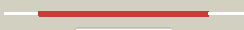
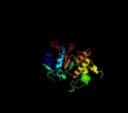


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1q1bD_	 Alignment		100.0	33	PDB header: transport protein Chain: D: PDB Molecule: maltose/maltodextrin transport atp-binding protein malk; PDBTitle: crystal structure of e. coli malk in the nucleotide-free form
2	c2yyzA_	 Alignment		100.0	31	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
3	c2it1B_	 Alignment		100.0	30	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
4	c3fvqB_	 Alignment		100.0	31	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
5	c1z47B_	 Alignment		100.0	30	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
6	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
7	c3dhwC_	 Alignment		100.0	30	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni
8	d1g2912	 Alignment		100.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
9	c1oxTB_	 Alignment		100.0	33	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
10	c2pcjB_	 Alignment		100.0	25	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
11	d3dhwC1	 Alignment		100.0	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like

12	clvciA_	Alignment		100.0	30	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
13	c2d62A_	Alignment		100.0	27	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
14	d1oxk2	Alignment		100.0	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
15	d3d31a2	Alignment		100.0	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
16	d1v43a3	Alignment		100.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
17	c3g5uB_	Alignment		100.0	26	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
18	c3gfoA_	Alignment		100.0	29	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.
19	c3d31B_	Alignment		100.0	27	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding PDBTitle: modbc from methanosarcina acetivorans
20	d1vp1a_	Alignment		100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
21	d1g6ha_	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
22	d1l2ta_	Alignment	not modelled	100.0	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
23	d1b0ua_	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
24	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
25	d1jj7a_	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
26	d2pmk1	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
27	c2yl4A_	Alignment	not modelled	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
28	d1mv5a_	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 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.
29	c2nq2C_	Alignment	not modelled	100.0	29
30	c2d2fA_	Alignment	not modelled	100.0	26
31	c2hydB_	Alignment	not modelled	100.0	26
32	d3b60a1	Alignment	not modelled	100.0	25
33	c3nhaA_	Alignment	not modelled	100.0	26
34	c2yz2B_	Alignment	not modelled	100.0	28
35	c3b5wE_	Alignment	not modelled	100.0	26
36	d2hyda1	Alignment	not modelled	100.0	25
37	c3gd7C_	Alignment	not modelled	100.0	23
38	d2onka1	Alignment	not modelled	100.0	36
39	d1pf4a1	Alignment	not modelled	100.0	27
40	c3b5xB_	Alignment	not modelled	100.0	26
41	c2d3wB_	Alignment	not modelled	100.0	22
42	c2cbzA_	Alignment	not modelled	100.0	23
43	c1yqtA_	Alignment	not modelled	100.0	20
44	c3ozxA_	Alignment	not modelled	100.0	22
45	d1sgwa_	Alignment	not modelled	100.0	22
46	c2ihyB_	Alignment	not modelled	100.0	22
47	c2pzfB_	Alignment	not modelled	100.0	22
48	c2pjzA_	Alignment	not modelled	100.0	27
49	d2awna2	Alignment	not modelled	100.0	34
50	c3bk7A_	Alignment	not modelled	100.0	20
51	d1xmia_	Alignment	not modelled	100.0	23
52	c2ghiD_	Alignment	not modelled	100.0	22

53	d1r0wa_	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
54	c2iw3B_	Alignment	not modelled	100.0	24	PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
55	d1l7vc_	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
56	c2r6fA_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra
57	c2ygrD_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
58	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
59	c2vf7B_	Alignment	not modelled	100.0	23	PDB header: dna-binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
60	d1w1wa_	Alignment	not modelled	99.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
61	c3tauB_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of a putative guanylate monophosphate kinase from2 listeria monocytogenes egd-e
62	d1cr2a_	Alignment	not modelled	99.9	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
63	c2j41A_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
64	c3a4mB_	Alignment	not modelled	99.7	14	PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) kinase; PDBTitle: crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
65	d1ls1a2	Alignment	not modelled	99.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
66	c1f2uD_	Alignment	not modelled	99.6	26	PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
67	c2o5vA_	Alignment	not modelled	99.6	27	PDB header: replication/recombination Chain: A: PDB Molecule: dna replication and repair protein recf; PDBTitle: recombination mediator recf
68	c1xexB_	Alignment	not modelled	99.5	16	PDB header: cell cycle Chain: B: PDB Molecule: smc protein; PDBTitle: structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
69	d2qy9a2	Alignment	not modelled	99.5	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
70	c3lncB_	Alignment	not modelled	99.5	13	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of guanylate kinase from anaplasma2 phagocytophilum
71	d1np6a_	Alignment	not modelled	99.5	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
72	c1ii8B_	Alignment	not modelled	99.4	24	PDB header: replication Chain: B: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain
73	c1u9iA_	Alignment	not modelled	99.4	13	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
74	d1vmaa2	Alignment	not modelled	99.4	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
75	c3geiB_	Alignment	not modelled	99.4	12	PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
76	c1q57G_	Alignment	not modelled	99.1	8	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
77	d1okkd2	Alignment	not modelled	99.1	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
78	d2i3ba1	Alignment	not modelled	99.1	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
						Fold: P-loop containing nucleoside triphosphate hydrolases

