

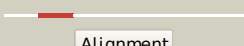

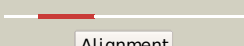

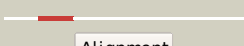

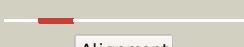
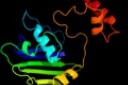






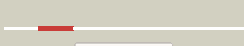





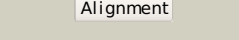


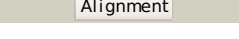
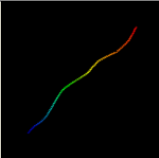
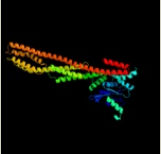
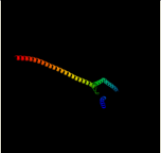
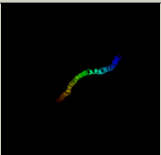


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3eukC_	 Alignment		100.0	72	PDB header: cell cycle Chain: C: PDB Molecule: chromosome partition protein mukb, linker; PDBTitle: crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, asymmetric dimer
2	d1qhla_	 Alignment		99.7	99	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
3	c3qg5A_	 Alignment		99.6	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
4	c1xexA_	 Alignment		99.5	14	PDB header: cell cycle Chain: A: PDB Molecule: smc protein; PDBTitle: structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
5	c3qkuB_	 Alignment		99.5	11	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
6	c3auyB_	 Alignment		99.5	11	PDB header: recombination Chain: B: PDB Molecule: dna double-strand break repair rad50 atpase; PDBTitle: crystal structure of rad50 bound to adp
7	c1ii8A_	 Alignment		99.4	10	PDB header: replication Chain: A: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain
8	d1wlwa_	 Alignment		99.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
9	d1e69a_	 Alignment		99.4	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
10	c2o5vA_	 Alignment		99.2	23	PDB header: replication/recombination Chain: A: PDB Molecule: dna replication and repair protein recf; PDBTitle: recombination mediator recf
11	c1us8A_	 Alignment		99.2	25	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

12	c1ii8B_	Alignment		98.5	17	PDB header: replication Chain: B: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of the p. furiosus rad50 atpase domain
13	c1xexB_	Alignment		98.4	15	PDB header: cell cycle Chain: B: PDB Molecule: smc protein; PDBTitle: structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
14	c3ibpA_	Alignment		98.2	99	PDB header: cell cycle Chain: A: PDB Molecule: chromosome partition protein mukb; PDBTitle: the crystal structure of the dimerization domain of escherichia coli2 structural maintenance of chromosomes protein mukb
15	d1v43a3	Alignment		97.9	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
16	c1z47B_	Alignment		97.9	16	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
17	c1vciA_	Alignment		97.9	24	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
18	d2awna2	Alignment		97.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
19	d1g2912	Alignment		97.8	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
20	c2it1B_	Alignment		97.8	24	PDB header: transport protein Chain: B: PDB Molecule: 362aa long hypothetical maltose/maltodextrin PDBTitle: structure of ph0203 protein from pyrococcus horikoshii
21	c2yz2B_	Alignment	not modelled	97.8	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
22	d2onka1	Alignment	not modelled	97.8	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
23	c1f2uD_	Alignment	not modelled	97.8	20	PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
24	c3d31B_	Alignment	not modelled	97.7	19	PDB header: transport protein Chain: B: PDB Molecule: sulfate/molybdate abc transporter, atp-binding PDBTitle: modbc from methanosarcina acetivorans
25	c2ghiD_	Alignment	not modelled	97.7	21	PDB header: transport protein Chain: D: PDB Molecule: transport protein; PDBTitle: crystal structure of plasmodium yoelii multidrug resistance2 protein 2
26	c3gfoA_	Alignment	not modelled	97.7	31	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.
27	c2nq2C_	Alignment	not modelled	97.7	28	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.
28	d1l7vc_	Alignment	not modelled	97.6	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

						Family: ABC transporter ATPase domain-like
29	c2d62A_	 Alignment	not modelled	97.6	15	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
30	c3gd7C_	 Alignment	not modelled	97.6	29	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)
31	c2ihyB_	 Alignment	not modelled	97.6	19	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
32	d1sgwa_	 Alignment	not modelled	97.6	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
33	c2yyzA_	 Alignment	not modelled	97.6	18	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, atp-binding protein; PDBTitle: crystal structure of sugar abc transporter, atp-binding protein
34	d3b60a1	 Alignment	not modelled	97.6	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
35	c1oxtb_	 Alignment	not modelled	97.6	17	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
36	d1g6ha_	 Alignment	not modelled	97.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
37	c2d2fA_	 Alignment	not modelled	97.6	30	PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
38	d1b0ua_	 Alignment	not modelled	97.6	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
39	c2pcjB_	 Alignment	not modelled	97.6	13	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
40	c2d3wB_	 Alignment	not modelled	97.6	26	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
41	d1ji0a_	 Alignment	not modelled	97.6	30	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
42	d3d31a2	 Alignment	not modelled	97.5	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
43	d3dhwc1	 Alignment	not modelled	97.5	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
44	c3fvqB_	 Alignment	not modelled	97.5	21	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
45	d1xmia_	 Alignment	not modelled	97.5	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
46	d1oxxk2	 Alignment	not modelled	97.5	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
47	c2cbzA_	 Alignment	not modelled	97.5	26	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
48	c1q1bD_	 Alignment	not modelled	97.5	16	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
49	c2olkD_	 Alignment	not modelled	97.5	20	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
50	d1vp1a_	 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
51	d1jj7a_	Alignment	not modelled	97.5	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
52	d1l2ta_	Alignment	not modelled	97.5	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases

						Family: ABC transporter ATPase domain-like Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
53	d2pmka1	Alignment	not modelled	97.5	21	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
54	c2pzfB_	Alignment	not modelled	97.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
55	d1mv5a_	Alignment	not modelled	97.4	19	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)
56	c3nhaA_	Alignment	not modelled	97.4	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
57	d1vmaa2	Alignment	not modelled	97.4	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
58	d1np6a_	Alignment	not modelled	97.4	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
59	d1r0wa_	Alignment	not modelled	97.3	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
60	d1okkd2	Alignment	not modelled	97.3	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
61	d2qy9a2	Alignment	not modelled	97.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
62	c1c1gA_	Alignment		97.2	11	PDB header: contractile protein Chain: A: PDB Molecule: tropomyosin; PDBTitle: crystal structure of tropomyosin at 7 angstroms resolution2 in the spermine-induced crystal form
63	c2vf7B_	Alignment	not modelled	97.2	25	PDB header: dna-binding protein Chain: B: PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
64	c2j41A_	Alignment	not modelled	97.2	36	PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
65	d1ls1a2	Alignment	not modelled	97.1	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
66	c3tauB_	Alignment	not modelled	97.1	41	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of a putative guanylate monophosphate kinase from2 listeria monocytogenes egd-e
67	d1cr2a_	Alignment	not modelled	97.0	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
68	c2r6fA_	Alignment	not modelled	97.0	28	PDB header: hydrolase Chain: A: PDB Molecule: excinuclease abc subunit a; PDBTitle: crystal structure of bacillus stearothermophilus uvra
69	d1pf4a1	Alignment	not modelled	97.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
70	c3pihA_	Alignment	not modelled	96.9	25	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
71	c2ygrD_	Alignment	not modelled	96.9	23	PDB header: hydrolase Chain: D: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
72	d1ewqa2	Alignment	not modelled	96.9	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
73	c2iw3B_	Alignment	not modelled	96.9	25	PDB header: translation Chain: B: PDB Molecule: elongation factor 3a; PDBTitle: elongation factor 3 in complex with adp
74	c1yqtA_	Alignment	not modelled	96.9	24	PDB header: hydrolase/translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: rnase-l inhibitor
75	c2pjzA_	Alignment	not modelled	96.8	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
76	c3bk7A_	Alignment	not modelled	96.7	23	PDB header: hydrolase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi
						PDB header: transferase

