

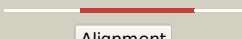













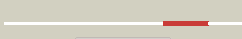





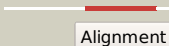






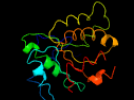










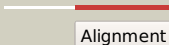
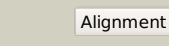

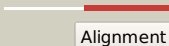



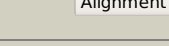


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0001_(dnaA)_1_1524
Date	Tue Jul 23 14:50:02 BST 2019
Unique Job ID	74b41116c2bc0842

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hcbC_	 Alignment		100.0	36	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
2	c2z4rB_	 Alignment		100.0	46	PDB header: dna binding protein Chain: B: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
3	d1l8qa2	 Alignment		100.0	40	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
4	c3bosA_	 Alignment		100.0	23	PDB header: hydrolase regulator,dna binding protein Chain: A: PDB Molecule: putative dna replication factor; PDBTitle: crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
5	c5x06G_	 Alignment		100.0	26	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
6	c3pvpA_	 Alignment		100.0	100	PDB header: dna binding protein/dna Chain: A: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
7	d1j1va_	 Alignment		100.0	39	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV
8	c2kjqA_	 Alignment		100.0	25	PDB header: replication Chain: A: PDB Molecule: dnaa-related protein; PDBTitle: solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
9	d1l8qa1	 Alignment		100.0	28	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV
10	c5bq5A_	 Alignment		100.0	18	PDB header: atp-binding protein Chain: A: PDB Molecule: insertion sequence is5376 putative atp-binding protein; PDBTitle: crystal structure of the istb aaa+ domain bound to adp-bef3
11	c6qell_	 Alignment		100.0	16	PDB header: replication Chain: L: PDB Molecule: dna replication protein dnac; PDBTitle: e. coli dnabc apo complex

12	c3ec2A_	 Alignment		99.9	17	PDB header: replication Chain: A: PDB Molecule: dna replication protein dnac; PDBTitle: crystal structure of the dnac helicase loader
13	c2w58B_	 Alignment		99.9	22	PDB header: hydrolase Chain: B: PDB Molecule: primosome component (helicase loader); PDBTitle: crystal structure of the dnai
14	c3pfiB_	 Alignment		99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
15	c4m4wO_	 Alignment		99.9	21	PDB header: replication Chain: O: PDB Molecule: primosomal protein dnai; PDBTitle: mechanistic implications for the bacterial primosome assembly of the2 structure of a helicase-helicase loader complex
16	c2qqzA_	 Alignment		99.9	18	PDB header: hydrolase Chain: A: PDB Molecule: putative primosome component; PDBTitle: crystal structure of a putative primosome component from streptococcus2 pyogenes serotype m3. northeast structural genomics target dr58
17	c1in8A_	 Alignment		99.9	20	PDB header: dna binding protein Chain: A: PDB Molecule: holliday junction dna helicase ruvb; PDBTitle: thermotoga maritima ruvb t158v
18	d1in4a2	 Alignment		99.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
19	c5he8J_	 Alignment		99.9	22	PDB header: protein binding Chain: J: PDB Molecule: helicase loader; PDBTitle: bacterial initiation protein
20	c3pvsA_	 Alignment		99.9	17	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
21	c6blbA_	 Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: holliday junction atp-dependent dna helicase ruvb; PDBTitle: 1.88 angstrom resolution crystal structure holliday junction atp-2 dependent dna helicase (ruvb) from pseudomonas aeruginosa in complex3 with adp
22	c3hu2C_	 Alignment	not modelled	99.8	19	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs
23	c3b9pA_	 Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
24	c3vfdA_	 Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
25	c4b4tM_	 Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
26	c2chgB_	 Alignment	not modelled	99.8	13	PDB header: dna-binding protein Chain: B: PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c domains 1 and 2
27	c5e7pA_	 Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qq54), a aaa atpase.
28	c1xwiA_	 Alignment	not modelled	99.8	17	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b

29	c4b4tH	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: H: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
30	c6epdM	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
31	d1ixsb2	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
32	c4xguB	Alignment	not modelled	99.8	13	PDB header: atp-binding protein Chain: B: PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
33	c5w0tA	Alignment	not modelled	99.8	18	PDB header: hydrolase Chain: A: PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
34	c4b4tJ	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
35	c3eihB	Alignment	not modelled	99.8	17	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein sorting-associated protein 4; PDBTitle: crystal structure of s.cerevisiae vps4 in the presence of atpgammas
36	c4l16A	Alignment	not modelled	99.8	16	PDB header: hydrolase Chain: A: PDB Molecule: figetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
37	c5g4gF	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: F: PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
38	c1iy2A	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsh; PDBTitle: crystal structure of the ftsh atpase domain from thermus2 thermophilus
39	c4z8xC	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: truncated ftsh from a. aeolicus
40	c3d8bB	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: B: PDB Molecule: figetin-like protein 1; PDBTitle: crystal structure of human figetin-like protein 1 in complex with adp
41	c6nyyC	Alignment	not modelled	99.8	17	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
42	c2zamA	Alignment	not modelled	99.8	17	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associating protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
43	d2ce7a2	Alignment	not modelled	99.8	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
44	c6hecH	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
45	c6epcJ	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
46	d1sxb2	Alignment	not modelled	99.8	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
47	d1iqpa2	Alignment	not modelled	99.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
48	c6b5cA	Alignment	not modelled	99.8	23	PDB header: cell cycle Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
49	c5t0gA	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: A: PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
50	c6nyyA	Alignment	not modelled	99.8	17	PDB header: translocase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
51	c2dhrC	Alignment	not modelled	99.8	21	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
52	c4b4tI	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
53	c5mpaL	Alignment	not modelled	99.8	14	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
54	d1fnna2	Alignment	not modelled	99.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain

55	d1sxc2	Alignment	not modelled	99.8	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
56	c2ce7B	Alignment	not modelled	99.8	21	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
57	c3cf1C	Alignment	not modelled	99.8	20	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
58	d1ixza	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
59	c4b4tK	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
60	c1hqcb	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: B: PDB Molecule: ruvb; PDBTitle: structure of ruvb from thermus thermophilus hb8
61	c5gjqL	Alignment	not modelled	99.8	17	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
62	d1njfa	Alignment	not modelled	99.8	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
63	d1sxd2	Alignment	not modelled	99.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
64	d1w5sa2	Alignment	not modelled	99.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
65	c4b4tL	Alignment	not modelled	99.8	15	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
66	c3zw6B	Alignment	not modelled	99.8	16	PDB header: photosynthesis Chain: B: PDB Molecule: ribulose biphosphate carboxylase/oxygenase activase 1, PDBTitle: model of hexameric aaa domain arrangement of green-type rubisco2 activase from tobacco.
67	c3h4mC	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: C: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: aaa atpase domain of the proteasome- activating nucleotidase
68	d1sxja2	Alignment	not modelled	99.7	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
69	c1s3sA	Alignment	not modelled	99.7	18	PDB header: protein binding Chain: A: PDB Molecule: transitional endoplasmic reticulum atpase (ter PDBTitle: crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
70	c5ifwB	Alignment	not modelled	99.7	16	PDB header: signaling protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: quantitative interaction mapping reveals an extended ubiquitin2 regulatory domain in aspl that disrupts functional p97 hexamers and3 induces cell death
71	c2c9oC	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: C: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1l
72	c6az0A	Alignment	not modelled	99.7	18	PDB header: hydrolase Chain: A: PDB Molecule: mitochondrial inner membrane i-aaa protease supercomplex PDBTitle: mitochondrial atpase protease yme1
73	c5ubvB	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: B: PDB Molecule: atpase domain of i-aaa protease; PDBTitle: atpase domain of i-aaa protease from myceliophthora thermophila
74	c5vq9D	Alignment	not modelled	99.7	12	PDB header: protein binding Chain: D: PDB Molecule: pachytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
75	c2c9oA	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: 3d structure of the human ruvb-like helicase ruvb1l
76	c6genX	Alignment	not modelled	99.7	25	PDB header: nuclear protein Chain: X: PDB Molecule: ruvb-like protein 1; PDBTitle: chromatin remodeller-nucleosome complex at 4.5 a resolution.
77	c3sylB	Alignment	not modelled	99.7	14	PDB header: chaperone Chain: B: PDB Molecule: protein cbbx; PDBTitle: crystal structure of the aaa+ protein cbbx, native structure
78	c3cf2B	Alignment	not modelled	99.7	14	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
79	c5oafB	Alignment	not modelled	99.7	19	PDB header: gene regulation Chain: B: PDB Molecule: ruvb-like 2; PDBTitle: human rvb1/rvb2 heterohexameric in ino80 complex
80	c5kzfJ	Alignment	not modelled	99.7	14	PDB header: hydrolase Chain: J: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of near full-length hexameric

						mycobacterium2 tuberculosis proteasomal atpase mpa in apo form PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
81	c6matE_	Alignment	not modelled	99.7	16	PDB header: motor protein Chain: D: PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
82	c5wc0D_	Alignment	not modelled	99.7	15	PDB header: dna binding protein/dna Chain: A: PDB Molecule: origin recognition complex subunit 1; PDBTitle: saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
83	c5zr1A_	Alignment	not modelled	99.7	14	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear valosin-containing protein-like; PDBTitle: human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
84	c2x8aA_	Alignment	not modelled	99.7	16	PDB header: replication Chain: A: PDB Molecule: activator 1 95 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
85	c1sxjA_	Alignment	not modelled	99.7	15	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen assimilation regulatory protein; PDBTitle: crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
86	c5m7nA_	Alignment	not modelled	99.7	19	PDB header: hydrolase Chain: A: PDB Molecule: cell division protease ftsh homolog; PDBTitle: crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
87	c2r65A_	Alignment	not modelled	99.7	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
88	c1ny5A_	Alignment	not modelled	99.7	21	PDB header: hydrolase Chain: H: PDB Molecule: ruvb-like 2; PDBTitle: crystal structure of the tip48 (tip49b) hexamer
89	c3uk6H_	Alignment	not modelled	99.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
90	d1sxje2	Alignment	not modelled	99.6	13	PDB header: replication/dna Chain: A: PDB Molecule: cell division control protein 6 homolog 1; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
91	c2qbyA_	Alignment	not modelled	99.6	21	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
92	c4ciuA_	Alignment	not modelled	99.6	18	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
93	c4lcbA_	Alignment	not modelled	99.6	17	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
94	c1iqpF_	Alignment	not modelled	99.6	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (ntrc family); PDBTitle: crystal structure of sigma54 activator ntrc4 in the inactive2 state
95	c3dzdA_	Alignment	not modelled	99.6	19	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
96	c1fnnB_	Alignment	not modelled	99.6	18	PDB header: dna binding protein Chain: C: PDB Molecule: origin recognition complex subunit 4; PDBTitle: structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
97	c5uj7C_	Alignment	not modelled	99.6	15	PDB header: transcription Chain: A: PDB Molecule: putative repressor protein luxo; PDBTitle: quorum-sensing signal integrator luxo - receiver+catalytic domains
98	c5ep0A_	Alignment	not modelled	99.6	19	PDB header: hydrolase Chain: A: PDB Molecule: paraplegin; PDBTitle: human paraplegin, aaa domain in complex with adp
99	c2qz4A_	Alignment	not modelled	99.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
100	d1r7ra3	Alignment	not modelled	99.6	16	PDB header: replication/dna Chain: B: PDB Molecule: cell division control protein 6 homolog 3; PDBTitle: crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
101	c2qbyB_	Alignment	not modelled	99.6	18	PDB header: motor protein Chain: C: PDB Molecule: atp-dependent clp protease atp-binding subunit clpx; PDBTitle: crystal structure of nucleotide-free hexameric clpx
102	c3hteC_	Alignment	not modelled	99.6	18	PDB header: hydrolase Chain: F: PDB Molecule: vesicle-fusing atpase; PDBTitle: structure of 20s supercomplex determined by single particle2 cryoelectron microscopy (state i)
103	c3j96F_	Alignment	not modelled	99.6	20	PDB header: hydrolase Chain: A: PDB Molecule: ruvb-like 1; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
104	c4ww4A_	Alignment	not modelled	99.6	21	PDB header: replication Chain: B: PDB Molecule: activator 1 37 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
105	c1sxjB_	Alignment	not modelled	99.6	12	PDB header: transferase

106	c1xxhB_	Alignment	not modelled	99.6	16	Chain: B; PDB Molecule: dna polymerase iii subunit gamma; PDBTitle: atpgs bound e. coli clamp loader complex
107	d1lv7a_	Alignment	not modelled	99.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
108	d1e32a2	Alignment	not modelled	99.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
109	d1ny5a2	Alignment	not modelled	99.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
110	c5kneF_	Alignment	not modelled	99.6	17	PDB header: chaperone Chain: F; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
111	c2chvE_	Alignment	not modelled	99.6	13	PDB header: dna-binding protein Chain: E; PDB Molecule: replication factor c small subunit; PDBTitle: replication factor c adnp complex
112	c3u5zM_	Alignment	not modelled	99.6	16	PDB header: dna binding protein/dna Chain: M; PDB Molecule: dna polymerase accessory protein 44; PDBTitle: structure of t4 bacteriophage clamp loader bound to the t4 clamp, 2 primer-template dna, and atp analog
113	c5kneA_	Alignment	not modelled	99.5	18	PDB header: chaperone Chain: A; PDB Molecule: heat shock protein 104; PDBTitle: cryoem reconstruction of hsp104 hexamer
114	c6opcF_	Alignment	not modelled	99.5	17	PDB header: motor protein Chain: F; PDB Molecule: cell division control protein 48; PDBTitle: cdc48 hexamer in a complex with substrate and shp1(ubx domain)
115	d1r6bx2	Alignment	not modelled	99.5	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
116	c5vy9C_	Alignment	not modelled	99.5	19	PDB header: chaperone Chain: C; PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
117	c2v1uA_	Alignment	not modelled	99.5	16	PDB header: replication Chain: A; PDB Molecule: cell division control protein 6 homolog; PDBTitle: structure of the aeropyrum pernix orc1 protein in complex2 with dna
118	c1sxC_	Alignment	not modelled	99.5	10	PDB header: replication Chain: C; PDB Molecule: activator 1 40 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor 2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear 3 antigen, pcna)
119	c6qi8E_	Alignment	not modelled	99.5	17	PDB header: chaperone Chain: E; PDB Molecule: ruvb-like 2; PDBTitle: truncated human r2tp complex, structure 3 (adp-filled)
120	c4ww4B_	Alignment	not modelled	99.5	20	PDB header: hydrolase Chain: B; PDB Molecule: ruvb-like 2; PDBTitle: double-heterohexameric rings of full-length ruv1(adp)/ruv2(adp)