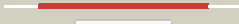


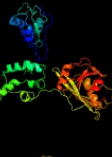
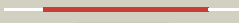




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3585_(radA)_4026623_4028065
Date	Fri Aug 9 18:20:26 BST 2019
Unique Job ID	fd24d238d8ed3496

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5lkmB_	 Alignment		100.0	45	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein rada; PDBTitle: rada bound to dtdp
2	c6on2A_	 Alignment		100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease la; PDBTitle: lon protease from yersinia pestis with y2853 substrate
3	c3m6aC_	 Alignment		100.0	17	PDB header: hydrolase Chain: C: PDB Molecule: atp-dependent protease la 1; PDBTitle: crystal structure of bacillus subtilis lon c-terminal domain
4	c5e7sG_	 Alignment		100.0	20	PDB header: hydrolase Chain: G: PDB Molecule: lon protease; PDBTitle: hexameric structure of a lona protease domain in active state
5	c4yplE_	 Alignment		100.0	18	PDB header: hydrolase Chain: E: PDB Molecule: lon protease; PDBTitle: crystal structure of a hexameric lona protease bound to three adps
6	c3k1jA_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent protease lon; PDBTitle: crystal structure of lon protease from thermococcus onnurineus na1
7	c5h45A_	 Alignment		100.0	41	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rada; PDBTitle: crystal structure of the c-terminal lon protease-like domain of 2 thermus thermophilus rada/sms
8	c2zroA_	 Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: protein reca; PDBTitle: msreca adp form iv
9	c2recB_	 Alignment		100.0	18	PDB header: helicase PDB COMPND:
10	d1xhka_	 Alignment		100.0	19	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: ATP-dependent protease Lon (La), catalytic domain
11	c1z0eF_	 Alignment		100.0	20	PDB header: hydrolase Chain: F: PDB Molecule: putative protease la homolog type; PDBTitle: crystal structure of a. fulgidus lon proteolytic domain

12	c2x36F_	Alignment		100.0	22	PDB header: hydrolase Chain: F: PDB Molecule: lon protease homolog, mitochondrial; PDBTitle: structure of the proteolytic domain of the human2 mitochondrial lon protease
13	d1mo6a1	Alignment		100.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
14	c4fw9A_	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: ttc1975 peptidase; PDBTitle: crystal structure of the lon-like protease mtalonc
15	d1xp8a1	Alignment		100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
16	d1tf7a2	Alignment		100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
17	d1tf7a1	Alignment		100.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
18	d1u94a1	Alignment		100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
19	c2q6tB_	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
20	c3ldaA_	Alignment		100.0	23	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
21	c6qe1B_	Alignment	not modelled	100.0	21	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
22	c4nmnA_	Alignment	not modelled	100.0	24	PDB header: replication Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: aquifex aeolicus replicative helicase (dnab) complexed with adp, at2 3.3 resolution
23	c1xp8A_	Alignment	not modelled	99.9	24	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
24	c3bgwD_	Alignment	not modelled	99.9	20	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
25	c2cvhB_	Alignment	not modelled	99.9	24	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair and recombination protein radb; PDBTitle: crystal structure of the radb recombinase
26	c6bbmA_	Alignment	not modelled	99.9	21	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
27	d1rrea_	Alignment	not modelled	99.9	20	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: ATP-dependent protease Lon (La), catalytic domain
28	c5jzcG_	Alignment	not modelled	99.9	21	PDB header: dna binding protein Chain: G: PDB Molecule: dna repair protein rad51 homolog 1; PDBTitle: helical filament

29	d1ubea1	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
30	c3bh0A	Alignment	not modelled	99.9	20	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
31	d2i1qa2	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
32	d1n0wa	Alignment	not modelled	99.9	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
33	d1v5wa	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
34	d1szpa2	Alignment	not modelled	99.9	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
35	c2ztsB	Alignment	not modelled	99.9	22	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
36	c4zc0A	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
37	c4wiaA	Alignment	not modelled	99.9	18	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
38	c2zjbB	Alignment	not modelled	99.9	19	PDB header: recombination Chain: B: PDB Molecule: meiotic recombination protein dmc1/lim15 homolog; PDBTitle: crystal structure of the human dmc1-m200v polymorphic2 variant
39	c4a1fB	Alignment	not modelled	99.9	24	PDB header: hydrolase Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase
40	c2df1A	Alignment	not modelled	99.9	24	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: crystal structure of left-handed rada filament
41	c1szpC	Alignment	not modelled	99.9	24	PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
42	c3hr8A	Alignment	not modelled	99.9	17	PDB header: recombination Chain: A: PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca
43	c1t4gA	Alignment	not modelled	99.9	22	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rada; PDBTitle: atpase in complex with amp-pnp
44	d1nlfa	Alignment	not modelled	99.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
45	c1u9iA	Alignment	not modelled	99.9	21	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
46	c4ydsA	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: A: PDB Molecule: flagella-related protein h; PDBTitle: flah from sulfobolus acidocaldarius with atp and mg-ion
47	c1pznA	Alignment	not modelled	99.9	23	PDB header: recombination Chain: A: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
48	c2vyeA	Alignment	not modelled	99.9	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnac-ssdna complex
49	c2w0mA	Alignment	not modelled	99.9	20	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfobolus solfataricus p2
50	d1pzna2	Alignment	not modelled	99.9	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
51	c1pznG	Alignment	not modelled	99.9	23	PDB header: recombination Chain: G: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
52	c1q57G	Alignment	not modelled	99.9	19	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
53	c5jwqA	Alignment	not modelled	99.9	21	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
54	c2dr3A	Alignment	not modelled	99.9	29	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
55	c3cmvG	Alignment	not modelled	99.8	21	PDB header: recombination Chain: G: PDB Molecule: protein reca;

55	c3cmvG	Alignment	not modelled	99.8	21	PDBTitle: mechanism of homologous recombination from the recA-dsdna/dsdna2 structures
56	d1cr2a	Alignment	not modelled	99.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
57	c3io5B	Alignment	not modelled	99.8	20	PDB header: dna binding protein Chain: B: PDB Molecule: recombination and repair protein; PDBTitle: crystal structure of a dimeric form of the uvsx recombinase core2 domain from enterobacteria phage t4
58	c3bs4A	Alignment	not modelled	99.8	16	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
59	c3cmwA	Alignment	not modelled	99.6	22	PDB header: recombination/dna Chain: A: PDB Molecule: protein recA; PDBTitle: mechanism of homologous recombination from the recA-dsdna/dsdna2 structures
60	c3cmuA	Alignment	not modelled	99.4	22	PDB header: recombination/dna Chain: A: PDB Molecule: protein recA; PDBTitle: mechanism of homologous recombination from the recA-dsdna/dsdna2 structures
61	c2cnwF	Alignment	not modelled	98.5	18	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
62	c2og2A	Alignment	not modelled	98.5	26	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
63	c3b9qA	Alignment	not modelled	98.4	25	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
64	c2qy9A	Alignment	not modelled	98.4	22	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
65	c6cy1B	Alignment	not modelled	98.4	22	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
66	c1zu4A	Alignment	not modelled	98.4	19	PDB header: protein transport Chain: A: PDB Molecule: ftsyt; PDBTitle: crystal structure of ftsyt from mycoplasma mycoides-space2 group p21212
67	c2j7pA	Alignment	not modelled	98.3	21	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsyt
68	c2q9cA	Alignment	not modelled	98.3	17	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsyt; PDBTitle: structure of ftsyt:gmppnp with mgcl complex
69	c2yhsA	Alignment	not modelled	98.3	22	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsyt; PDBTitle: structure of the e. coli srp receptor ftsyt
70	c2j37W	Alignment	not modelled	98.3	20	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
71	c6epcJ	Alignment	not modelled	98.3	22	PDB header: hydrolase Chain: J: PDB Molecule: 26s proteasome regulatory subunit 8; PDBTitle: ground state 26s proteasome (gs2)
72	c4ak9A	Alignment	not modelled	98.3	22	PDB header: protein transport Chain: A: PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsyt from physcomitrella patens
73	d1skyb3	Alignment	not modelled	98.3	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
74	c3dmdA	Alignment	not modelled	98.3	20	PDB header: transport protein Chain: A: PDB Molecule: signal recognition particle receptor; PDBTitle: structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
75	c5l3sF	Alignment	not modelled	98.3	17	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsyt; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsyt
76	c6hecH	Alignment	not modelled	98.2	26	PDB header: hydrolase Chain: H: PDB Molecule: proteasome-activating nucleotidase; PDBTitle: pan-proteasome in state 4
77	c1xwiA	Alignment	not modelled	98.2	17	PDB header: protein transport Chain: A: PDB Molecule: skd1 protein; PDBTitle: crystal structure of vps4b
78	d1skye3	Alignment	not modelled	98.2	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
79	c5l3rC	Alignment	not modelled	98.2	27	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 ftsyt from2 arabidopsis thaliana
80	d2did3	Alignment	not modelled	98.2	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
						PDB header: ribosomal protein

81	c6matE	Alignment	not modelled	98.2	21	Chain: E; PDB Molecule: rix7 mutant; PDBTitle: cryo-em structure of the essential ribosome assembly aaa-atpase rix7
82	c5mpaL	Alignment	not modelled	98.2	21	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: 26s proteasome in presence of atp (s2)
83	c5l3qB	Alignment	not modelled	98.2	20	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
84	c6epdM	Alignment	not modelled	98.2	19	PDB header: hydrolase Chain: M; PDB Molecule: 26s proteasome regulatory subunit 6a; PDBTitle: substrate processing state 26s proteasome (sps1)
85	d1fx0a3	Alignment	not modelled	98.2	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
86	c1vmaA	Alignment	not modelled	98.2	23	PDB header: protein transport Chain: A; PDB Molecule: cell division protein ftsy; PDBTitle: crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
87	c5gafi	Alignment	not modelled	98.2	21	PDB header: ribosome Chain: I; PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
88	c3dm5A	Alignment	not modelled	98.2	23	PDB header: rna binding protein, transport protein Chain: A; PDB Molecule: signal recognition 54 kda protein; PDBTitle: structures of srp54 and srp19, the two proteins assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
89	c6focD	Alignment	not modelled	98.2	19	PDB header: hydrolase Chain: D; PDB Molecule: atp synthase subunit beta; PDBTitle: f1-atpase from mycobacterium smegmatis
90	c1skyE	Alignment	not modelled	98.2	19	PDB header: atp synthase Chain: E; PDB Molecule: f1-atpase; PDBTitle: crystal structure of the nucleotide free alpha3beta3 sub-complex of2 f1-atpase from the thermophilic bacillus ps3
91	c5uj7C	Alignment	not modelled	98.2	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
92	c4b4tH	Alignment	not modelled	98.2	21	PDB header: hydrolase Chain: H; PDB Molecule: 26s protease regulatory subunit 7 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
93	c4b4tJ	Alignment	not modelled	98.1	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
94	d1vmaa2	Alignment	not modelled	98.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
95	c30aaC	Alignment	not modelled	98.1	20	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
96	c5gjqL	Alignment	not modelled	98.1	19	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease regulatory subunit 10b; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
97	d2jdia3	Alignment	not modelled	98.1	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
98	d1qzxa3	Alignment	not modelled	98.1	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
99	c4b4tL	Alignment	not modelled	98.1	20	PDB header: hydrolase Chain: L; PDB Molecule: 26s protease subunit rpt4; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
100	c5syrA	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: A; PDB Molecule: probable atp synthase spa1/mxib; PDBTitle: crystal structure of atpase delta1-79 spa47 r350a
101	c5he8J	Alignment	not modelled	98.1	14	PDB header: protein binding Chain: J; PDB Molecule: helicase loader; PDBTitle: bacterial initiation protein
102	c5bq5A	Alignment	not modelled	98.1	17	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
103	c4a8jA	Alignment	not modelled	98.1	14	PDB header: transcription Chain: A; PDB Molecule: elongator complex protein 4; PDBTitle: crystal structure of the elongator subcomplex elp456
104	c2iy3A	Alignment	not modelled	98.1	24	PDB header: rna-binding Chain: A; PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
105	c6nyyC	Alignment	not modelled	98.1	19	PDB header: translocase Chain: C; PDB Molecule: afg3-like protein 2; PDBTitle: human m-aaa protease afg3l2, substrate-bound
106	c6q45C	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: C; PDB Molecule: atp synthase subunit alpha;

						PDBTitle: f1-atpase from fusobacterium nucleatum
107	c2hcbC_	Alignment	not modelled	98.1	23	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
108	c4b4tK_	Alignment	not modelled	98.1	25	PDB header: hydrolase Chain: K: PDB Molecule: 26s protease regulatory subunit 6b homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
109	d1fx0b3	Alignment	not modelled	98.1	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
110	c5bo5B_	Alignment	not modelled	98.1	15	PDB header: hydrolase Chain: B: PDB Molecule: neq263; PDBTitle: structure of a unique atp synthase subunit neqb from nanoarchaeum2 equitans
111	c4b4tM_	Alignment	not modelled	98.1	19	PDB header: hydrolase Chain: M: PDB Molecule: 26s protease regulatory subunit 6a; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
112	c2qe7C_	Alignment	not modelled	98.1	18	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
113	c4xd7B_	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: B: PDB Molecule: atp synthase subunit alpha; PDBTitle: structure of thermophilic f1-atpase inhibited by epsilon subunit
114	c4b4tI_	Alignment	not modelled	98.1	18	PDB header: hydrolase Chain: I: PDB Molecule: 26s protease regulatory subunit 4 homolog; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
115	c6focB_	Alignment	not modelled	98.1	19	PDB header: hydrolase Chain: B: PDB Molecule: atp synthase subunit alpha,atp synthase subunit alpha,atp PDBTitle: f1-atpase from mycobacterium smegmatis
116	c6f5dE_	Alignment	not modelled	98.1	20	PDB header: hydrolase Chain: E: PDB Molecule: atp synthase subunit beta, mitochondrial; PDBTitle: trypanosoma brucei f1-atpase
117	c1nsfA_	Alignment	not modelled	98.0	20	PDB header: protein transport Chain: A: PDB Molecule: n-ethylmaleimide sensitive factor; PDBTitle: d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
118	c1s3sA_	Alignment	not modelled	98.0	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
119	d1ls1a2	Alignment	not modelled	98.0	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
120	c2qmoA_	Alignment	not modelled	98.0	14	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori