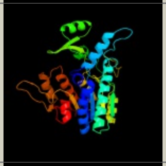
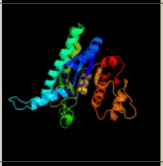
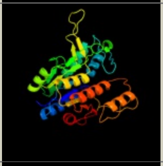
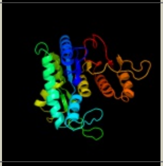
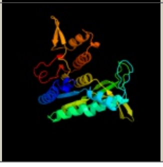
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	Q46807
Date	Thu Jan 5 12:34:33 GMT 2012
Unique Job ID	a3425bf2dff664be

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1e19a_	Alignment		100.0	48	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase
2	c2e9yA_	Alignment		100.0	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**carbamate kinase; **PDBTitle:** crystal structure of project ape1968 from aeropyrum pernix k1
3	d1b7ba_	Alignment		100.0	51	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**Carbamate kinase
4	c3kzfC_	Alignment		100.0	44	**PDB header:**transferase **Chain:** C: **PDB Molecule:**carbamate kinase; **PDBTitle:** structure of giardia carbamate kinase
5	c2rd5A_	Alignment		100.0	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**acetylglutamate kinase-like protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
6	d2ap9a1	Alignment		100.0	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
7	d2bufa1	Alignment		100.0	22	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
8	d1gs5a_	Alignment		100.0	22	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
9	c2r98A_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetylglutamate synthase; **PDBTitle:** crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
10	c2v5hB_	Alignment		100.0	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** controlling the storage of nitrogen as arginine: the2 complex of pii and acetylglutamate kinase from3 synechococcus elongatus pcc 7942
11	d2btya1	Alignment		100.0	26	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase

12	c3l86A_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetylglutamate kinase; **PDBTitle:** the crystal structure of smu.665 from streptococcus mutans ua159
13	c2j5tF_	Alignment		100.0	19	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** glutamate 5-kinase from escherichia coli complexed with2 glutamate
14	c2w21A_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** crystal structure of the aminoacid kinase domain of the2 glutamate 5 kinase of escherichia coli.
15	d2hmfa1	Alignment		100.0	14	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
16	c2egxA_	Alignment		100.0	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative acetylglutamate kinase; **PDBTitle:** crystal structure of the putative acetylglutamate kinase from thermus2 thermophilus
17	d2bnea1	Alignment		100.0	22	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
18	d1ybda1	Alignment		100.0	18	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
19	c3c1nA_	Alignment		100.0	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable aspartokinase; **PDBTitle:** crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
20	d2akoa1	Alignment		100.0	18	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
21	d2cdqa1	Alignment	not modelled	100.0	10	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
22	c3l76B_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of aspartate kinase from synechocystis
23	d1z9da1	Alignment	not modelled	100.0	18	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
24	c3ek5A_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridylate kinase; **PDBTitle:** unique gtp-binding pocket and allostery of ump kinase from a gram-2 negative phytopathogen bacterium
25	c2jjxC_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridylate kinase; **PDBTitle:** the crystal structure of ump kinase from bacillus anthracis2 (ba1797)
26	c3ll5C_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** C: **PDB Molecule:**gamma-glutamyl kinase related protein; **PDBTitle:** crystal structure of t. acidophilum isopentenyl phosphate kinase2 product complex
27	c3ll9A_	Alignment	not modelled	100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** x-ray structures of isopentenyl phosphate kinase
28	d2a1fa1	Alignment	not modelled	100.0	22	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
						Fold: Carbamate kinase-like

29	d2j0wa1	Alignment	not modelled	100.0	15	**Superfamily:**Carbamate kinase-like **Family:**PyrH-like
30	c3nwyB_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridylate kinase; **PDBTitle:** structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
31	d2ij9a1	Alignment	not modelled	100.0	27	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
32	c3k4yB_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** crystal structure of isopentenyl phosphate kinase from m. jannaschii2 in complex with ipp
33	c2cdqB_	Alignment	not modelled	100.0	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
34	d2brxa1	Alignment	not modelled	100.0	23	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
35	c3ab4K_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** K: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
36	c3d40A_	Alignment	not modelled	100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**foma protein; **PDBTitle:** crystal structure of fosfomycin resistance kinase foma from2 streptomyces wedmorensis complexed with diphosphate
37	c2j0wA_	Alignment	not modelled	100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lysine-sensitive aspartokinase 3; **PDBTitle:** crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
38	c2ogxB_	Alignment	not modelled	100.0	20	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**molybdenum storage protein subunit beta; **PDBTitle:** the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
39	c2va1A_	Alignment	not modelled	100.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of ump kinase from ureaplasma parvum
40	c2ogxA_	Alignment	not modelled	100.0	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**molybdenum storage protein subunit alpha; **PDBTitle:** the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
41	c2j4kC_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridylate kinase; **PDBTitle:** crystal structure of uridylate kinase from sulfolobus2 solfataricus in complex with ump to 2.2 angstrom3 resolution
42	d2zdra2	Alignment	not modelled	85.2	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
43	c1xuzA_	Alignment	not modelled	63.0	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**polysialic acid capsule biosynthesis protein siac; **PDBTitle:** crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
44	d2obba1	Alignment	not modelled	61.7	10	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
45	c3bq9A_	Alignment	not modelled	59.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**predicted rossmann fold nucleotide-binding domain- **PDBTitle:** crystal structure of predicted nucleotide-binding protein from2 idiomarina baltica os145
46	d1iowa1	Alignment	not modelled	49.9	20	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
47	c2q4dB_	Alignment	not modelled	45.3	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
48	c3mn1B_	Alignment	not modelled	43.0	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable yrbi family phosphatase; **PDBTitle:** crystal structure of probable yrbi family phosphatase from pseudomonas2 syringae pv.phaseolica 1448a
49	c4a1al_	Alignment	not modelled	41.1	24	**PDB header:**ribosome **Chain:** I: **PDB Molecule:**60s ribosomal protein l13a; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 3.
50	d1weka_	Alignment	not modelled	40.9	19	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
51	d1ydha_	Alignment	not modelled	38.4	14	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
52	c2dlnA_	Alignment	not modelled	36.9	20	**PDB header:**ligase(peptidoglycan synthesis) **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
53	d2q4oa1	Alignment	not modelled	36.4	10	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like

						Family: MoCo carrier protein-like
54	c2q4oA_	Alignment	not modelled	36.4	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein at2g37210/t2n18.3; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
55	d1xpja_	Alignment	not modelled	33.2	13	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
56	d1vlia2	Alignment	not modelled	30.9	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**NeuB-like
57	d2nx2a1	Alignment	not modelled	29.0	25	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**YpsA-like
58	d1t35a_	Alignment	not modelled	23.7	17	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
59	d1weha_	Alignment	not modelled	21.9	6	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
60	d1z6za1	Alignment	not modelled	20.7	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
61	c1vliA_	Alignment	not modelled	19.4	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
62	c3fzqA_	Alignment	not modelled	19.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of putative haloacid dehalogenase-like hydrolase2 (yp_001086940.1) from clostridium difficile 630 at 2.10 a resolution
63	c3gk0H_	Alignment	not modelled	18.3	33	**PDB header:**transferase **Chain:** H: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
64	c3g8rA_	Alignment	not modelled	18.2	21	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**probable spore coat polysaccharide biosynthesis protein e; **PDBTitle:** crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472
65	d2b0ja2	Alignment	not modelled	16.9	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
66	c3izcK_	Alignment	not modelled	16.8	18	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein rpl16 (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
67	c1x3lA_	Alignment	not modelled	16.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ph0495; **PDBTitle:** crystal structure of the ph0495 protein from pyrococccus horikoshii2 ot3
68	c3ewiB_	Alignment	not modelled	15.8	8	**PDB header:**transferase **Chain:** B: **PDB Molecule:**n-acylneuraminate cytidylyltransferase; **PDBTitle:** structural analysis of the c-terminal domain of murine cmp-2 sialic acid synthetase
69	c3e8mD_	Alignment	not modelled	15.0	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**acylneuraminate cytidylyltransferase; **PDBTitle:** structure-function analysis of 2-keto-3-deoxy-d-glycero-d-galacto-2 nononate-9-phosphate (kdn) phosphatase defines a new clad within the3 type c0 had subfamily
70	c3r4cA_	Alignment	not modelled	14.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase, haloacid dehalogenase-like hydrolase; **PDBTitle:** divergence of structure and function among phosphatases of the2 haloalkanoate (had) enzyme superfamily: analysis of bt1666 from3 bacteroides thetaiotaomicron
71	d1m5wa_	Alignment	not modelled	14.4	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**Pyridoxine 5'-phosphate synthase **Family:**Pyridoxine 5'-phosphate synthase
72	c3o6cA_	Alignment	not modelled	14.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyridoxine 5'-phosphate synthase; **PDBTitle:** pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
73	d2bdua1	Alignment	not modelled	14.2	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Pyrimidine 5'-nucleotidase (UMPH-1)
74	c3lqkA_	Alignment	not modelled	13.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit b; **PDBTitle:** crystal structure of dipicolinate synthase subunit b from bacillus2 halodurans c
75	c3nbuC_	Alignment	not modelled	13.4	11	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of pgi glucosephosphate isomerase
76	c1xrsB_	Alignment	not modelled	13.3	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-lysine 5,6-aminomutase beta subunit; **PDBTitle:** crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine
						Fold:SIS domain

77	d1gzda_	Alignment	not modelled	13.2	11	**Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
78	c2pr7A_	Alignment	not modelled	12.9	8	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase/epoxide hydrolase family; **PDBTitle:** crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
79	c3f46A_	Alignment	not modelled	12.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**5,10-methenyltetrahydromethanopterin hydrogenase; **PDBTitle:** the crystal structure of c176a mutated [fe]-hydrogenase (hmd)2 holoenzyme from methanocaldococcus jannaschii
80	c3mmzA_	Alignment	not modelled	12.9	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative had family hydrolase; **PDBTitle:** crystal structure of putative had family hydrolase from streptomyces2 avermitilis ma-4680
81	d1k1ea_	Alignment	not modelled	12.8	14	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Probable phosphatase YrbI
82	c3mcuF_	Alignment	not modelled	12.4	24	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dipicolinate synthase, b chain; **PDBTitle:** crystal structure of the dipicolinate synthase chain b from2 bacillus cereus. northeast structural genomics consortium3 target bcr215.
83	d1rkqa_	Alignment	not modelled	12.4	28	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
84	d1g5qa_	Alignment	not modelled	12.3	19	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
85	c3ujhB_	Alignment	not modelled	12.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
86	c3dnpA_	Alignment	not modelled	11.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**stress response protein yhax; **PDBTitle:** crystal structure of stress response protein yhax from bacillus2 subtilis
87	d1xrsb1	Alignment	not modelled	11.6	15	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
88	c1xviA_	Alignment	not modelled	11.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative mannosyl-3-phosphoglycerate phosphatase; **PDBTitle:** crystal structure of yedp, phosphatase-like domain protein2 from escherichia coli k12
89	d1xvia_	Alignment	not modelled	11.4	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
90	d1iata_	Alignment	not modelled	11.2	11	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
91	c3pr3B_	Alignment	not modelled	11.1	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
92	c3bsuF_	Alignment	not modelled	10.9	10	**PDB header:**hydrolase/rna/dna **Chain:** F: **PDB Molecule:**ribonuclease h1; **PDBTitle:** hybrid-binding domain of human rnase h1 in complex with 12-2 mer rna/dna
93	c2wu8A_	Alignment	not modelled	10.9	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
94	d1xkla_	Alignment	not modelled	10.8	25	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Hydroxynitrile lyase-like
95	c3iz5K_	Alignment	not modelled	10.5	24	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein l13a (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
96	d1u0fa_	Alignment	not modelled	10.0	13	**Fold:**SIS domain **Superfamily:**SIS domain **Family:**Phosphoglucose isomerase, PGI
97	c3ljkA_	Alignment	not modelled	9.5	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** glucose-6-phosphate isomerase from francisella tularensis.
98	c2o2cB_	Alignment	not modelled	9.4	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase, glycosomal; **PDBTitle:** crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
99	c3iabB_	Alignment	not modelled	9.4	18	**PDB header:**hydrolase/rna **Chain:** B: **PDB Molecule:**ribonucleases p/mrp protein subunit pop7; **PDBTitle:** crystal structure of rnase p /rnase mrp proteins pop6, pop72 in a complex with the p3 domain of rnase mrp rna