

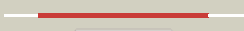






























Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hydB_	 Alignment		100.0	30	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
2	c2yl4A_	 Alignment		100.0	28	PDB header: membrane protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 10, PDBTitle: structure of the human mitochondrial abc transporter, abcb10
3	c3b5wE_	 Alignment		100.0	28	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
4	c3g5uB_	 Alignment		100.0	25	PDB header: membrane protein Chain: B: PDB Molecule: multidrug resistance protein 1a; PDBTitle: structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
5	c3b5xB_	 Alignment		100.0	28	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
6	c3nhaA_	 Alignment		100.0	39	PDB header: transport protein Chain: A: PDB Molecule: atp-binding cassette sub-family b member 6, mitochondrial; PDBTitle: nucleotide binding domain of human abcb6 (adp mg bound structure)
7	d2pmka1	 Alignment		100.0	40	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
8	d3b60a1	 Alignment		100.0	43	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
9	d2hyda1	 Alignment		100.0	43	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
10	d1jj7a_	 Alignment		100.0	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
11	d1mv5a_	 Alignment		100.0	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like

12	c2cbzA	Alignment		100.0	34	PDB header: transport Chain: A: PDB Molecule: multidrug resistance-associated protein 1; PDBTitle: structure of the human multidrug resistance protein 12 nucleotide binding domain 1
13	c2iw3B	Alignment		100.0	14	PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
14	c2r6fA	Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearotherophilus uvra
15	c2ghiD	Alignment		100.0	36	PDB header: transport protein Chain: D: PDB Molecule: transport protein; PDBTitle: crystal structure of plasmodium yoelii multidrug resistance2 protein 2
16	d1pf4a1	Alignment		100.0	40	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
17	c2pzfB	Alignment		100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508
18	c3gd7C	Alignment		100.0	30	PDB header: hydrolase Chain: C: PDB Molecule: fusion complex of cystic fibrosis transmembrane PDBTitle: crystal structure of human nbd2 complexed with n6-2 phenylethyl-atp (p-atp)
19	c2olkD	Alignment		100.0	27	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
20	d1xmia	Alignment		100.0	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
21	d1r0wa	Alignment	not modelled	100.0	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
22	c3gfoA	Alignment	not modelled	100.0	27	PDB header: atp binding protein Chain: A: PDB Molecule: cobalt import atp-binding protein cbio 1; PDBTitle: structure of cbio1 from clostridium perfringens: part of2 the abc transporter complex cbionq.
23	d1ji0a	Alignment	not modelled	100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
24	c3fvqB	Alignment	not modelled	100.0	30	PDB header: hydrolase Chain: B: PDB Molecule: fe(3+) ions import atp-binding protein fbpc; PDBTitle: crystal structure of the nucleotide binding domain fbpc2 complexed with atp
25	c1oxtb	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, atp binding protein; PDBTitle: crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
26	c2yyzA	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
27	d1oxxk2	Alignment	not modelled	100.0	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
28	c1z47B	Alignment	not modelled	100.0	26	PDB header: ligand binding protein Chain: B: PDB Molecule: putative abc-transporter atp-binding protein; PDBTitle: structure of the atpase subunit cysa of the putative2

						sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius
29	d1vp1a_	Alignment	not modelled	100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
30	c2d2fA_	Alignment	not modelled	100.0	20	PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufC from thermus2 thermophilus hb8
31	d1b0ua_	Alignment	not modelled	100.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
32	c2it1B_	Alignment	not modelled	100.0	30	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
33	d3d31a2	Alignment	not modelled	100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
34	d3dhwc1	Alignment	not modelled	100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
35	c2yz2B_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: putative abc transporter atp-binding protein tm_0222; PDBTitle: crystal structure of the abc transporter in the cobalt transport2 system
36	d1v43a3	Alignment	not modelled	100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
37	d1g6ha_	Alignment	not modelled	100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
38	c1vc1A_	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: A: PDB Molecule: sugar-binding transport atp-binding protein; PDBTitle: crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp
39	c3dhwc_	Alignment	not modelled	100.0	25	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni
40	d1g2912	Alignment	not modelled	100.0	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
41	d1l2ta_	Alignment	not modelled	100.0	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
42	c2d62A_	Alignment	not modelled	100.0	26	PDB header: sugar binding protein Chain: A: PDB Molecule: multiple sugar-binding transport atp-binding PDBTitle: crystal structure of multiple sugar binding transport atp-2 binding protein
43	c1q1bD_	Alignment	not modelled	100.0	26	PDB header: transport protein Chain: D: PDB Molecule: maltose/maltodextrin transport atp-binding protein malk; PDBTitle: crystal structure of e. coli malk in the nucleotide-free form
44	c2pcjB_	Alignment	not modelled	100.0	21	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
45	c3d31B_	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding PDBTitle: modbc from methanosarcina acetivorans
46	d2onka1	Alignment	not modelled	100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
47	c2nq2C_	Alignment	not modelled	100.0	26	PDB header: metal transport Chain: C: PDB Molecule: hypothetical abc transporter atp-binding protein PDBTitle: an inward-facing conformation of a putative metal-chelate2 type abc transporter.
48	c2d3wB_	Alignment	not modelled	100.0	22	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufC; PDBTitle: crystal structure of escherichia coli sufC, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
49	c2ihyB_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: B: PDB Molecule: abc transporter, atp-binding protein; PDBTitle: structure of the staphylococcus aureus putative atpase subunit of an2 atp-binding cassette (abc) transporter
50	c2ygrD_	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
51	c2pjzA_	Alignment	not modelled	100.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st1066; PDBTitle: the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), st1066
52	d1l7vc	Alignment	not modelled	100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate

52	d17vc_	Alignment	not modelled	100.0	24	hydrolases Family: ABC transporter ATPase domain-like
53	d1sgwa_	Alignment	not modelled	100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
54	c3ozxA_	Alignment	not modelled	100.0	20	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
55	c1yqtA_	Alignment	not modelled	100.0	23	PDB header: hydrolase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
56	d2awna2	Alignment	not modelled	100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
57	d3b60a2	Alignment	not modelled	100.0	18	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
58	c3bk7A_	Alignment	not modelled	100.0	20	PDB header: hydrolase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abce1/rnaase-I inhibitor protein2 from pyrococcus abyssi
59	c2vf7B_	Alignment	not modelled	100.0	26	PDB header: dna-binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
60	c3pihA_	Alignment	not modelled	100.0	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
61	d2hyda2	Alignment	not modelled	100.0	18	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
62	d1wlwa_	Alignment	not modelled	99.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
63	d1pf4a2	Alignment	not modelled	99.8	20	Fold: ABC transporter transmembrane region Superfamily: ABC transporter transmembrane region Family: ABC transporter transmembrane region
64	d1cr2a_	Alignment	not modelled	99.7	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
65	c3tauB_	Alignment	not modelled	99.6	11	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of a putative guanylate monophosphate kinase from2 listeria monocytogenes egd-e
66	c1xexB_	Alignment	not modelled	99.6	17	PDB header: cell cycle Chain: B: PDB Molecule: smc protein; PDBTitle: structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
67	c2j41A_	Alignment	not modelled	99.6	12	PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
68	c1f2uD_	Alignment	not modelled	99.5	21	PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
69	c3a4mB_	Alignment	not modelled	99.4	11	PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) kinase; PDBTitle: crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
70	c1ii8B_	Alignment	not modelled	99.4	25	PDB header: replication Chain: B: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain
71	d2qy9a2	Alignment	not modelled	99.2	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
72	d1e69a_	Alignment	not modelled	99.2	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
73	c3geiB_	Alignment	not modelled	99.2	16	PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
74	d1ls1a2	Alignment	not modelled	99.1	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
75	d1vmaa2	Alignment	not modelled	99.1	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	c3lncB_	Alignment	not modelled	99.1	12	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of guanylate kinase from anaplasma2 phagocytophilum
77	c1u9iA_	Alignment	not modelled	98.8	18	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
78	d1okkd2	Alignment	not modelled	98.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

					Family: Nitrogenase iron protein-like
79	c2o5vA_	Alignment	not modelled	98.8	17 PDB header: replication/recombination Chain: A: PDB Molecule: dna replication and repair protein recf; PDBTitle: recombination mediator recf
80	d1ye8a1	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)
81	c3auyB_	Alignment	not modelled	98.2	18 PDB header: recombination Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: crystal structure of rad50 bound to adp
82	d1np6a_	Alignment	not modelled	98.2	18 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
83	d2i3ba1	Alignment	not modelled	98.2	10 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
84	d1qzxa3	Alignment	not modelled	98.2	13 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
85	c1q57G_	Alignment	not modelled	98.1	8 PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
86	c2w0mA_	Alignment	not modelled	98.0	11 PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfolobus solfataricus2 p2
87	c2dr3A_	Alignment	not modelled	97.9	12 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
88	d1ewqa2	Alignment	not modelled	97.8	13 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
89	c3thxB_	Alignment	not modelled	97.8	15 PDB header: dna binding protein/dna Chain: B: PDB Molecule: dna mismatch repair protein msh3; PDBTitle: human mutsbeta complexed with an idl of 3 bases (loop3) and adp
90	c1ewqA_	Alignment	not modelled	97.7	12 PDB header: replication/dna Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure taq muts complexed with a heteroduplex2 dna at 2.2 a resolution
91	c2o8bA_	Alignment	not modelled	97.5	15 PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna mismatch repair protein msh2; PDBTitle: human mutsalph (msh2/msh6) bound to adp and a g t mispair
92	d1nlfa_	Alignment	not modelled	97.4	14 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
93	c2j3eA_	Alignment	not modelled	97.3	12 PDB header: protein transport Chain: A: PDB Molecule: t7i23.11 protein; PDBTitle: dimerization is important for the gtpase activity of2 chloroplast translocon components attoc33 and pstoc159
94	d1tf7a2	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)
95	c3qkuB_	Alignment	not modelled	97.2	20 PDB header: replication Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: mre11 rad50 binding domain in complex with rad50 and amp-pnp
96	d1wb9a2	Alignment	not modelled	97.2	16 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
97	c1ewrA_	Alignment	not modelled	97.1	19 PDB header: hydrolase Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of taq muts
98	c1wxqA_	Alignment	not modelled	97.1	13 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
99	c2o8dB_	Alignment	not modelled	97.0	16 PDB header: dna binding protein/dna Chain: B: PDB Molecule: dna mismatch repair protein msh6; PDBTitle: human mutsalph (msh2/msh6) bound to adp and a g du mispair
100	c1wbdA_	Alignment	not modelled	97.0	14 PDB header: dna-binding Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of e. coli dna mismatch repair enzyme2 muts, e38q mutant, in complex with a g.t mismatch
101	c3pxiB_	Alignment	not modelled	97.0	25 PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/mechb; PDBTitle: structure of meca108:clpc
102	d1tf7a1	Alignment	not modelled	97.0	16 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
103	c2cvhB_	Alignment	not modelled	96.9	15 PDB header: dna binding protein Chain: B: PDB Molecule: dna repair and recombination protein radb; PDBTitle: crystal structure of the radb recombinase

104	c2recB_	Alignment	not modelled	96.7	20	PDB header: helicase PDB COMPND:
105	c3ldaA_	Alignment	not modelled	96.6	19	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
106	d2ilqa2	Alignment	not modelled	96.6	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
107	d1g41a_	Alignment	not modelled	96.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
108	c2j289_	Alignment	not modelled	96.5	22	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
109	c3bh0A_	Alignment	not modelled	96.5	14	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
110	d1xp8a1	Alignment	not modelled	96.5	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
111	d1zp6a1	Alignment	not modelled	96.5	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Atu3015-like
112	d1v5wa_	Alignment	not modelled	96.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
113	c1xx6B_	Alignment	not modelled	96.4	25	PDB header: transferase Chain: B: PDB Molecule: thymidine kinase; PDBTitle: x-ray structure of clostridium acetobutylicum thymidine kinase with2 adp. northeast structural genomics target car26.
114	c2j7pA_	Alignment	not modelled	96.3	17	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and tfsy
115	c3cmvG_	Alignment	not modelled	96.3	19	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
116	c2hcbC_	Alignment	not modelled	96.3	24	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
117	d1n0wa_	Alignment	not modelled	96.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
118	c2ztsB_	Alignment	not modelled	96.3	16	PDB header: atp-binding protein Chain: B: PDB Molecule: putative uncharacterized protein ph0186; PDBTitle: crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
119	d1yrba1	Alignment	not modelled	96.3	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
120	d1znwa1	Alignment	not modelled	96.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases