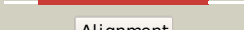
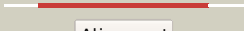
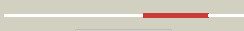


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wlwa_	 Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
2	c2o5vA_	 Alignment		100.0	29	PDB header: replication/recombination Chain: A: PDB Molecule: dna replication and repair protein recf; PDBTitle: recombination mediator recf
3	c3auyB_	 Alignment		100.0	22	PDB header: recombination Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: crystal structure of rad50 bound to adp
4	c3g5uB_	 Alignment		99.9	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	c1yqtA_	 Alignment		99.9	21	PDB header: hydrolase/translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: rnase-l inhibitor
6	d1e69a_	 Alignment		99.9	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
7	c1z47B_	 Alignment		99.9	24	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
8	c3dhwC_	 Alignment		99.9	32	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni
9	c1xexB_	 Alignment		99.9	20	PDB header: cell cycle Chain: B: PDB Molecule: smc protein; PDBTitle: structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
10	c3fvqB_	 Alignment		99.9	19	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
11	c1oxtb_	 Alignment		99.9	24	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

12	c3qg5A_	Alignment		99.9	14	PDB header: hydrolase Chain: A: PDB Molecule: rad50; PDBTitle: the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
13	c2it1B_	Alignment		99.9	20	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
14	cli18B_	Alignment		99.8	14	PDB header: replication Chain: B: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain
15	dlj17a_	Alignment		99.8	34	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
16	clxexA_	Alignment		99.8	26	PDB header: cell cycle Chain: A: PDB Molecule: smc protein; PDBTitle: structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
17	cli18A_	Alignment		99.8	15	PDB header: replication Chain: A: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain
18	c2d3wB_	Alignment		99.8	24	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter sufcd; PDBTitle: crystal structure of escherichia coli sufcd, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
19	clf2uD_	Alignment		99.8	16	PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
20	c3qkuB_	Alignment		99.8	22	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
21	c3pihA_	Alignment	not modelled	99.7	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
22	c2vf7B_	Alignment	not modelled	99.7	22	PDB header: dna-binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
23	c2ygrD_	Alignment	not modelled	99.7	20	PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
24	c2hydB_	Alignment	not modelled	99.7	18	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
25	d2awna2	Alignment	not modelled	99.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
26	c2yl4A_	Alignment	not modelled	99.7	20	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
27	c3bk7A_	Alignment	not modelled	99.7	18	PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi
28	c2iw3B_	Alignment	not modelled	99.7	17	PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp

29	c2pcjB_	Alignment	not modelled	99.7	22	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
30	c3ozxA_	Alignment	not modelled	99.7	21	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
31	c3b5xB_	Alignment	not modelled	99.7	21	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
32	c1vciA_	Alignment	not modelled	99.7	16	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
33	c3b5wE_	Alignment	not modelled	99.6	22	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
34	d2pmka1	Alignment	not modelled	99.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
35	d1l2ta_	Alignment	not modelled	99.6	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
36	c2olkD_	Alignment	not modelled	99.6	24	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
37	c2yyzA_	Alignment	not modelled	99.6	17	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
38	c2yz2B_	Alignment		99.6	20	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
39	c2r6fA_	Alignment	not modelled	99.6	21	PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra
40	d1g2912	Alignment	not modelled	99.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
41	c2d62A_	Alignment	not modelled	99.6	16	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
42	d1qhla_	Alignment	not modelled	99.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
43	d1v43a3	Alignment	not modelled	99.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
44	d3b60a1	Alignment	not modelled	99.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
45	c1us8A_	Alignment	not modelled	99.6	26	PDB header: dna repair Chain: A: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: the rad50 signature motif: essential to atp binding and2 biological function
46	d2hyda1	Alignment	not modelled	99.6	17	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	99.6	24	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	d1vpla_	Alignment	not modelled	99.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
49	d3dhwc1	Alignment	not modelled	99.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
50	d1oxk2	Alignment	not modelled	99.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
51	c3gfoA_	Alignment	not modelled	99.6	22	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 cbioq. Fold: P-loop containing nucleoside triphosphate hydrolases

52	d1b0ua_	Alignment	not modelled	99.6	25	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
53	c3nhaA_	Alignment	not modelled	99.6	18	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)
54	c3d31B_	Alignment	not modelled	99.6	21	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding PDBTitle: modbc from methanosarcina acetivorans
55	c2cbzA_	Alignment	not modelled	99.6	16	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
56	d1mv5a_	Alignment	not modelled	99.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
57	c2pjzA_	Alignment	not modelled	99.6	11	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
58	d1pf4a1	Alignment	not modelled	99.5	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
59	d1r0wa_	Alignment	not modelled	99.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
60	c1qlbD_	Alignment	not modelled	99.5	15	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
61	d3d31a2	Alignment	not modelled	99.5	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
62	d1g6ha_	Alignment	not modelled	99.5	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
63	c3gd7C_	Alignment	not modelled	99.5	16	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)
64	c2d2fA_	Alignment	not modelled	99.5	18	PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
65	d1ji0a_	Alignment	not modelled	99.5	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
66	c2pzfB_	Alignment	not modelled	99.5	15	PDB header: hydrolase Chain: B: PDB Molecule: cystic fibrosis transmembrane conductance regulator; PDBTitle: minimal human cfr first nucleotide binding domain as a head-to-tail2 dimer with delta f508
67	d1xmia_	Alignment	not modelled	99.5	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
68	c3eukC_	Alignment	not modelled	99.5	13	PDB header: cell cycle linker; Chain: C: PDB Molecule: chromosome partition protein mukb, PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, asymmetric dimer
69	d2onka1	Alignment	not modelled	99.4	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
70	c2ihyB_	Alignment	not modelled	99.4	18	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
71	d1sgwa_	Alignment	not modelled	99.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
72	d1l7vc_	Alignment	not modelled	99.3	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
73	c2ghiD_	Alignment	not modelled	99.2	18	PDB header: transport protein Chain: D: PDB Molecule: transport protein; PDBTitle: crystal structure of plasmodium yoelii multidrug resistance2 protein 2
74	d1cr2a_	Alignment	not modelled	98.4	7	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
75	d1vmaa2	Alignment	not modelled	98.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	d2ev9a2	Alignment	not modelled	98.2	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate

76	d2qy2a2	Alignment	not modelled	98.2	23	hydrolases Family: Nitrogenase iron protein-like
77	c2j41A	Alignment	not modelled	98.0	23	PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
78	d1okkd2	Alignment	not modelled	98.0	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
79	d1ls1a2	Alignment	not modelled	97.9	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
80	d1np6a	Alignment	not modelled	97.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
81	c3tauB	Alignment	not modelled	97.9	10	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of a putative guanylate monophosphate kinase from2 listeria monocytogenes egd-e
82	d1ewqa2	Alignment	not modelled	97.7	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
83	d1ye8a1	Alignment	not modelled	97.7	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
84	d2i3ba1	Alignment	not modelled	97.6	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
85	d1qzxa3	Alignment	not modelled	97.5	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
86	c3a4mB	Alignment	not modelled	97.5	8	PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) kinase; PDBTitle: crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
87	c1ewqA	Alignment	not modelled	97.5	28	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
88	d1wb9a2	Alignment	not modelled	97.5	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
89	c2o8bA	Alignment	not modelled	97.4	26	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
90	c1wbdA	Alignment	not modelled	97.3	29	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
91	d1znwa1	Alignment	not modelled	97.3	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
92	c3geiB	Alignment	not modelled	97.3	50	PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
93	c2plrB	Alignment	not modelled	97.3	25	PDB header: transferase Chain: B: PDB Molecule: probable thymidylate kinase; PDBTitle: crystal structure of dtmp kinase (st1543) from sulfolobus tokodaii2 strain7
94	c3thxB	Alignment	not modelled	97.3	29	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
95	c1ewrA	Alignment	not modelled	97.2	28	PDB header: hydrolase Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of taq muts
96	c3cmvG	Alignment	not modelled	97.2	10	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
97	c2o8dB	Alignment	not modelled	97.2	28	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
98	d1s96a	Alignment	not modelled	97.2	41	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
99	d1tmka	Alignment	not modelled	97.2	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
100	c2yvua	Alignment	not modelled	97.2	30	PDB header: transferase Chain: A: PDB Molecule: probable adenyl-yl-sulfate kinase; PDBTitle: crystal structure of ape1195
101	d1zpa1	Alignment	not modelled	97.2	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Atu3015-like
						Fold: P-loop containing nucleoside triphosphate hydrolases

102	d1ki9a_	Alignment	not modelled	97.1	21	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
103	c2w0sB_	Alignment	not modelled	97.1	22	PDB header: transferase Chain: B: PDB Molecule: thymidylate kinase; PDBTitle: crystal structure of vaccinia virus thymidylate kinase2 bound to brivudin-5'-monophosphate
104	c1znyA_	Alignment	not modelled	97.1	33	PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp
105	d1yrba1	Alignment	not modelled	97.1	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
106	c1wxqA_	Alignment	not modelled	97.0	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
107	c2wwiC_	Alignment	not modelled	97.0	31	PDB header: transferase Chain: C: PDB Molecule: thymidilate kinase, putative; PDBTitle: plasmodium falciparum thymidylate kinase in complex with2 aztmp and adp
108	c2dr3A_	Alignment	not modelled	97.0	19	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
109	d1nn5a_	Alignment	not modelled	97.0	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
110	d1qhxa_	Alignment	not modelled	97.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Chloramphenicol phosphotransferase
111	c2vliB_	Alignment	not modelled	96.9	29	PDB header: transferase Chain: B: PDB Molecule: antibiotic resistance protein; PDBTitle: structure of deinococcus radiodurans tunicamycin resistance2 protein
112	c2rhmD_	Alignment	not modelled	96.9	26	PDB header: unknown function Chain: D: PDB Molecule: putative kinase; PDBTitle: crystal structure of a putative kinase (caur_3907) from chloroflexus2 aurantiacus j-10-fl at 1.70 a resolution
113	c3lncB_	Alignment	not modelled	96.9	11	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of guanylate kinase from anaplasma2 phagocytophilum
114	c3ievA_	Alignment	not modelled	96.9	21	PDB header: nucleotide binding protein/rna Chain: A: PDB Molecule: gtp-binding protein era; PDBTitle: crystal structure of era in complex with mggnp and the 3' end of 16s2 rrna
115	c3jvva_	Alignment	not modelled	96.9	38	PDB header: atp binding protein Chain: A: PDB Molecule: twitching mobility protein; PDBTitle: crystal structure of p. aeruginosa pilt with bound amp-pcp
116	c2grjH_	Alignment	not modelled	96.9	33	PDB header: transferase Chain: H: PDB Molecule: dephospho-coa kinase; PDBTitle: crystal structure of dephospho-coa kinase (ec 2.7.1.24)2 (dephosphocoenzyme a kinase) (tm1387) from thermotoga maritima at3 2.60 a resolution
117	d1m8pa3	Alignment	not modelled	96.9	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ATP sulfurylase C-terminal domain
118	c3ld9D_	Alignment	not modelled	96.9	23	PDB header: transferase Chain: D: PDB Molecule: thymidylate kinase; PDBTitle: crystal structure of thymidylate kinase from ehrlichia chaffeensis at2 2.15a resolution
119	c2z0hA_	Alignment	not modelled	96.9	33	PDB header: transferase Chain: A: PDB Molecule: thymidylate kinase; PDBTitle: crystal structure of thymidylate kinase in complex with dtdp2 and adp from thermotoga maritima
120	d1knqa_	Alignment	not modelled	96.9	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Gluconate kinase