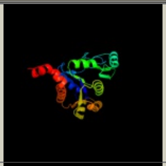
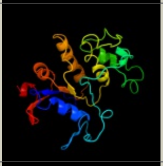
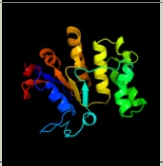
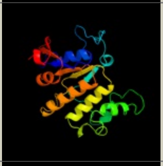
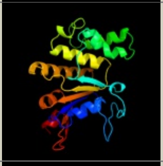
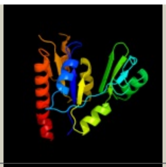
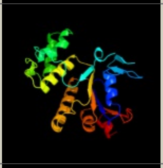
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P60546
Date	Thu Jan 5 12:06:52 GMT 2012
Unique Job ID	6ad84f9ac11fa705

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1s96a_	Alignment		100.0	98	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
2	c3tr0A_	Alignment		100.0	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** structure of guanylate kinase (gmk) from coxiella burnetii
3	c3tauB_	Alignment		99.9	39	**PDB header:**transferase **Chain:** B: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of a putative guanylate monophosphaste kinase from2 listeria monocytogenes egd-e
4	c1q1bD_	Alignment		99.9	12	**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
5	c2it1B_	Alignment		99.9	13	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**362aa long hypothetical maltose/maltodextrin **PDBTitle:** structure of ph0203 protein from pyrococcus horikoshii
6	c2yyzA_	Alignment		99.9	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar abc transporter, atp-binding protein; **PDBTitle:** crystal structure of sugar abc transporter, atp-binding protein
7	c1z47B_	Alignment		99.9	12	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative abc-transporter atp-binding protein; **PDBTitle:** structure of the atpase subunit cysa of the putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius
8	c3d31B_	Alignment		99.9	11	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**sulfate/molybdate abc transporter, atp-binding **PDBTitle:** modbc from methanosarcina acetivorans
9	c1vciA_	Alignment		99.9	13	**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
10	c3fvqB_	Alignment		99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fe(3+) ions import atp-binding protein fbpc; **PDBTitle:** crystal structure of the nucleotide binding domain fbpc2 complexed with atp
11	c1oxtB_	Alignment		99.9	12	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, atp binding protein; **PDBTitle:** crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus

12	c2j41A_	Alignment		99.9	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
13	d3d31a2	Alignment		99.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
14	d1g2912	Alignment		99.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
15	c1z6gA_	Alignment		99.9	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of guanylate kinase from plasmodium falciparum
16	d1oxxk2	Alignment		99.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
17	d3dhwc1	Alignment		99.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
18	c3dhwC_	Alignment		99.9	11	**PDB header:**membrane protein/hydrolase **Chain:** C: **PDB Molecule:**methionine import atp-binding protein metn; **PDBTitle:** crystal structure of methionine importer metni
19	c2d62A_	Alignment		99.9	10	**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
20	c3neyC_	Alignment		99.9	27	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**55 kda erythrocyte membrane protein; **PDBTitle:** crystal structure of the kinase domain of mpp1/p55
21	c3lncB_	Alignment	not modelled	99.9	42	**PDB header:**transferase **Chain:** B: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of guanylate kinase from anaplasma2 phagocytophilum
22	c2olkD_	Alignment	not modelled	99.9	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**amino acid abc transporter; **PDBTitle:** abc protein artp in complex with adp-beta-s
23	c2qorA_	Alignment	not modelled	99.9	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of plasmodium vivax guanylate kinase
24	d1kgda_	Alignment	not modelled	99.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
25	d2onka1	Alignment	not modelled	99.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
26	d1ji0a_	Alignment	not modelled	99.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
27	d1vpla_	Alignment	not modelled	99.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
28	c3g5uB_	Alignment	not modelled	99.9	11	**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
						Fold:P-loop containing nucleoside triphosphate hydrolases

