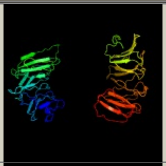
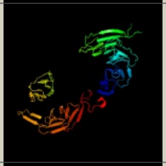
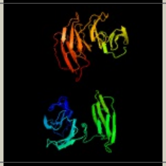
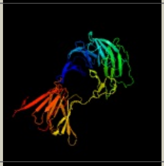
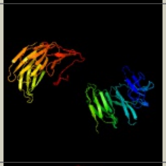
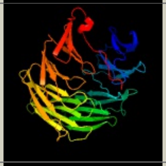
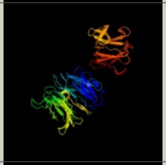
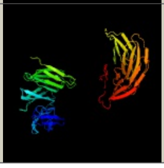
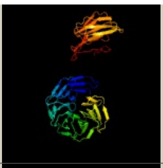
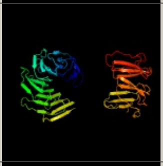
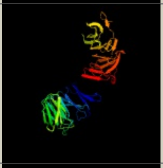
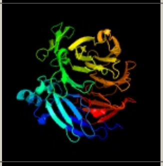
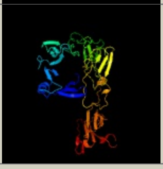
Phyre^2

Email	mdejesus@rockefeller.edu
Description	RVBD1057_(-)_1179401_1180582
Date	Wed Jul 31 22:05:13 BST 2019
Unique Job ID	5b2972e5d40c2ee7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5juyB_	Alignment		100.0	17	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**apoptotic protease-activating factor 1; **PDBTitle:** active human apoptosome with procaspase-9
2	c6nd4O_	Alignment		100.0	14	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**utp1; **PDBTitle:** conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
3	c6nd4Q_	Alignment		100.0	12	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**utp12; **PDBTitle:** conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
4	c5n1aB_	Alignment		100.0	18	**PDB header:**translation **Chain:** B: **PDB Molecule:**utp4; **PDBTitle:** crystal structure of utp4 from chaetomium thermophilum
5	c5i2tA_	Alignment		100.0	15	**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
6	c5tzsT_	Alignment		100.0	13	**PDB header:**translation **Chain:** T: **PDB Molecule:**utp21; **PDBTitle:** architecture of the yeast small subunit processome
7	c5a5uB_	Alignment		100.0	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
8	c3dm0A_	Alignment		100.0	17	**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
9	c1nr0A_	Alignment		100.0	18	**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).
10	c4uerb_	Alignment		100.0	10	**PDB header:**translation **Chain:** B: **PDB Molecule:**us2; **PDBTitle:** 40s-eif1-eif1a-eif3-eif3j translation initiation complex from2 lachancea kluyveri
11	c6nd4T_	Alignment		100.0	12	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**utp21; **PDBTitle:** conformational switches control early maturation of the eukaryotic2 small ribosomal subunit

12	c2ymuA_	Alignment		100.0	23	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**wd-40 repeat protein; **PDBTitle:** structure of a highly repetitive propeller structure
13	c3iytG_	Alignment		100.0	15	**PDB header:**apoptosis **Chain:** G: **PDB Molecule:**apoptotic protease-activating factor 1; **PDBTitle:** structure of an apoptosome-procaspase-9 card complex
14	c5a1vK_	Alignment		100.0	15	**PDB header:**transport protein **Chain:** K: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** the structure of the copi coat linkage i
15	c5thaA_	Alignment		100.0	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**gem-associated protein 5; **PDBTitle:** gemin5 wd40 repeats in complex with a guanosyl moiety
16	c5f30B_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thiocyanate dehydrogenase; **PDBTitle:** thiocyanate dehydrogenase from thioalkalivibrio paradoxus
17	c5cvlA_	Alignment		100.0	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**wd repeat-containing protein 48; **PDBTitle:** wdr48 (uaf-1), residues 2-580
18	c5cvoD_	Alignment		100.0	13	**PDB header:**hydrolase/protein binding **Chain:** D: **PDB Molecule:**wd repeat-containing protein 48; **PDBTitle:** wdr48:usp46~ubiquitin ternary complex
19	c5cvoA_	Alignment		100.0	13	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**wd repeat-containing protein 48; **PDBTitle:** wdr48:usp46~ubiquitin ternary complex
20	c6nd4H_	Alignment		100.0	16	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**utp17; **PDBTitle:** conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
21	c1pi6A_	Alignment	not modelled	100.0	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**actin interacting protein 1; **PDBTitle:** yeast actin interacting protein 1 (aip1), orthorhombic crystal form
22	c4xfvA_	Alignment	not modelled	100.0	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongator complex protein 2; **PDBTitle:** crystal structure of elp2
23	c4yczA_	Alignment	not modelled	100.0	16	**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)
24	c4nsxA_	Alignment	not modelled	100.0	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**u3 small nucleolar rna-associated protein 21; **PDBTitle:** crystal structure of the utp21 tandem wd domain
25	c5k1bB_	Alignment	not modelled	100.0	11	**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
26	c5ch2A_	Alignment	not modelled	100.0	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
27	c3wj9A_	Alignment	not modelled	100.0	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 2a; **PDBTitle:** crystal structure of the eukaryotic initiation factor
28	c4ci8B_	Alignment	not modelled	100.0	15	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**echinoderm microtubule-associated protein-like 1; **PDBTitle:** crystal structure of the tandem atypical beta-propeller domain of eml1

29	c3bwsA_	Alignment	not modelled	100.0	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein lp49; **PDBTitle:** crystal structure of the leptospiral antigen lp49
30	c4u1fA_	Alignment	not modelled	100.0	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
31	c4yhcA_	Alignment	not modelled	100.0	12	**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
32	c6nd4N_	Alignment	not modelled	100.0	11	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**utp4; **PDBTitle:** conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
33	c4noxA_	Alignment	not modelled	100.0	12	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit b; **PDBTitle:** structure of the nine-bladed beta-propeller of eif3b
34	c4wjsA_	Alignment	not modelled	100.0	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**rsa4; **PDBTitle:** crystal structure of rsa4 from chaetomium thermophilum
35	c6chgD_	Alignment	not modelled	100.0	10	**PDB header:**transferase **Chain:** D: **PDB Molecule:**klla0a08800p; **PDBTitle:** crystal structure of the yeast compass catalytic module
36	c5mzhB_	Alignment	not modelled	100.0	11	**PDB header:**motor protein **Chain:** B: **PDB Molecule:**dynein assembly factor with wdr repeat domains 1; **PDBTitle:** crystal structure of oda16 from chlamydomonas reinhardtii
37	c6rteB_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome c; **PDBTitle:** dihydro-heme d1 dehydrogenase nirn in complex with dhe
38	c4o9dA_	Alignment	not modelled	100.0	10	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**rik1-associated factor 1; **PDBTitle:** structure of dos1 propeller
39	c4wjuB_	Alignment	not modelled	100.0	9	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**ribosome assembly protein 4; **PDBTitle:** crystal structure of rsa4 from saccharomyces cerevisiae
40	d1l0qa2	Alignment	not modelled	100.0	26	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**YVTN repeat
41	c5nzvC_	Alignment	not modelled	100.0	8	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**coatomer subunit beta'; **PDBTitle:** the structure of the copi coat linkage iv
42	c1gq1B_	Alignment	not modelled	100.0	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome cd1 nitrite reductase; **PDBTitle:** cytochrome cd1 nitrite reductase, y25s mutant, oxidised form
43	c3mkqA_	Alignment	not modelled	100.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**coatomer beta'-subunit; **PDBTitle:** crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat
44	d1fwxa2	Alignment	not modelled	100.0	14	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
45	d1jmxb_	Alignment	not modelled	100.0	13	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
46	c5a1vL_	Alignment	not modelled	100.0	7	**PDB header:**transport protein **Chain:** L: **PDB Molecule:**coatomer subunit beta; **PDBTitle:** the structure of the copi coat linkage i
47	c1nnoA_	Alignment	not modelled	100.0	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrite reductase; **PDBTitle:** conformational changes occurring upon no binding in nitrite reductase2 from pseudomonas aeruginosa
48	c5nnzB_	Alignment	not modelled	100.0	10	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**dynein assembly factor with wdr repeat domains 1; **PDBTitle:** crystal structure of human oda16
49	c4e54B_	Alignment	not modelled	100.0	13	**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
50	c6iczW_	Alignment	not modelled	100.0	12	**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
51	c6nd4U_	Alignment	not modelled	100.0	13	**PDB header:**ribosome **Chain:** U: **PDB Molecule:**sof1; **PDBTitle:** conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
52	c2oajA_	Alignment	not modelled	100.0	12	**PDB header:**endocytosis/exocytosis **Chain:** A: **PDB Molecule:**protein sni1; **PDBTitle:** crystal structure of sro7 from s. cerevisiae
53	c4lg9A_	Alignment	not modelled	100.0	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**f-box-like/wd repeat-containing protein tbl1xr1; **PDBTitle:** crystal structure of tbl1xr1 wd40 repeats
54	c6em5m_	Alignment	not modelled	100.0	11	**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

55	d1pbyb_	Alignment	not modelled	100.0	14	**Fold:**7-bladed beta-propeller **Superfamily:**YVTN repeat-like/Quinoprotein amine dehydrogenase **Family:**Quinohemoprotein amine dehydrogenase B chain
56	c3jcmB_	Alignment	not modelled	100.0	16	**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
57	d2ovrb2	Alignment	not modelled	100.0	10	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
58	c6nd4S_	Alignment	not modelled	100.0	14	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**utp18; **PDBTitle:** conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
59	d1nira2	Alignment	not modelled	100.0	11	**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
60	c5a1uC_	Alignment	not modelled	100.0	10	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**coatomer subunit alpha; **PDBTitle:** the structure of the copi coat triad
61	c6cb1s_	Alignment	not modelled	100.0	13	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**60s ribosomal protein l20-a; **PDBTitle:** yeast nucleolar pre-60s ribosomal subunit (state 3)
62	c2ovqB_	Alignment	not modelled	100.0	11	**PDB header:**transcription/cell cycle **Chain:** B: **PDB Molecule:**f-box/wd repeat protein 7; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex
63	d1gxra_	Alignment	not modelled	100.0	12	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
64	c5n4aA_	Alignment	not modelled	100.0	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**intraflagellar transport protein 80; **PDBTitle:** crystal structure of chlamydomonas ift80
65	c3jroA_	Alignment	not modelled	100.0	13	**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
66	c3j65q_	Alignment	not modelled	100.0	17	**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.
67	c4zovB_	Alignment	not modelled	100.0	10	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**ribosome assembly protein sqt1; **PDBTitle:** crystal structure of the saccharomyces cerevisiae sqt1
68	c6eojD_	Alignment	not modelled	100.0	11	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**polyadenylation factor subunit 2,polyadenylation factor **PDBTitle:** polya polymerase module of the cleavage and polyadenylation factor2 (cpf) from saccharomyces cerevisiae
69	c1nexD_	Alignment	not modelled	100.0	12	**PDB header:**ligase, cell cycle **Chain:** D: **PDB Molecule:**cdc4 protein; **PDBTitle:** crystal structure of scskp1-sccdc4-cpd peptide complex
70	c6iyyA_	Alignment	not modelled	100.0	13	**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
71	d1nexb2	Alignment	not modelled	100.0	13	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
72	c4bzkA_	Alignment	not modelled	100.0	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec31; **PDBTitle:** the structure of the copii coat assembled on membranes
73	c2pm9A_	Alignment	not modelled	100.0	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein transport protein sec31; **PDBTitle:** crystal structure of yeast sec13/31 vertex element of the copii2 vesicular coat
74	c3frxB_	Alignment	not modelled	100.0	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide-binding protein subunit beta- **PDBTitle:** crystal structure of the yeast orthologue of rack1, asc1.
75	c2j57J_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**methylamine dehydrogenase heavy chain; **PDBTitle:** x-ray reduced paraccocus denitrificans methylamine2 dehydrogenase n-quinol in complex with amicyanin.
76	c4a11B_	Alignment	not modelled	100.0	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna excision repair protein ercc-8; **PDBTitle:** structure of the hsddb1-hscsa complex
77	c5a31R_	Alignment	not modelled	100.0	13	**PDB header:**cell cycle **Chain:** R: **PDB Molecule:**the anaphase-promoting complex chain r; **PDBTitle:** structure of the human apc-cdh1-hsl1-ubch10 complex.
78	c5ov3B_	Alignment	not modelled	100.0	14	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**retinoblastoma-binding protein 5; **PDBTitle:** structure of the rbbp5 beta-propeller domain
79	c5dfzB_	Alignment	not modelled	100.0	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase vps15; **PDBTitle:** structure of vps34 complex ii from s. cerevisiae.
80	c6nd4W_	Alignment	not modelled	100.0	14	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**utp7; **PDBTitle:** conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
						Fold:7-bladed beta-propeller

81	d1tbga_	Alignment	not modelled	100.0	13	**Superfamily:**WD40 repeat-like **Family:**WD40-repeat
82	c3zwlB_	Alignment	not modelled	100.0	12	**PDB header:**translation **Chain:** B: **PDB Molecule:**eukaryotic translation initiation factor 3 subunit i; **PDBTitle:** structure of eukaryotic translation initiation factor eif3i complex2 with eif3b c-terminus (655-700)
83	c3jb9K_	Alignment	not modelled	100.0	11	**PDB header:**rna binding protein/rna **Chain:** K: **PDB Molecule:**pre-mrna-splicing factor prp5; **PDBTitle:** cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
84	c6nd4J_	Alignment	not modelled	100.0	16	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**utp15; **PDBTitle:** conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
85	c3u4yA_	Alignment	not modelled	100.0	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** the crystal structure of a functionally unknown protein (dtox_1751)2 from desulfotomaculum acetoxidans dsm 771.
86	c6e29C_	Alignment	not modelled	100.0	11	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**swd1-like protein; **PDBTitle:** crystal structure of myceliophteria_thermophila cps50 (swd1) beta-2 propeller domain
87	c2xznR_	Alignment	not modelled	100.0	11	**PDB header:**ribosome **Chain:** R: **PDB Molecule:**rack1; **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 2
88	c5g04R_	Alignment	not modelled	100.0	16	**PDB header:**cell cycle **Chain:** R: **PDB Molecule:**cell division cycle protein 20 homolog; **PDBTitle:** structure of the human apc-cdc20-hsl1 complex
89	c4jspC_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**target of rapamycin complex subunit lst8; **PDBTitle:** structure of mtordeltan-mlst8-atpgammas-mg complex
90	d1nr0a1	Alignment	not modelled	99.9	13	**Fold:**7-bladed beta-propeller **Superfamily:**WD40 repeat-like **Family:**WD40-repeat
91	c2pbiB_	Alignment	not modelled	99.9	11	**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
92	c5o9zL_	Alignment	not modelled	99.9	17	**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)
93	c3acpA_	Alignment	not modelled	99.9	11	**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
94	c6bm0B_	Alignment	not modelled	99.9	10	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**pre-mrna 3' end processing protein wdr33; **PDBTitle:** cryo-em structure of human cpsf-160-wdr33 complex at 3.8 a resolution
95	c4ui9R_	Alignment	not modelled	99.9	17	**PDB header:**cell cycle **Chain:** R: **PDB Molecule:**fizzy-related protein homolog; **PDBTitle:** atomic structure of the human anaphase-promoting complex
96	c3mmyE_	Alignment	not modelled	99.9	9	**PDB header:**nuclear protein **Chain:** E: **PDB Molecule:**mrna export factor; **PDBTitle:** structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1
97	c6bk8D_	Alignment	not modelled	99.9	12	**PDB header:**rna binding protein **Chain:** D: **PDB Molecule:**pre-mrna-splicing factor prp46; **PDBTitle:** s. cerevisiae spliceosomal post-catalytic p complex
98	c3iz6a_	Alignment	not modelled	99.9	8	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein sa (s2p); **PDBTitle:** localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
99	c1r5mA_	Alignment	not modelled	99.9	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sir4-interacting protein sif2; **PDBTitle:** crystal structure of the c-terminal wd40 domain of sif2
100	c6mzcG_	Alignment	not modelled	99.9	16	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription initiation factor tfiid subunit 5; **PDBTitle:** human tfiid bc core
101	c2w18A_	Alignment	not modelled	99.9	15	**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
102	c5wbiA_	Alignment	not modelled	99.9	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**regulatory-associated protein of tor 1; **PDBTitle:** crystal structure of the arabidopsis thaliana raptor
103	c5o9zF_	Alignment	not modelled	99.9	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	d1k32a3	Alignment	not modelled	99.9	11	**Fold:**7-bladed beta-propeller **Superfamily:**Tricorn protease domain 2 **Family:**Tricorn protease domain 2
105	c4zoyA_	Alignment	not modelled	99.9	10	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**sqt1; **PDBTitle:** crystal structure of the chaetomium thermophilum sqt1
106	d1qksa2	Alignment	not modelled	99.9	11	**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
107	c1k32E_	Alignment	not modelled	99.9	12	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** crystal structure of the tricorn protease
108	c2gnqA_	Alignment	not modelled	99.9	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**wd-repeat protein 5; **PDBTitle:** structure of wdr5
109	c5mqfE_	Alignment	not modelled	99.9	10	**PDB header:**splicing **Chain:** E: **PDB Molecule:**pre-mrna-processing factor 17; **PDBTitle:** cryo-em structure of a human spliceosome activated for step 2 of2 splicing (c* complex)
110	c5c2vB_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**hydrazine synthase beta subunit; **PDBTitle:** kuenenia stuttgartiensis hydrazine synthase
111	c1n6dE_	Alignment	not modelled	99.9	12	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**tricorn protease; **PDBTitle:** tricorn protease in complex with tetrapeptide chloromethyl2 ketone derivative
112	c6fqlA_	Alignment	not modelled	99.9	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
113	c6n8sA_	Alignment	not modelled	99.9	14	**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 (lgl2). apkc phosphorylated, crystal form 3.
114	d1qnia2	Alignment	not modelled	99.9	16	**Fold:**7-bladed beta-propeller **Superfamily:**Nitrous oxide reductase, N-terminal domain **Family:**Nitrous oxide reductase, N-terminal domain
115	c1qniE_	Alignment	not modelled	99.9	16	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nitrous-oxide reductase; **PDBTitle:** crystal structure of nitrous oxide reductase from pseudomonas nautica,2 at 2.4a resolution
116	c3jzhA_	Alignment	not modelled	99.9	11	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**polycomb protein eed; **PDBTitle:** eed-h3k79me3
117	c3jcrD_	Alignment	not modelled	99.9	13	**PDB header:**splicing **Chain:** D: **PDB Molecule:**u5-40k; **PDBTitle:** 3d structure determination of the human*u4/u6.u5* tri-snrnp complex
118	c3ei3B_	Alignment	not modelled	99.9	9	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna damage-binding protein 2; **PDBTitle:** structure of the hsddb1-drddb2 complex
119	c4u7aA_	Alignment	not modelled	99.9	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**ribosome biogenesis protein erb1; **PDBTitle:** the carboxy-terminal domain of erb1 is a seven-bladed beta-propeller2 that binds rna.
120	c6cmkB_	Alignment	not modelled	99.9	13	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**aztd protein; **PDBTitle:** crystal structure of citrobacter koseri aztd