
































Phyre2

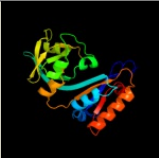
Email	I.a.kelley@imperial.ac.uk
Description	P75831
Date	Thu Jan 5 12:14:48 GMT 2012
Unique Job ID	3a25593692bfb9aa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dhwC_	 Alignment		100.0	35	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni
2	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
3	c2pcjB_	 Alignment		100.0	43	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding protein Iold; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
4	c2olkD_	 Alignment		100.0	35	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
5	c2yyzA_	 Alignment		100.0	32	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
6	c2it1B_	 Alignment		100.0	37	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
7	c1oxTB_	 Alignment		100.0	30	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	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
9	d1g2912	 Alignment		100.0	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
10	d1l2ta_	 Alignment		100.0	46	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
11	c1z47B_	 Alignment		100.0	35	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

12	d1oxxk2	Alignment		100.0	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
13	c3gfoA_	Alignment		100.0	30	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.
14	c2d62A_	Alignment		100.0	29	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
15	c3g5uB_	Alignment		100.0	27	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
16	d1g6ha_	Alignment		100.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
17	d1vp1a_	Alignment		100.0	26	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	38	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
19	c1q1bD_	Alignment		100.0	32	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
20	c1vc1A_	Alignment		100.0	29	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
21	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
22	d1ji0a_	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
23	d1v43a3	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	c3d31B_	Alignment	not modelled	100.0	28	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding PDBTitle: modbc from methanosarcina acetivorans
25	d1jj7a_	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
26	c2yl4A_	Alignment	not modelled	100.0	33	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	c2hydB_	Alignment	not modelled	100.0	31	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
28	d2pmka1	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

29	d3b60a1	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
30	c2d2fA	Alignment	not modelled	100.0	23	PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
31	c2yz2B	Alignment	not modelled	100.0	25	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
32	d1mv5a	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
33	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.
34	c3nhaA	Alignment	not modelled	100.0	31	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	d2hyda1	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
36	c2d3wB	Alignment	not modelled	100.0	28	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
37	c3b5xB	Alignment	not modelled	100.0	31	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
38	c3b5wE	Alignment	not modelled	100.0	31	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba
39	c3gd7C	Alignment	not modelled	100.0	23	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)
40	c2cbzA	Alignment	not modelled	100.0	24	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
41	d2onka1	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	d1pf4a1	Alignment	not modelled	100.0	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
43	c2ihyB	Alignment	not modelled	100.0	30	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
44	c2pzfB	Alignment	not modelled	100.0	23	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
45	c2pjzA	Alignment	not modelled	100.0	23	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
46	c2ghiD	Alignment	not modelled	100.0	27	PDB header: transport protein Chain: D: PDB Molecule: transport protein; PDBTitle: crystal structure of plasmodium yoelii multidrug resistance2 protein 2
47	d1sgwa	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
48	c1yqtA	Alignment	not modelled	100.0	26	PDB header: hydrolase/translation Chain: A: PDB Molecule: rnase i inhibitor; PDBTitle: rnase-i inhibitor
49	d1xmia	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
50	c3ozxA	Alignment	not modelled	100.0	25	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase i inhibitor; PDBTitle: crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
51	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
52	d1l7vc	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
						PDB header: hydrolase/translation

53	c3bk7A	Alignment	not modelled	100.0	27	Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abc1/rnaase-i inhibitor protein2 from pyrococcus abyssi
54	d2awna2	Alignment	not modelled	100.0	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
55	c2r6fA	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra
56	c2iw3B	Alignment	not modelled	100.0	21	PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
57	c2ygrD	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
58	c3pihA	Alignment	not modelled	100.0	27	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	32	PDB header: dna-binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
60	d1wlwa	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
61	d1cr2a	Alignment	not modelled	99.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
62	c3tauB	Alignment	not modelled	99.8	15	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of a putative guanylate monophosphate kinase from2 listeria monocytogenes egd-e
63	c2j41A	Alignment	not modelled	99.7	13	PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
64	c3ftjA	Alignment		99.7	36	PDB header: hydrolase Chain: A: PDB Molecule: macrolide export atp-binding/permease protein PDBTitle: crystal structure of the periplasmic region of macb from2 actinobacillus actinomycetemcomitans
65	c1xexB	Alignment	not modelled	99.6	21	PDB header: cell cycle Chain: B: PDB Molecule: smc protein; PDBTitle: structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
66	c1f2uD	Alignment	not modelled	99.6	27	PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
67	c3a4mB	Alignment	not modelled	99.6	14	PDB header: transferase Chain: B: PDB Molecule: l-seryl-trna(sec) kinase; PDBTitle: crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
68	d2qy9a2	Alignment	not modelled	99.5	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
69	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
70	c2o5vA	Alignment	not modelled	99.5	27	PDB header: replication/recombination Chain: A: PDB Molecule: dna replication and repair protein recf; PDBTitle: recombination mediator recf
71	d1ls1a2	Alignment	not modelled	99.4	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
72	c3lncB	Alignment	not modelled	99.4	14	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of guanylate kinase from anaplasma2 phagocytophilum
73	d1vmaa2	Alignment	not modelled	99.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
74	c1u9iA	Alignment	not modelled	99.3	16	PDB header: circadian clock protein Chain: A: PDB Molecule: kaic; PDBTitle: crystal structure of circadian clock protein kaic with phosphorylation2 sites
75	d1e69a	Alignment	not modelled	99.2	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
76	d1okkd2	Alignment	not modelled	99.2	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
77	c3geiB	Alignment	not modelled	99.1	14	PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
78	d1ve8a1	Alignment	not modelled	99.0	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate

78	d1ye0a1	Alignment	not modelled	99.0	42	hydrolases Family: RecA protein-like (ATPase-domain)
79	d1np6a	Alignment	not modelled	98.9	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
80	c1q57G	Alignment	not modelled	98.9	13	PDB header: transferase Chain: G: PDB Molecule: dna primase/helicase; PDBTitle: the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
81	c3auyB	Alignment	not modelled	98.8	28	PDB header: recombination Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: crystal structure of rad50 bound to adp
82	c2dr3A	Alignment	not modelled	98.7	14	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	c3is6A	Alignment	not modelled	98.5	13	PDB header: transport protein Chain: A: PDB Molecule: putative permease protein, abc transporter; PDBTitle: the crystal structure of a domain of a putative permease protein from2 porphyromonas gingivalis to 2a
84	d1qzxa3	Alignment	not modelled	98.5	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
85	d1ewqa2	Alignment	not modelled	98.5	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
86	c2o8bA	Alignment	not modelled	98.4	25	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
87	c3thxB	Alignment	not modelled	98.4	18	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
88	c2w0mA	Alignment	not modelled	98.3	12	PDB header: unknown function Chain: A: PDB Molecule: sso2452; PDBTitle: crystal structure of sso2452 from sulfolobus solfataricus2 p2
89	c2o8dB	Alignment	not modelled	98.3	32	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
90	c3qkuB	Alignment	not modelled	98.3	21	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
91	d1wb9a2	Alignment	not modelled	98.3	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
92	d2i3ba1	Alignment	not modelled	98.3	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
93	c1ewqA	Alignment	not modelled	98.2	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
94	c1wxqA	Alignment	not modelled	98.2	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
95	d1nlfa	Alignment	not modelled	98.2	15	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	98.1	21	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	c1ewrA	Alignment	not modelled	98.1	24	PDB header: hydrolase Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of taq muts
98	d1tf7a1	Alignment	not modelled	97.9	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
99	c2recB	Alignment	not modelled	97.7	23	PDB header: helicase PDB COMPND:
100	c3qg5A	Alignment	not modelled	97.7	26	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	c3bh0A	Alignment	not modelled	97.7	10	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
102	d1yrba1	Alignment	not modelled	97.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
103	c1pznG	Alignment	not modelled	97.6	16	PDB header: recombination Chain: G: PDB Molecule: dna repair and recombination protein rad51; PDBTitle: rad51 (rada)

104	c1xx6B_	Alignment	not modelled	97.5	36	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.
105	d1tf7a2	Alignment	not modelled	97.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
106	c3cmvG_	Alignment	not modelled	97.5	15	PDB header: recombination Chain: G: PDB Molecule: protein reca; PDBTitle: mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
107	c2q6tB_	Alignment	not modelled	97.4	19	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
108	d1xp8a1	Alignment	not modelled	97.4	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
109	c1xp8A_	Alignment	not modelled	97.4	23	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: "deinococcus radiodurans reca in complex with atp-gamma-s"
110	c2vyeA_	Alignment	not modelled	97.4	13	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of the dnac-ssdna complex
111	d1mo6a1	Alignment	not modelled	97.4	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
112	c2hcbC_	Alignment	not modelled	97.4	17	PDB header: replication Chain: C: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of amppcp-bound dnaa from aquifex aeolicus
113	c2ztsB_	Alignment	not modelled	97.3	17	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
114	c1ii8A_	Alignment	not modelled	97.3	32	PDB header: replication Chain: A: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain
115	d1u94a1	Alignment	not modelled	97.3	23	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	97.3	16	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair and recombination protein radb; PDBTitle: crystal structure of the radb recombinase
117	c3ldaA_	Alignment	not modelled	97.3	20	PDB header: dna binding protein Chain: A: PDB Molecule: dna repair protein rad51; PDBTitle: yeast rad51 h352y filament interface mutant
118	d1v5wa_	Alignment	not modelled	97.2	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
119	c1us8A_	Alignment	not modelled	97.2	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
120	c3pxiB_	Alignment	not modelled	97.2	21	PDB header: protein binding Chain: B: PDB Molecule: negative regulator of genetic competence clpc/meccb; PDBTitle: structure of meca108:clpc