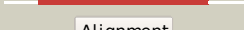
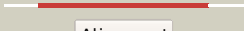
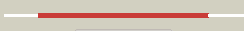
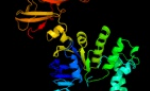


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yyzA_	 Alignment		100.0	39	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
2	c1qlbD_	 Alignment		100.0	36	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
3	c2it1B_	 Alignment		100.0	36	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
4	c1vciA_	 Alignment		100.0	40	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
5	c1z47B_	 Alignment		100.0	37	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	c3fvqB_	 Alignment		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
7	c1oxTB_	 Alignment		100.0	35	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
8	c3d31B_	 Alignment		100.0	33	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding PDBTitle: modbc from methanosarcina acetivorans
9	c2d62A_	 Alignment		100.0	36	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
10	c3gd7C_	 Alignment		100.0	24	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)
11	d1g2912	 Alignment		100.0	49	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like

12	d1oxxk2	Alignment		100.0	42	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
13	c2olkD_	Alignment		100.0	38	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
14	d3dhwc1	Alignment		100.0	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
15	c3dhwc_	Alignment		100.0	34	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni
16	d3d31a2	Alignment		100.0	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
17	d1v43a3	Alignment		100.0	51	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
18	d1b0ua_	Alignment		100.0	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
19	c3gfoA_	Alignment		100.0	28	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.
20	d1vp1a_	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	d1ji0a_	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
22	c2pcjB_	Alignment	not modelled	100.0	30	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
23	d1g6ha_	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
24	d2pmka1	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
25	c3g5uB_	Alignment	not modelled	100.0	32	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
26	d1jj7a_	Alignment	not modelled	100.0	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
27	d2onka1	Alignment	not modelled	100.0	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
28	c2nq2C_	Alignment	not modelled	100.0	25	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	c2yz2B_	Alignment	not modelled	100.0	27	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
30	d1l2ta_	Alignment	not modelled	100.0	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
31	c2d2fA_	Alignment	not modelled	100.0	27	PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase suf from thermus2 thermophilus hb8
32	d1mv5a_	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
33	d3b60a1	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
34	c3nhaA_	Alignment	not modelled	100.0	30	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)
35	d2awna2	Alignment	not modelled	100.0	49	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
36	d2hya1	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
37	c2d3wB_	Alignment	not modelled	100.0	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: probable atp-dependent transporter suf; PDBTitle: crystal structure of escherichia coli suf, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
38	c2hydB_	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
39	c2ihyB_	Alignment	not modelled	100.0	24	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
40	c2yl4A_	Alignment	not modelled	100.0	31	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
41	c2cbzA_	Alignment	not modelled	100.0	29	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
42	c1yqtA_	Alignment	not modelled	100.0	30	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: rnase-l inhibitor
43	c3b5xB_	Alignment	not modelled	100.0	32	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
44	c3ozxA_	Alignment	not modelled	100.0	20	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
45	c2pjzA_	Alignment	not modelled	100.0	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein stl066; PDBTitle: the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), stl066
46	c3b5wE_	Alignment	not modelled	100.0	33	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
47	d1pf4a1	Alignment	not modelled	100.0	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
48	c2pzfB_	Alignment	not modelled	100.0	26	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
49	d1xmia_	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
50	d1r0wa_	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
51	c3bk7A_	Alignment	not modelled	100.0	29	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
52	d1l7vc_	Alignment	not modelled	100.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like

53	c2ghiD	Alignment	not modelled	100.0	29	PDB header: transport protein Chain: D: PDB Molecule: transport protein; PDBTitle: crystal structure of plasmodium yoelii multidrug resistance2 protein 2
54	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
55	c2iw3B	Alignment	not modelled	100.0	18	PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
56	c2r6fA	Alignment	not modelled	100.0	18	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	24	PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
58	c3pihA	Alignment	not modelled	100.0	23	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	27	PDB header: dna-binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
60	d1cr2a	Alignment	not modelled	99.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
61	c3tauB	Alignment	not modelled	99.9	17	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of a putative guanylate monophosphate kinase from2 listeria monocytogenes egd-e
62	d1wlwa	Alignment	not modelled	99.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
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	99.8	11	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	99.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
66	d2qy9a2	Alignment	not modelled	99.8	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
67	c2o5vA	Alignment	not modelled	99.7	22	PDB header: replication/recombination Chain: A: PDB Molecule: dna replication and repair protein recf; PDBTitle: recombination mediator recf
68	d1vmaa2	Alignment	not modelled	99.7	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
69	c1xexB	Alignment	not modelled	99.6	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.
70	c1f2uD	Alignment	not modelled	99.6	24	PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
71	c1u9iA	Alignment	not modelled	99.6	19	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
72	d1okkd2	Alignment	not modelled	99.5	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
73	c3geiB	Alignment	not modelled	99.5	11	PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
74	c3lncB	Alignment	not modelled	99.5	12	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of guanylate kinase from anaplasma2 phagocytophilum
75	c1ii8B	Alignment	not modelled	99.5	29	PDB header: replication Chain: B: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain
76	d1np6a	Alignment	not modelled	99.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
77	d1ye8a1	Alignment	not modelled	99.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
78	c1q57G	Alignment	not modelled	99.3	14	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
						Fold: P-loop containing nucleoside triphosphate hydrolases

79	d1e69a_	Alignment	not modelled	99.2	19	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
80	d1qzxa3	Alignment	not modelled	99.2	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
81	d2i3ba1	Alignment	not modelled	99.2	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
82	c2dr3A_	Alignment	not modelled	99.1	16	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
83	c3auyB_	Alignment	not modelled	99.1	24	PDB header: recombination Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: crystal structure of rad50 bound to adp
84	c2w0mA_	Alignment	not modelled	98.9	14	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfolobus solfataricus2 p2
85	d1loxk1	Alignment	not modelled	98.9	18	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
86	d2awna1	Alignment	not modelled	98.9	17	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
87	d1nfa_	Alignment	not modelled	98.8	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
88	d3d31a1	Alignment	not modelled	98.8	19	Fold: OB-fold Superfamily: MOP-like Family: ABC-transporter additional domain
89	d1ewqa2	Alignment	not modelled	98.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
90	c3thxB_	Alignment	not modelled	98.8	21	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
91	c2o8bA_	Alignment	not modelled	98.8	19	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	d1wb9a2	Alignment	not modelled	98.7	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
93	c2o8dB_	Alignment	not modelled	98.7	21	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
94	c1pznG_	Alignment	not modelled	98.7	14	PDB header: recombination Chain: G: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)
95	d1tf7a1	Alignment	not modelled	98.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
96	c1wbdA_	Alignment	not modelled	98.6	22	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
97	c1ewqA_	Alignment	not modelled	98.5	20	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
98	c1ewrA_	Alignment	not modelled	98.5	22	PDB header: hydrolase Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of taq muts
99	d2i1qa2	Alignment	not modelled	98.4	9	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
100	d1yrba1	Alignment	not modelled	98.4	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
101	c1wxqA_	Alignment	not modelled	98.4	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: gtp-binding protein; PDBTitle: crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
102	c3bh0A_	Alignment	not modelled	98.3	11	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
103	d1tf7a2	Alignment	not modelled	98.2	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
104	c2vyeA_	Alignment	not modelled	98.2	11	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnac-ssdna complex
						PDB header: dna binding protein

105	c1szpC_	Alignment	not modelled	98.2	18	Chain: C: PDB Molecule: dna repair protein rad51; PDBTitle: a crystal structure of the rad51 filament
106	d1v5wa_	Alignment	not modelled	98.2	11	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	98.1	22	PDB header: helicase PDB COMPND:
108	c3cmvG_	Alignment	not modelled	98.1	9	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
109	c2zjbB_	Alignment	not modelled	98.1	10	PDB header: recombination Chain: B: PDB Molecule: meiotic recombination protein dmc1/lim15 homolog; PDBTitle: crystal structure of the human dmc1-m200v polymorphic2 variant
110	d1znwa1	Alignment	not modelled	98.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
111	c3qkuB_	Alignment	not modelled	98.1	26	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
112	d1szpa2	Alignment	not modelled	98.1	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
113	d1n0wa_	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)
114	c2q6tB_	Alignment	not modelled	98.0	9	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
115	d1mo6a1	Alignment	not modelled	98.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
116	c2cvhB_	Alignment	not modelled	98.0	13	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair and recombination protein radb; PDBTitle: crystal structure of the radb recombinase
117	d1xp8a1	Alignment	not modelled	98.0	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
118	c3ldaA_	Alignment	not modelled	98.0	17	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
119	c3qg5A_	Alignment	not modelled	98.0	18	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
120	c2ztsB_	Alignment	not modelled	97.9	24	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