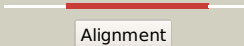

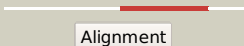

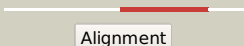







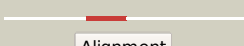















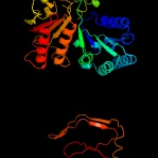
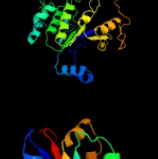
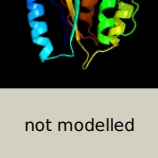


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3447c_(-)_3864707_3868417
Date	Fri Aug 9 18:20:12 BST 2019
Unique Job ID	926f1c1157c28bb7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4nh0A_	 Alignment		100.0	52	PDB header: cell cycle Chain: A: PDB Molecule: cell divisionftsk/spoiii; PDBTitle: cytoplasmic domain of the thermomonospora curvata type vii secretion2 atpase eccc
2	c4n1aE_	 Alignment		100.0	48	PDB header: protein binding/protein binding Chain: E: PDB Molecule: cell divisionftsk/spoiii; PDBTitle: thermomonospora curvata eccc (atpases 2 and 3) in complex with a2 signal sequence peptide
3	c4lyaA_	 Alignment		100.0	23	PDB header: cell cycle Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: essc (atpases 2 and 3) from geobacillus thermodenitrificans (semet)
4	c2iuuE_	 Alignment		100.0	27	PDB header: membrane protein Chain: E: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, hexamer
5	c2iutA_	 Alignment		100.0	27	PDB header: membrane protein Chain: A: PDB Molecule: dna translocase ftsk; PDBTitle: p. aeruginosa ftsk motor domain, dimeric
6	c2iusB_	 Alignment		100.0	24	PDB header: membrane protein Chain: B: PDB Molecule: dna translocase ftsk; PDBTitle: e. coli ftsk motor domain
7	c4kfuC_	 Alignment		99.9	13	PDB header: hydrolase Chain: C: PDB Molecule: genome packaging ntpase b204; PDBTitle: structure of the genome packaging ntpase b204 from sulfolobus turreted2 icosahedral virus 2 in complex with amppcp
8	c4d2iB_	 Alignment		99.9	21	PDB header: hydrolase Chain: B: PDB Molecule: hera; PDBTitle: crystal structure of the hera hexameric dna translocase2 from sulfolobus solfataricus bound to amp-pnp
9	c4ag5A_	 Alignment		99.8	21	PDB header: hydrolase Chain: A: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus
10	d1e9ra_	 Alignment		99.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
11	c4ag5D_	 Alignment		99.1	23	PDB header: hydrolase Chain: D: PDB Molecule: type iv secretory pathway virb4 components-like protein; PDBTitle: structure of virb4 of thermoanaerobacter pseudethanolicus

12	c1u9iA_	Alignment		99.0	19	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
13	c6matE_	Alignment		99.0	19	PDB header: ribosomal protein Chain: E: PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
14	c5g4gF_	Alignment		98.9	20	PDB header: hydrolase Chain: F: PDB Molecule: vcp-like atpase; PDBTitle: structure of the atpgs-bound vat complex
15	c5jwqA_	Alignment		98.8	15	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
16	c5ifwB_	Alignment		98.7	18	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
17	c3cf2B_	Alignment		98.7	16	PDB header: transport protein Chain: B: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/amp-pnp
18	c5e7pA_	Alignment		98.6	22	PDB header: hydrolase Chain: A: PDB Molecule: cell division control protein cdc48; PDBTitle: crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.
19	c1yqtA_	Alignment		98.2	16	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnaase I inhibitor; PDBTitle: rnaase-I inhibitor
20	c5udbD_	Alignment		98.0	14	PDB header: replication Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
21	c5vq9D_	Alignment	not modelled	97.9	18	PDB header: protein binding Chain: D: PDB Molecule: pacchytene checkpoint protein 2 homolog; PDBTitle: structure of human trip13, apo form
22	c3l0oA_	Alignment	not modelled	97.9	19	PDB header: hydrolase Chain: A: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
23	c4xgcE_	Alignment	not modelled	97.9	16	PDB header: dna binding protein Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: crystal structure of the eukaryotic origin recognition complex
24	c4xgcD_	Alignment	not modelled	97.9	13	PDB header: dna binding protein Chain: D: PDB Molecule: origin recognition complex subunit 4; PDBTitle: crystal structure of the eukaryotic origin recognition complex
25	c1xwiA_	Alignment	not modelled	97.9	23	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
26	c2zamA_	Alignment	not modelled	97.9	22	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 4b; PDBTitle: crystal structure of mouse skd1/vps4b apo-form
27	c3b9pA_	Alignment	not modelled	97.9	18	PDB header: hydrolase Chain: A: PDB Molecule: cg5977-pa, isoform a; PDBTitle: spastin
28	c3l0oB_	Alignment	not modelled	97.9	17	PDB header: hydrolase Chain: B: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
						PDB header: ribosome

29	c3j16B_	Alignment	not modelled	97.9	12	Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
30	c4b4tj_	Alignment	not modelled	97.9	21	PDB header: hydrolase Chain: J: PDB Molecule: 26s protease regulatory subunit 8 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
31	c5uj7C_	Alignment	not modelled	97.8	13	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
32	c3d8bB_	Alignment	not modelled	97.8	18	PDB header: hydrolase Chain: B: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of human fidgetin-like protein 1 in complex with adp
33	c6b5cA_	Alignment	not modelled	97.8	23	PDB header: cell cycle Chain: A: PDB Molecule: katanin p60 atpase-containing subunit a-like 1; PDBTitle: structural basis for katanin self-assembly
34	c4z8xC_	Alignment	not modelled	97.8	21	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent zinc metalloprotease ftsH; PDBTitle: truncated ftsH from a. aeolicus
35	c4xguB_	Alignment	not modelled	97.8	13	PDB header: atp-binding protein Chain: B: PDB Molecule: putative pachytene checkpoint protein 2; PDBTitle: structure of c. elegans pch-2
36	c6nyyC_	Alignment	not modelled	97.8	22	PDB header: translocase Chain: C: PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
37	c6epcJ_	Alignment	not modelled	97.8	20	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
38	c6opcF_	Alignment	not modelled	97.8	24	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)
39	c2r2aB_	Alignment	not modelled	97.7	14	PDB header: toxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis
40	c4kxfF_	Alignment	not modelled	97.7	11	PDB header: immune system Chain: F: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
41	d1fnna2	Alignment	not modelled	97.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
42	d1nlfa_	Alignment	not modelled	97.7	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
43	c1xpuB_	Alignment	not modelled	97.7	21	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)
44	c5l3rC_	Alignment	not modelled	97.7	15	PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
45	c4phtC_	Alignment	not modelled	97.7	25	PDB header: protein transport Chain: C: PDB Molecule: general secretory pathway protein e; PDBTitle: atpase gspe in complex with the cytoplasmic domain of gspI from the2 vibrio vulnificus type ii secretion system
46	c5vy9C_	Alignment	not modelled	97.6	15	PDB header: chaperone Chain: C: PDB Molecule: heat shock protein 104; PDBTitle: s. cerevisiae hsp104:casein complex, middle domain conformation
47	c5wc0D_	Alignment	not modelled	97.6	20	PDB header: motor protein Chain: D: PDB Molecule: meiotic spindle formation protein mei-1; PDBTitle: katanin hexamer in spiral conformation
48	c4l16A_	Alignment	not modelled	97.6	22	PDB header: hydrolase Chain: A: PDB Molecule: fidgetin-like protein 1; PDBTitle: crystal structure of figl-1 aaa domain in complex with adp
49	c4b4tH_	Alignment	not modelled	97.6	18	PDB header: hydrolase Chain: H: PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
50	c1s3sA_	Alignment	not modelled	97.6	21	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
51	c2v1uA_	Alignment	not modelled	97.6	17	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
52	c3cmvG_	Alignment	not modelled	97.6	19	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-sdna/dsdna2 structures
53	c3hu2C_	Alignment	not modelled	97.6	21	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97 n-d1 r86a mutant in complex with atpgs PDB header: dna binding protein/dna

54	c5zr1A_	Alignment	not modelled	97.5	10	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
55	c3cf1C_	Alignment	not modelled	97.5	20	PDB header: transport protein Chain: C: PDB Molecule: transitional endoplasmic reticulum atpase; PDBTitle: structure of p97/vcp in complex with adp/adp.alfx
56	c2ja1A_	Alignment	not modelled	97.5	12	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
57	d1w5sa2	Alignment	not modelled	97.5	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
58	d1p9ra_	Alignment	not modelled	97.5	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
59	c3bk7A_	Alignment	not modelled	97.5	15	PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abce1/rnaase-i inhibitor protein from2 pyrococcus abyssi
60	c5w0tA_	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: A: PDB Molecule: protein msp1; PDBTitle: crystal structure of monomeric msp1 from s. cerevisiae
61	c3vfdA_	Alignment	not modelled	97.5	20	PDB header: hydrolase Chain: A: PDB Molecule: spastin; PDBTitle: human spastin aaa domain
62	c6hecH_	Alignment	not modelled	97.5	23	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
63	c5mpaL_	Alignment	not modelled	97.5	20	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
64	c4kxfP_	Alignment	not modelled	97.5	10	PDB header: immune system Chain: P: PDB Molecule: nlr family card domain-containing protein 4; PDBTitle: crystal structure of nlrc4 reveals its autoinhibition mechanism
65	d1xpua3	Alignment	not modelled	97.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
66	c5uj7B_	Alignment	not modelled	97.5	13	PDB header: dna binding protein Chain: B: PDB Molecule: origin recognition complex subunit 1; PDBTitle: structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
67	c2ce7B_	Alignment	not modelled	97.4	29	PDB header: cell division protein Chain: B: PDB Molecule: cell division protein ftsh; PDBTitle: edta treated
68	c2dhrC_	Alignment	not modelled	97.4	25	PDB header: hydrolase Chain: C: PDB Molecule: ftsh; PDBTitle: whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
69	d1w36d1	Alignment	not modelled	97.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
70	c5kzfl_	Alignment	not modelled	97.4	16	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
71	c3sylvB_	Alignment	not modelled	97.4	19	PDB header: chaperone Chain: B: PDB Molecule: protein cbbx; PDBTitle: crystal structure of the aaa+ protein cbbx, native structure
72	c5gjqL_	Alignment	not modelled	97.4	20	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
73	c5l3qB_	Alignment	not modelled	97.4	18	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
74	c3pvsA_	Alignment	not modelled	97.4	19	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
75	c5ujmE_	Alignment	not modelled	97.4	17	PDB header: replication Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: structure of the active form of human origin recognition complex and2 its atpase motor module
76	c1fnnB_	Alignment	not modelled	97.4	17	PDB header: cell cycle Chain: B: PDB Molecule: cell division control protein 6; PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
77	c4lcbA_	Alignment	not modelled	97.4	13	PDB header: protein transport Chain: A: PDB Molecule: cell division protein cdvc, vps4; PDBTitle: structure of vps4 homolog from acidianus hospitalis
78	c5tshF_	Alignment	not modelled	97.3	23	PDB header: atp-binding protein Chain: F: PDB Molecule: type iv pilus biogenesis atpase pilb; PDBTitle: pilb from geobacter metallireducens bound to amp-pnp
79	c1sxjD_	Alignment	not modelled	97.3	14	PDB header: replication Chain: D: PDB Molecule: activator 1 41 kda subunit; PDBTitle: crystal structure of the eukaryotic clamp loader (replication factor 2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)

80	c2qbyA	Alignment	not modelled	97.3	12	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)
81	c4b4tL	Alignment	not modelled	97.3	21	PDB header: hydrolase Chain: L: PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
82	c1nsfA	Alignment	not modelled	97.3	26	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
83	c3eihB	Alignment	not modelled	97.3	25	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
84	c5x06G	Alignment	not modelled	97.3	15	PDB header: replication Chain: G: PDB Molecule: dnaa regulatory inactivator hda; PDBTitle: dna replication regulation protein
85	c5x40A	Alignment	not modelled	97.3	25	PDB header: transport protein Chain: A: PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp
86	c2vyeA	Alignment	not modelled	97.3	17	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dna-c-ssdna complex
87	d1n0wa	Alignment	not modelled	97.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
88	d1szpa2	Alignment	not modelled	97.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
89	d1jbka	Alignment	not modelled	97.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
90	c4b4tK	Alignment	not modelled	97.3	23	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
91	d1tf7a1	Alignment	not modelled	97.3	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
92	c6amxA	Alignment	not modelled	97.3	15	PDB header: transport protein Chain: A: PDB Molecule: abc transporter; PDBTitle: crystal structure of nucelotide binding domain of o-antigen2 polysaccharide abc-transporter
93	c4b4tM	Alignment	not modelled	97.3	23	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
94	c6epdM	Alignment	not modelled	97.3	22	PDB header: hydrolase Chain: M: PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
95	d1u94a1	Alignment	not modelled	97.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
96	c2j7pA	Alignment	not modelled	97.3	15	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
97	c1iy2A	Alignment	not modelled	97.2	22	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent metalloprotease ftsH; PDBTitle: crystal structure of the ftsH atpase domain from thermus2 thermophilus
98	c2q6tB	Alignment	not modelled	97.2	14	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
99	d1d2na	Alignment	not modelled	97.2	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
100	c3bh0A	Alignment	not modelled	97.2	13	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
101	c5t0gA	Alignment	not modelled	97.2	24	PDB header: hydrolase Chain: A: PDB Molecule: 26s protease regulatory subunit 7; PDBTitle: structural basis for dynamic regulation of the human 26s proteasome
102	c1iqpF	Alignment	not modelled	97.2	20	PDB header: replication Chain: F: PDB Molecule: rfcs; PDBTitle: crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
103	c4ciuA	Alignment	not modelled	97.2	21	PDB header: chaperone Chain: A: PDB Molecule: chaperone protein clpb; PDBTitle: crystal structure of e. coli clpb
104	c6azyA	Alignment	not modelled	97.2	17	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein hsp104; PDBTitle: crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
105	c2pcjB	Alignment	not modelled	97.2	13	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding protein lold; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5

106	c3te6A_	Alignment	not modelled	97.2	9	PDB header: gene regulation Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: crystal structure of the s. cerevisiae sir3 aaa+ domain
107	c1sxA_	Alignment	not modelled	97.2	15	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)
108	c3ldaA_	Alignment	not modelled	97.2	21	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
109	c5udbE_	Alignment	not modelled	97.1	16	PDB header: replication Chain: E: PDB Molecule: origin recognition complex subunit 5; PDBTitle: structural basis of mcm2-7 replicative helicase loading by orc-cdc62 and cdt1
110	d1l8qa2	Alignment	not modelled	97.1	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
111	d2awna2	Alignment	not modelled	97.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
112	c2kjqA_	Alignment	not modelled	97.1	16	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.
113	d1skyb3	Alignment	not modelled	97.1	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
114	d2jdia3	Alignment	not modelled	97.1	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
115	d1tf7a2	Alignment	not modelled	97.1	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
116	c2hcbC_	Alignment	not modelled	97.1	15	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
117	d2i1qa2	Alignment	not modelled	97.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
118	c6b5bA_	Alignment	not modelled	97.1	16	PDB header: immune system Chain: A: PDB Molecule: baculoviral iap repeat-containing protein 1e; PDBTitle: cryo-em structure of the naip5-nlrc4-flagellin inflammasome
119	c3ec2A_	Alignment	not modelled	97.1	13	PDB header: replication Chain: A: PDB Molecule: dna replication protein dnac; PDBTitle: crystal structure of the dnac helicase loader
120	c1sxC_	Alignment	not modelled	97.1	23	PDB header: replication Chain: C: PDB Molecule: activator 1 40 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)