29	d1lvga_	Alignment	not modelled	99.9	42	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
30	d1b0ua_	Alignment	not modelled	99.9	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
31	d1gkya_	Alignment	not modelled	99.9	45	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
32	c3gfoA_	Alignment	not modelled	99.9	13	**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.
33	d1v43a3	Alignment	not modelled	99.9	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
34	c1znyA_	Alignment	not modelled	99.9	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp
35	d1znwa1	Alignment	not modelled	99.9	36	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
36	c2pcjB_	Alignment	not modelled	99.9	14	**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
37	d1g6ha_	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
38	d1l2ta_	Alignment	not modelled	99.9	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
39	c2yz2B_	Alignment	not modelled	99.8	15	**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
40	d1jj7a_	Alignment	not modelled	99.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
41	d2awna2	Alignment	not modelled	99.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
42	d2pmka1	Alignment	not modelled	99.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
43	c2hydB_	Alignment	not modelled	99.8	18	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
44	c2nq2C_	Alignment	not modelled	99.8	13	**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.
45	c3nhaA_	Alignment	not modelled	99.8	13	**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)
46	d1mv5a_	Alignment	not modelled	99.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
47	c2yl4A_	Alignment	not modelled	99.8	12	**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
48	d3b60a1	Alignment	not modelled	99.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
49	c3b5xB_	Alignment	not modelled	99.8	10	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of msba from vibrio cholerae
50	c3b5wE_	Alignment	not modelled	99.8	11	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of eschericia coli msba
51	c3gd7C_	Alignment	not modelled	99.8	10	**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)
52	c2d3wB_	Alignment	not modelled	99.8	13	**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
53	d1xmja	Alignment	not modelled	99.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate

		Alignment	not modelled	99.8	12	hydrolases **Family:**ABC transporter ATPase domain-like
54	c2d2fA_	Alignment	not modelled	99.8	11	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sufc protein; **PDBTitle:** crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
55	c1yqtA_	Alignment	not modelled	99.8	11	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
56	d1l7vc_	Alignment	not modelled	99.8	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
57	c2ihyB_	Alignment	not modelled	99.8	14	**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
58	d2hyda1	Alignment	not modelled	99.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
59	d1pf4a1	Alignment	not modelled	99.8	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
60	c3ozxA_	Alignment	not modelled	99.8	10	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
61	c2pjzA_	Alignment	not modelled	99.8	12	**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
62	c2cbzA_	Alignment	not modelled	99.7	17	**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
63	c2pzfB_	Alignment	not modelled	99.7	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cystic fibrosis transmembrane conductance regulator; **PDBTitle:** minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508
64	d1r0wa_	Alignment	not modelled	99.7	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
65	d1kjwa2	Alignment	not modelled	99.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
66	c2ghiD_	Alignment	not modelled	99.7	11	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**transport protein; **PDBTitle:** crystal structure of plasmodium yoelii multidrug resistance2 protein 2
67	c3bk7A_	Alignment	not modelled	99.7	14	**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 abysii
68	c3uatA_	Alignment	not modelled	99.7	24	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**disks large homolog 1; **PDBTitle:** guanylate kinase domains of the maguk family scaffold proteins as2 specific phospho-protein binding modules
69	d1sgwa_	Alignment	not modelled	99.7	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
70	c1kjwA_	Alignment	not modelled	99.7	23	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**postsynaptic density protein 95; **PDBTitle:** sh3-guanylate kinase module from psd-95
71	c2xkxB_	Alignment	not modelled	99.6	22	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**disks large homolog 4; **PDBTitle:** single particle analysis of psd-95 in negative stain
72	c2r6fA_	Alignment	not modelled	99.6	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**excinuclease abc subunit a; **PDBTitle:** crystal structure of bacillus stearothermophilus uvra
73	c2iw3B_	Alignment	not modelled	99.6	16	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 3a; **PDBTitle:** elongation factor 3 in complex with adp
74	d2qy9a2	Alignment	not modelled	99.3	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
75	c2ygrD_	Alignment	not modelled	99.3	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
76	d1vmaa2	Alignment	not modelled	99.2	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
77	c3a4mB_	Alignment	not modelled	99.2	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-seryl-trna(sec) kinase; **PDBTitle:** crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
78	c2yvuA_	Alignment	not modelled	99.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable adenylyl-sulfate kinase; **PDBTitle:** crystal structure of ape1195
						Fold:P-loop containing nucleoside triphosphate hydrolases

79	d1okkd2	Alignment	not modelled	99.1	19	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
80	d1ls1a2	Alignment	not modelled	99.1	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
81	c2f6rA_	Alignment	not modelled	99.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional coenzyme a synthase; **PDBTitle:** crystal structure of bifunctional coenzyme a synthase (coa synthase):2 (18044849) from mus musculus at 1.70 a resolution
82	c1vyuB_	Alignment	not modelled	99.1	18	**PDB header:**ion transport **Chain:** B: **PDB Molecule:**calcium channel beta-3 subunit; **PDBTitle:** beta3 subunit of voltage-gated ca2+-channel
83	c2w0sB_	Alignment	not modelled	99.1	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of vaccinia virus thymidylate kinase2 bound to brivudin-5'-monophosphate
84	c3h0kA_	Alignment	not modelled	99.1	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0200 protein sso1041; **PDBTitle:** crystal structure of an adenylated kinase related protein from2 sulfolobus solfataricus to 3.25a
85	c3ch4B_	Alignment	not modelled	99.1	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphomevalonate kinase; **PDBTitle:** the crystal structure of human phosphomavelonate kinase at2 1.8 a resolution
86	c2wwiC_	Alignment	not modelled	99.0	9	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidilate kinase, putative; **PDBTitle:** plasmodium falciparum thymidylate kinase in complex with2 aztmp and adp
87	c3pihA_	Alignment	not modelled	99.0	13	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
88	d1w1wa_	Alignment	not modelled	99.0	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
89	c2if2C_	Alignment	not modelled	99.0	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**dephospho-coa kinase; **PDBTitle:** crystal structure of the putative dephospho-coa kinase from aquifex2 aeolicus, northeast structural genomics target qr72.
90	d1vhta_	Alignment	not modelled	99.0	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
91	d1ki9a_	Alignment	not modelled	99.0	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
92	d1jjva_	Alignment	not modelled	99.0	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
93	c3lh5A_	Alignment	not modelled	98.9	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of the sh3-guanylate kinase core domain of zo-1
94	d1np6a_	Alignment	not modelled	98.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
95	d1zp6a1	Alignment	not modelled	98.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Atu3015-like
96	d1cr2a_	Alignment	not modelled	98.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
97	d1nn5a_	Alignment	not modelled	98.9	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
98	d4tmka_	Alignment	not modelled	98.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
99	d1uf9a_	Alignment	not modelled	98.9	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
100	c2ccjA_	Alignment	not modelled	98.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of s. aureus thymidylate kinase complexed2 with thymidine monophosphate
101	c3geiB_	Alignment	not modelled	98.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from chlorobium tepidum in complex2 with gcp
102	c2plrB_	Alignment	not modelled	98.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thymidylate kinase; **PDBTitle:** crystal structure of dtmp kinase (st1543) from sulfolobus tokodaii2 strain7
103	c2pbrB_	Alignment	not modelled	98.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of thymidylate kinase (aq_969) from aquifex aeolicus2 vf5
104	c3kfvA_	Alignment	not modelled	98.8	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**tight junction protein zo-3; **PDBTitle:** crystal structure of the sh3-kinase fragment of tight2

							junction protein 3 (tjp3) in apo-form
105	d1e6ca_		Alignment	not modelled	98.8	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
106	d1ye8a1		Alignment	not modelled	98.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
107	d1m7gb_		Alignment	not modelled	98.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Adenosine-5'phosphosulfate kinase (APS kinase)
108	c2z0hA_		Alignment	not modelled	98.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of thymidylate kinase in complex with dtdp2 and adp from thermotoga maritima
109	d1m8pa3		Alignment	not modelled	98.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ATP sulfurylase C-terminal domain
110	d1qzxa3		Alignment	not modelled	98.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
111	c1zuiA_		Alignment	not modelled	98.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**shikimate kinase; **PDBTitle:** structural basis for shikimate-binding specificity of helicobacter2 pylori shikimate kinase
112	c2bwjC_		Alignment	not modelled	98.7	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**adenylate kinase 5; **PDBTitle:** structure of adenylate kinase 5
113	c3akcA_		Alignment	not modelled	98.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cytidylate kinase; **PDBTitle:** crystal structure of cmp kinase in complex with cdp and adp from2 thermus thermophilus hb8
114	d1khta_		Alignment	not modelled	98.7	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
115	d1tmka_		Alignment	not modelled	98.7	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
116	c2vf7B_		Alignment	not modelled	98.7	17	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
117	d1rkba_		Alignment	not modelled	98.6	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
118	d1knqa_		Alignment	not modelled	98.6	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Gluconate kinase
119	c2grjH_		Alignment	not modelled	98.6	9	**PDB header:**transferase **Chain:** H: **PDB Molecule:**dephospho-coa kinase; **PDBTitle:** crystal structure of dephospho-coa kinase (ec 2.7.1.24)2 (dephosphocoenzyme a kinase) (tm1387) from thermotoga maritima at3 2.60 a resolution
120	c3hdtB_		Alignment	not modelled	98.6	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of putative kinase from clostridium symbiosum atcc2 14940