77	c3a4mB_	Alignment	not modelled	96.7	17	Chain: B: PDB Molecule: l-seryl-trna(sec) kinase; PDBTitle: crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
78	d1qzxa3	Alignment	not modelled	96.7	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
79	c2yl4A_	Alignment	not modelled	96.7	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
80	c3dhwC_	Alignment	not modelled	96.6	25	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metni; PDBTitle: crystal structure of methionine importer metni
81	c3ozxA_	Alignment	not modelled	96.6	21	PDB header: hydrolase, translation Chain: A: PDB Molecule: rnase l inhibitor; PDBTitle: crystal structure of abce1 of sulfolobus solfataricus (-fes domain)
82	c2hydB_	Alignment	not modelled	96.5	26	PDB header: transport protein Chain: B: PDB Molecule: abc transporter homolog; PDBTitle: multidrug abc transporter sav1866
83	c1ewqA_	Alignment	not modelled	96.5	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
84	c3g5uB_	Alignment	not modelled	96.5	31	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
85	d2i3ba1	Alignment	not modelled	96.5	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
86	c2o8dB_	Alignment	not modelled	96.4	24	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
87	d1wb9a2	Alignment	not modelled	96.4	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
88	c2o8bA_	Alignment	not modelled	96.4	20	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
89	d2hyda1	Alignment	not modelled	96.4	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
90	c1f5nA_	Alignment		96.3	11	PDB header: signaling protein Chain: A: PDB Molecule: interferon-induced guanylate-binding protein 1; PDBTitle: human guanylate binding protein-1 in complex with the gtp2 analogue, gmppnp.
91	d1ye8a1	Alignment	not modelled	96.3	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
92	c3ojaB_	Alignment		96.3	14	PDB header: protein binding Chain: B: PDB Molecule: anopheles plasmodium-responsive leucine-rich repeat protein PDBTitle: crystal structure of lrim1/apl1c complex
93	c1ewrA_	Alignment	not modelled	96.2	23	PDB header: hydrolase Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of taq muts
94	c3thxB_	Alignment	not modelled	96.2	26	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	c3ghgK_	Alignment		96.1	11	PDB header: blood clotting Chain: K: PDB Molecule: fibrinogen beta chain; PDBTitle: crystal structure of human fibrinogen
96	c2cnwF_	Alignment	not modelled	96.1	27	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
97	c2f1rA_	Alignment	not modelled	96.1	10	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobbb)
98	d1yrba1	Alignment	not modelled	96.1	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
99	c3b5wE_	Alignment	not modelled	96.1	28	PDB header: membrane protein Chain: E: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of eschericia coli msba

100	dlp9ra	Alignment	not modelled	96.1	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
101	dls96a	Alignment	not modelled	96.1	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
102	clwbdA	Alignment	not modelled	96.0	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
103	c3jvvA	Alignment	not modelled	96.0	38	PDB header: atp binding protein Chain: A: PDB Molecule: twitching mobility protein; PDBTitle: crystal structure of p. aeruginosa pilt with bound amp-pcp
104	dlzp6a1	Alignment	not modelled	96.0	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Atu3015-like
105	dlznwa1	Alignment	not modelled	96.0	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
106	cldegO	Alignment		96.0	12	PDB header: PDB COMPND:
107	c2j7pA	Alignment	not modelled	96.0	20	PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
108	c3b9qA	Alignment	not modelled	95.9	27	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpfts from arabidopsis thaliana
109	clciiA	Alignment		95.9	14	PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia
110	c2qy9A	Alignment	not modelled	95.9	20	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
111	c2yhsA	Alignment	not modelled	95.9	20	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
112	c2og2A	Alignment	not modelled	95.8	32	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
113	c3geiB	Alignment	not modelled	95.7	33	PDB header: hydrolase Chain: B: PDB Molecule: trna modification gtpase mnme; PDBTitle: crystal structure of mnme from chlorobium tepidum in complex2 with gcp
114	clu9iA	Alignment	not modelled	95.7	30	PDB header: circadian clock protein Chain: A: PDB Molecule: kaiC; PDBTitle: crystal structure of circadian clock protein kaiC with phosphorylation2 sites
115	clzu4A	Alignment	not modelled	95.7	32	PDB header: protein transport Chain: A: PDB Molecule: ftsy; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
116	dl1nija1	Alignment	not modelled	95.7	43	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
117	c2eyuA	Alignment	not modelled	95.7	35	PDB header: protein transport Chain: A: PDB Molecule: twitching motility protein pilt; PDBTitle: the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
118	dlg6oa	Alignment	not modelled	95.6	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
119	c3b5xB	Alignment	not modelled	95.6	28	PDB header: membrane protein Chain: B: PDB Molecule: lipid a export atp-binding/permease protein msba; PDBTitle: crystal structure of msba from vibrio cholerae
120	dlki9a	Alignment	not modelled	95.6	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases