cpd peptide complex
76	c4czvB_	Alignment	not modelled	99.7	10	PDB header: gene regulation Chain: B: PDB Molecule: pab-dependent poly(a)-specific ribonuclease subunit pan2; PDBTitle: structure of the neurospora crassa pan2 wd40 domain
77	c5o9zL_	Alignment	not modelled	99.7	11	PDB header: splicing Chain: L: PDB Molecule: wd40 repeat-containing protein smu1; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
78	c1nnoA_	Alignment	not modelled	99.7	9	PDB header: oxidoreductase Chain: A: PDB Molecule: nitrite reductase; PDBTitle: conformational changes occurring upon no binding in nitrite reductase2 from pseudomonas aeruginosa
79	c6nd4H_	Alignment	not modelled	99.7	8	PDB header: ribosome Chain: H: PDB Molecule: utp17; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
80	d1nira2	Alignment	not modelled	99.7	10	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
81	c5nzc_	Alignment	not modelled	99.7	8	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit beta'; PDBTitle: the structure of the copi coat linkage iv
82	c5ch2A_	Alignment	not modelled	99.7	11	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
83	c2ovqB_	Alignment	not modelled	99.7	10	PDB header: transcription/cell cycle Chain: B: PDB Molecule: f-box/wd repeat protein 7; PDBTitle: structure of the skp1-fbw7-cyclinedegc complex
84	c6nd4S_	Alignment	not modelled	99.7	8	PDB header: ribosome Chain: S: PDB Molecule: utp18; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
85	c6nd4L_	Alignment	not modelled	99.7	11	PDB header: ribosome Chain: L: PDB Molecule: utp5; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
86	c2pbiB_	Alignment	not modelled	99.7	13	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
87	c2i0tB_	Alignment	not modelled	99.7	8	PDB header: oxidoreductase Chain: B: PDB Molecule: aromatic amine dehydrogenase; PDBTitle: crystal structure of phenylacetaldehyde derived r-2 carbinolamine adduct of aromatic amine dehydrogenase
88	c4jpc_	Alignment	not modelled	99.7	9	PDB header: transferase Chain: C: PDB Molecule: target of rapamycin complex subunit lst8; PDBTitle: structure of mtor/delta-n-mlst8-atpgamma-s-mg complex
89	c2be1A_	Alignment	not modelled	99.7	16	PDB header: transcription Chain: A: PDB Molecule: serine/threonine-protein kinase/endoribonuclease ire1; PDBTitle: structure of the compact luminal domain of yeast ire1
90	c6cmkB_	Alignment	not modelled	99.7	10	PDB header: metal binding protein Chain: B: PDB Molecule: aztd protein; PDBTitle: crystal structure of citrobacter koseri aztd
91	c6nd4N_	Alignment	not modelled	99.7	10	PDB header: ribosome Chain: N: PDB Molecule: utp4; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
92	d1l0qa2	Alignment	not modelled	99.6	10	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: YVTN repeat
93	c6iyA_	Alignment	not modelled	99.6	14	PDB header: lipid binding protein Chain: A: PDB Molecule: wd repeat domain phosphoinositide-interacting protein 3; PDBTitle: crystal structure of human wipi3,loop deletion mutant
94	c5a1uC_	Alignment	not modelled	99.6	9	PDB header: transport protein Chain: C: PDB Molecule: coatomer subunit alpha; PDBTitle: the structure of the copi coat triad
95	c5a1vL_	Alignment	not modelled	99.6	8	PDB header: transport protein Chain: L: PDB Molecule: coatomer subunit beta; PDBTitle: the structure of the copi coat linkage i
96	d1gxra_	Alignment	not modelled	99.6	12	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like Family: WD40-repeat
97	d1erja_	Alignment	not modelled	99.6	12	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like Family: WD40-repeat
98	d2ovrb2	Alignment	not modelled	99.6	6	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like Family: WD40-repeat
99	c6ck1C_	Alignment	not modelled	99.6	8	PDB header: metal binding protein Chain: C: PDB Molecule: a1b2f4 protein; PDBTitle: crystal structure of paracoccus denitrificans aztd
100	c4h5jB_	Alignment	not modelled	99.6	9	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)
101	d1nr0a1	Alignment	not modelled	99.6	8	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like Family: WD40-repeat
102	c6dloA_	Alignment	not modelled	99.6	10	PDB header: cytosolic protein Chain: A: PDB Molecule: leucine-rich repeat serine/threonine-protein kinase 2; PDBTitle: crystal structure of lrrk2 wd40 domain dimer
103	c5o9zF_	Alignment	not modelled	99.6	11	PDB header: splicing Chain: F: PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp4; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
104	c3jcmB_	Alignment	not modelled	99.6	14	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
105	c6fqIA_	Alignment	not modelled	99.6	13	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
						PDB header: protein binding

106	c5cxcA_	Alignment	not modelled	99.6	9	Chain: A: PDB Molecule: ribosome biogenesis protein ytm1; PDBTitle: structure of ytm1 bound to the c-terminal domain of erb1 in p 65 2 22 space group
107	c4zovB_	Alignment	not modelled	99.6	11	PDB header: chaperone Chain: B: PDB Molecule: ribosome assembly protein sqt1; PDBTitle: crystal structure of the saccharomyces cerevisiae sqt1
108	c2j57J_	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: J: PDB Molecule: methylamine dehydrogenase heavy chain; PDBTitle: x-ray reduced paracoccus denitrificans methylamine2 dehydrogenase n-quinol in complex with amicyanin.
109	c6r5kA_	Alignment	not modelled	99.6	10	PDB header: rna binding protein Chain: A: PDB Molecule: pan2-pan3 deadenylation complex catalytic subunit pan2; PDBTitle: cryo-em structure of a poly(a) rnp bound to the pan2-pan3 deadenylase
110	c5m89B_	Alignment	not modelled	99.6	17	PDB header: splicing Chain: B: PDB Molecule: spliceosome wd40 sc; PDBTitle: spliceosome component
111	c4xfvA_	Alignment	not modelled	99.6	10	PDB header: translation Chain: A: PDB Molecule: elongator complex protein 2; PDBTitle: crystal structure of elp2
112	d1pbyb_	Alignment	not modelled	99.6	12	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Quinohemoprotein amine dehydrogenase B chain
113	d2madh_	Alignment	not modelled	99.6	15	Fold: 7-bladed beta-propeller Superfamily: YVTN repeat-like/Quinoprotein amine dehydrogenase Family: Methylamine dehydrogenase, H-chain
114	c3ei4D_	Alignment	not modelled	99.6	7	PDB header: dna binding protein Chain: D: PDB Molecule: dna damage-binding protein 2; PDBTitle: structure of the hsddb1-hsddb2 complex
115	c6nd4J_	Alignment	not modelled	99.6	9	PDB header: ribosome Chain: J: PDB Molecule: utp15; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
116	c5ov3B_	Alignment	not modelled	99.6	11	PDB header: structural protein Chain: B: PDB Molecule: retinoblastoma-binding protein 5; PDBTitle: structure of the rbbp5 beta-propeller domain
117	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.
118	c4a11B_	Alignment	not modelled	99.6	12	PDB header: dna binding protein Chain: B: PDB Molecule: dna excision repair protein ercc-8; PDBTitle: structure of the hsddb1-hscsa complex
119	d1yfqg_	Alignment	not modelled	99.6	10	Fold: 7-bladed beta-propeller Superfamily: WD40 repeat-like Family: Cell cycle arrest protein BUB3
120	c3jzhA_	Alignment	not modelled	99.6	12	PDB header: gene regulation Chain: A: PDB Molecule: polycomb protein eed; PDBTitle: eed-h3k79me3