79	dlqza3	Alignment	not modelled	99.0	14	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
80	dle69a	Alignment	not modelled	98.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
81	dlye8a1	Alignment	not modelled	98.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
82	clwxqA	Alignment	not modelled	98.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
83	c2w0mA	Alignment	not modelled	98.7	12	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfolobus solfataricus2 p2
84	clpznG	Alignment	not modelled	98.7	11	PDB header: recombination Chain: G: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
85	c3auyB	Alignment	not modelled	98.7	24	PDB header: recombination Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: crystal structure of rad50 bound to adp
86	c3thxB	Alignment	not modelled	98.6	16	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
87	c2dr3A	Alignment	not modelled	98.6	11	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	dlewqa2	Alignment	not modelled	98.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
89	dlwb9a2	Alignment	not modelled	98.5	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
90	c2o8bA	Alignment	not modelled	98.5	21	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
91	c3cmvG	Alignment	not modelled	98.5	20	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
92	dl1f7a1	Alignment	not modelled	98.4	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
93	dl1nfa	Alignment	not modelled	98.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
94	c2o8dB	Alignment	not modelled	98.4	22	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
95	clwbdA	Alignment	not modelled	98.3	18	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
96	clewqA	Alignment	not modelled	98.3	23	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
97	clewrA	Alignment	not modelled	98.3	20	PDB header: hydrolase Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of taq muts
98	dlznwa1	Alignment	not modelled	98.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
99	c3qkuB	Alignment	not modelled	98.1	32	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
100	c3qg5A	Alignment	not modelled	98.1	42	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
101	d2ilqa2	Alignment	not modelled	97.8	8	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
102	dlyrba1	Alignment	not modelled	97.7	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
103	c3r8cB	Alignment	not modelled	97.7	19	PDB header: transferase Chain: B: PDB Molecule: cytidylate kinase; PDBTitle: crystal structure of cytidylate kinase (cmk) from mycobacterium2 abscessus
104	clus8A	Alignment	not modelled	97.7	24	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
105	c1ii8A_	Alignment	not modelled	97.7	32 PDB header: replication Chain: A: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain
106	d1xp8a1	Alignment	not modelled	97.7	15 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
107	c2recB_	Alignment	not modelled	97.7	19 PDB header: helicase PDB COMPND:
108	c1xp8A_	Alignment	not modelled	97.6	16 PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: "deinococcus radiodurans reca in complex with atp-gamma-s"
109	c2gesA_	Alignment	not modelled	97.6	17 PDB header: transferase Chain: A: PDB Molecule: pantothenate kinase; PDBTitle: pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
110	c2zjbB_	Alignment	not modelled	97.6	7 PDB header: recombination Chain: B: PDB Molecule: meiotic recombination protein dmc1/lm15 homolog; PDBTitle: crystal structure of the human dmc1-m200v polymorphic2 variant
111	c3bh0A_	Alignment	not modelled	97.6	8 PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
112	d1qhla_	Alignment	not modelled	97.6	24 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
113	c2cvhB_	Alignment	not modelled	97.6	18 PDB header: dna binding protein Chain: B: PDB Molecule: dna repair and recombination protein radb; PDBTitle: crystal structure of the radb recombinase
114	c1szpC_	Alignment	not modelled	97.5	14 PDB header: dna binding protein Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
115	d1v5wa_	Alignment	not modelled	97.5	7 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
116	d1tf7a2	Alignment	not modelled	97.5	16 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
117	d1n0wa_	Alignment	not modelled	97.5	11 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
118	d1mo6a1	Alignment	not modelled	97.5	19 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
119	d1s96a_	Alignment	not modelled	97.4	12 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
120	d1zp6a1	Alignment	not modelled	97.4	31 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Atu3015-like