







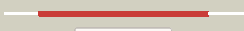












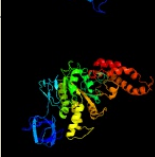



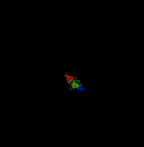







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1310_(atpD)_1465847_1467307
Date	Wed Jul 31 22:05:40 BST 2019
Unique Job ID	45e15379ab59114e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2w6jD_	 Alignment		100.0	61	PDB header: hydrolase Chain: D; PDB Molecule: atp synthase subunit beta, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 5.
2	c2jizD_	 Alignment		100.0	61	PDB header: hydrolase Chain: D; PDB Molecule: atp synthase subunit beta; PDBTitle: the structure of f1-atpase inhibited by resveratrol.
3	c1skyE_	 Alignment		100.0	65	PDB header: atp synthase Chain: E; PDB Molecule: f1-atpase; PDBTitle: crystal structure of the nucleotide free alpha3beta3 sub-complex of f2 f1-atpase from the thermophilic bacillus ps3
4	c6f5dE_	 Alignment		100.0	55	PDB header: hydrolase Chain: E; PDB Molecule: atp synthase subunit beta, mitochondrial; PDBTitle: trypanosoma brucei f1-atpase
5	c1fx0B_	 Alignment		100.0	62	PDB header: hydrolase Chain: B; PDB Molecule: atp synthase beta chain; PDBTitle: crystal structure of the chloroplast f1-atpase from spinach
6	c6focD_	 Alignment		100.0	94	PDB header: hydrolase Chain: D; PDB Molecule: atp synthase subunit beta; PDBTitle: f1-atpase from mycobacterium smegmatis
7	c6rdtY_	 Alignment		100.0	61	PDB header: proton transport Chain: Y; PDB Molecule: atp synthase subunit beta; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1e,2 composite map
8	c5b0oB_	 Alignment		100.0	26	PDB header: hydrolase/motor protein Chain: B; PDB Molecule: flagellum-specific atp synthase; PDBTitle: structure of the flih-flii complex
9	c2dpyA_	 Alignment		100.0	26	PDB header: hydrolase Chain: A; PDB Molecule: flagellum-specific atp synthase; PDBTitle: crystal structure of the flagellar type iii atpase flii
10	c2r9vA_	 Alignment		100.0	23	PDB header: hydrolase Chain: A; PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution
11	c6npjC_	 Alignment		100.0	26	PDB header: hydrolase Chain: C; PDB Molecule: translocator escn; PDBTitle: structure of the assembled atpase escn in complex with its central2 stalk esco from the enteropathogenic e. coli (epec) type iii3 secretion system

12	c2qe7C_	Alignment		100.0	25	PDB header: hydrolase Chain: C: PDB Molecule: atp synthase subunit alpha; PDBTitle: crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
13	c2w6fA_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase subunit alpha heart isoform, mitochondrial; PDBTitle: low resolution structures of bovine mitochondrial f1-atpase during2 controlled dehydration: hydration state 2.
14	c6re7U_	Alignment		100.0	23	PDB header: proton transport Chain: U: PDB Molecule: atp synthase subunit alpha; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 2c,2 focussed refinement of f1 head and rotor
15	c4b2gA_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: model of the yeast f1fo-atp synthase dimer based on subtomogram average
16	c3vr5D_	Alignment		100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: v-type sodium atpase subunit b; PDBTitle: crystal structure of nucleotide-free enterococcus hirae v1-atpase2 [ev1(l)]
17	c3a5dM_	Alignment		100.0	22	PDB header: hydrolase Chain: M: PDB Molecule: v-type atp synthase beta chain; PDBTitle: inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
18	c5bn4A_	Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: v-type atp synthase alpha chain; PDBTitle: structure of a unique atp synthase neqa-neqb in complex with anp from2 nanoarchaeum equitans
19	c5dn6A_	Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: atp synthase subunit alpha; PDBTitle: atp synthase from paracoccus denitrificans
20	c6fkhA_	Alignment		100.0	21	PDB header: membrane protein Chain: A: PDB Molecule: atp synthase subunit alpha, chloroplastic; PDBTitle: chloroplast f1fo conformation 2
21	c3vr5C_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: C: PDB Molecule: v-type sodium atpase catalytic subunit a; PDBTitle: crystal structure of nucleotide-free enterococcus hirae v1-atpase2 [ev1(l)]
22	c3j9uD_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: v-type proton atpase subunit b; PDBTitle: yeast v-atpase state 2
23	c1w0jB_	Alignment	not modelled	100.0	25	PDB header: hydrolase Chain: B: PDB Molecule: atp synthase alpha chain heart isoform, PDBTitle: beryllium fluoride inhibited bovine f1-atpase
24	c1kmhA_	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: atpase alpha subunit; PDBTitle: crystal structure of spinach chloroplast f1-atpase complexed with2 tentoxin
25	c30aaC_	Alignment	not modelled	100.0	23	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: atp synthase subunit alpha; PDBTitle: structure of the e.coli f1-atp synthase inhibited by subunit epsilon
26	c6focB_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: atp synthase subunit alpha,atp synthase subunit alpha,atp PDBTitle: f1-atpase from mycobacterium smegmatis
27	c3a5dB_	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: v-type atp synthase alpha chain; PDBTitle: inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
28	c3j9vC_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: C: PDB Molecule: v-type proton atpase catalytic subunit a; PDBTitle: yeast v-atpase state 3
						PDB header: hydrolase

29	c6q45C	Alignment	not modelled	100.0	25	Chain: C; PDB Molecule: atp synthase subunit alpha; PDBTitle: f1-atpase from fusobacterium nucleatum
30	c5t4oA	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: atp synthase subunit alpha; PDBTitle: autoinhibited e. coli atp synthase state 1
31	c4xd7B	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: atp synthase subunit alpha; PDBTitle: structure of thermophilic f1-atpase inhibited by epsilon subunit
32	c2c61A	Alignment	not modelled	100.0	22	PDB header: hydrolase Chain: A; PDB Molecule: a-type atp synthase non-catalytic subunit b; PDBTitle: crystal structure of the non-catalytic b subunit of a-type2 atpase from m. mazei go1
33	c6f5dB	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: atp synthase subunit alpha, mitochondrial; PDBTitle: trypanosoma brucei f1-atpase
34	c5bo5B	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B; PDB Molecule: neq263; PDBTitle: structure of a unique atp synthase subunit neqb from nanoarchaeum2 equitans
35	c3sdzA	Alignment	not modelled	100.0	28	PDB header: hydrolase Chain: A; PDB Molecule: v-type atp synthase alpha chain; PDBTitle: structural characterization of the subunit a mutant f427w of the a-atp2 synthase from pyrococcus horikoshii
36	c2oblA	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A; PDB Molecule: escn; PDBTitle: structural and biochemical analysis of a prototypical atpase from the2 type iii secretion system of pathogenic bacteria
37	c5syrA	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: A; PDB Molecule: probable atp synthase spa1/mxib; PDBTitle: crystal structure of atpase delta1-79 spa47 r350a
38	c1vdzA	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: A; PDB Molecule: a-type atpase subunit a; PDBTitle: crystal structure of a-type atpase catalytic subunit a from2 pyrococcus horikoshii ot3
39	c4nphA	Alignment	not modelled	100.0	28	PDB header: protein transport Chain: A; PDB Molecule: probable secretion system apparatus atp synthase ssan; PDBTitle: crystal structure of ssan from salmonella enterica
40	d2jdia3	Alignment	not modelled	100.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
41	d2jdid3	Alignment	not modelled	100.0	66	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
42	d1skye3	Alignment	not modelled	100.0	71	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
43	d1fx0b3	Alignment	not modelled	100.0	68	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
44	d1skyb3	Alignment	not modelled	100.0	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
45	d1fx0a3	Alignment	not modelled	100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
46	c3l0oB	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: B; PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
47	c1xpuB	Alignment	not modelled	100.0	17	PDB header: transcription/rna Chain: B; PDB Molecule: rho transcription termination factor; PDBTitle: structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
48	c3l0oA	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A; PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
49	d1xpua3	Alignment	not modelled	100.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
50	d2jdid1	Alignment	not modelled	100.0	57	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
51	d1skye1	Alignment	not modelled	100.0	59	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
52	d1fx0b1	Alignment	not modelled	100.0	58	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
53	d1skye2	Alignment	not modelled	99.2	55	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
						Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1

54	d1mabb2	Alignment	not modelled	99.2	48	ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
55	d1fx0b2	Alignment	not modelled	99.2	44	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
56	d2jdid2	Alignment	not modelled	99.1	53	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
57	c4ydsA_	Alignment	not modelled	99.0	13	PDB header: hydrolase Chain: A: PDB Molecule: flagella-related protein h; PDBTitle: flah from sulfolobus acidocaldarius with atp and mg-ion
58	c1u9iA_	Alignment	not modelled	98.9	11	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
59	d1fx0a1	Alignment	not modelled	98.8	15	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
60	d1tf7a1	Alignment	not modelled	98.7	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
61	d2jdia1	Alignment	not modelled	98.7	23	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
62	d1tf7a2	Alignment	not modelled	98.5	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
63	d1skyb1	Alignment	not modelled	98.5	20	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
64	d2f43a1	Alignment	not modelled	98.4	20	Fold: Left-handed superhelix Superfamily: C-terminal domain of alpha and beta subunits of F1 ATP synthase Family: C-terminal domain of alpha and beta subunits of F1 ATP synthase
65	d2i1qa2	Alignment	not modelled	98.4	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
66	c2w0mA_	Alignment	not modelled	98.3	21	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfolobus solfataricus p2
67	c3hr8A_	Alignment	not modelled	98.3	18	PDB header: recombination Chain: A: PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca
68	d1xp8a1	Alignment	not modelled	98.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
69	c2recB_	Alignment	not modelled	98.3	21	PDB header: helicase PDB COMPND:
70	c1pznA_	Alignment	not modelled	98.2	16	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
71	d1mo6a1	Alignment	not modelled	98.2	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
72	c5jwqA_	Alignment	not modelled	98.2	16	PDB header: transcription regulator Chain: A: PDB Molecule: circadian clock protein kinase kaic; PDBTitle: crystal structure of kaic s431e in complex with foldswitch-stabilized2 kaib from thermosynechococcus elongatus
73	c2zroA_	Alignment	not modelled	98.2	22	PDB header: hydrolase Chain: A: PDB Molecule: protein reca; PDBTitle: msreca adp form iv
74	c2dr3A_	Alignment	not modelled	98.2	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0273 protein ph0284; PDBTitle: crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
75	d1n0wa_	Alignment	not modelled	98.2	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
76	c2cvhB_	Alignment	not modelled	98.2	17	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair and recombination protein radb; PDBTitle: crystal structure of the radb recombinase
77	d1v5wa_	Alignment	not modelled	98.2	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
78	c5lkmB_	Alignment	not modelled	98.2	20	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein rada; PDBTitle: rada bound to dtdp
						Fold: P-loop containing nucleoside triphosphate hydrolases

79	d1ubea1	Alignment	not modelled	98.1	22	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
80	c3ldaA	Alignment	not modelled	98.1	21	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
81	c1t4gA	Alignment	not modelled	98.1	14	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: atpase in complex with amp-pnp
82	c2df1A	Alignment	not modelled	98.1	21	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament
83	c2ztsB	Alignment	not modelled	98.1	26	PDB header: atp-binding protein Chain: B: PDB Molecule: putative uncharacterized protein ph0186; PDBTitle: crystal structure of kaic-like protein ph0186 from hyperthermophilic2 archaea pyrococcus horikoshii ot3
84	c2zjbB	Alignment	not modelled	98.1	21	PDB header: recombination Chain: B: PDB Molecule: meiotic recombination protein dmc1/lim15 homolog; PDBTitle: crystal structure of the human dmc1-m200v polymorphic2 variant
85	d1pzna2	Alignment	not modelled	98.0	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
86	c1pznG	Alignment	not modelled	98.0	13	PDB header: recombination Chain: G: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
87	c1xp8A	Alignment	not modelled	98.0	23	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
88	c1szpC	Alignment	not modelled	97.9	18	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
89	d1szpa2	Alignment	not modelled	97.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
90	c3bh0A	Alignment	not modelled	97.9	12	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
91	c2q6tB	Alignment	not modelled	97.9	17	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
92	c2vyeA	Alignment	not modelled	97.8	16	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnc-ssdna complex
93	d1u94a1	Alignment	not modelled	97.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
94	c3io5B	Alignment	not modelled	97.8	16	PDB header: dna binding protein Chain: B: PDB Molecule: recombination and repair protein; PDBTitle: crystal structure of a dimeric form of the uvx3 recombinase core2 domain from enterobacteria phage t4
95	d1cr2a	Alignment	not modelled	97.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
96	d2jdia2	Alignment	not modelled	97.7	21	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
97	c3bs4A	Alignment	not modelled	97.6	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ph0321; PDBTitle: crystal structure of uncharacterized protein ph0321 from pyrococcus2 horikoshii in complex with an unknown peptide
98	c4a1fB	Alignment	not modelled	97.6	17	PDB header: hydrolase Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
99	d1skyb2	Alignment	not modelled	97.6	25	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
100	c5jzcG	Alignment	not modelled	97.5	16	PDB header: dna binding protein Chain: G: PDB Molecule: dna repair protein rad51 homolog 1; PDBTitle: helical filament
101	d1fx0a2	Alignment	not modelled	97.5	19	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
102	c4nmnA	Alignment	not modelled	97.5	25	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
103	c4wiaA	Alignment	not modelled	97.4	19	PDB header: atp-binding protein Chain: A: PDB Molecule: putative flagella-related protein h; PDBTitle: crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
104	c6bbmA	Alignment	not modelled	97.2	13	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: mechanisms of opening and closing of the bacterial replicative2 helicase: the dnab helicase and lambda p helicase

						loader complex
105	c6qe1B_	Alignment	not modelled	97.2	13	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
106	c4zc0A_	Alignment	not modelled	97.2	25	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
107	c3bgwD_	Alignment	not modelled	97.1	18	PDB header: replication Chain: D: PDB Molecule: dnab-like replicative helicase; PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
108	c3cmvG_	Alignment	not modelled	97.1	19	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-ssdna/dsdna2 structures
109	c3iz8F_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: F: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
110	c3iz8E_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: E: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
111	c3iz8A_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: A: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
112	c3iz8B_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: B: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
113	c3iz8G_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: G: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
114	c1vt4M_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: M: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
115	c1vt4P_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: P: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
116	c3iz8C_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: C: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
117	c3iz8H_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: H: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
118	c1vt4J_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: J: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
119	c1vt4K_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: K: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome
120	c3iz8D_	Alignment	not modelled	96.9	13	PDB header: apoptosis Chain: D: PDB Molecule: apaf-1 related killer dark; PDBTitle: structure of the drosophila apoptosome