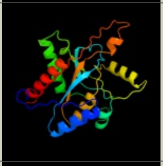
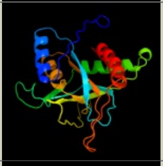
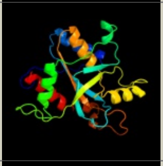
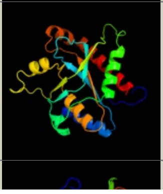
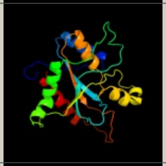
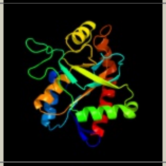
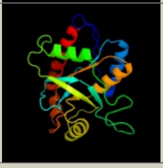
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AE12
Date	Wed Jan 25 15:20:29 GMT 2012
Unique Job ID	b19b75b5d91e45d5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t8sa_	Alignment		100.0	99	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
2	d1ybfa_	Alignment		100.0	32	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
3	c3mb8A_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from toxoplasma2 gondii in complex with immucillin-h
4	c1nw4C_	Alignment		100.0	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridine phosphorylase, putative; **PDBTitle:** crystal structure of plasmodium falciparum purine nucleoside2 phosphorylase in complex with immh and sulfate
5	d1q1ga_	Alignment		100.0	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
6	c3qpbB_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uridine phosphorylase; **PDBTitle:** crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
7	d1odka_	Alignment		100.0	20	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
8	c3bjeA_	Alignment		100.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nucleoside phosphorylase, putative; **PDBTitle:** crystal structure of trypanosoma brucei nucleoside phosphorylase shows2 uridine phosphorylase activity
9	d1k9sa_	Alignment		100.0	17	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
10	d1vhwa_	Alignment		100.0	16	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
11	d1rxya_	Alignment		100.0	21	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases

12	c1z34A_	Alignment		100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
13	c2xrfA_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uridine phosphorylase 2; **PDBTitle:** crystal structure of human uridine phosphorylase 2
14	d1je0a_	Alignment		100.0	18	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
15	c3tl6B_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of purine nucleoside phosphorylase from entamoeba2 histolytica
16	c3eufC_	Alignment		100.0	16	**PDB header:**transferase **Chain:** C: **PDB Molecule:**uridine phosphorylase 1; **PDBTitle:** crystal structure of bau-bound human uridine phosphorylase 1
17	d2ac7a1	Alignment		100.0	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
18	c3bl6A_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine nucleosidase/s- **PDBTitle:** crystal structure of staphylococcus aureus 5'-2 methylthioadenosine/s-adenosylhomocysteine nucleosidase in3 complex with formycin a
19	c3eeiA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5-methylthioadenosine nucleosidase/s- **PDBTitle:** crystal structure of 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from neisseria3 meningitidis in complex with methylthio-immucillin-a
20	c3dp9A_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mta/sah nucleosidase; **PDBTitle:** crystal structure of vibrio cholerae 5'-methylthioadenosine/s-adenosyl2 homocysteine nucleosidase (mtan) complexed with butylthio-dadme-3 immucillin a
21	c3nm5B_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mta/sah nucleosidase; **PDBTitle:** helicobacter pylori mtan complexed with formycin a
22	c1zosE_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**5'-methylthioadenosine / s-adenosylhomocysteine **PDBTitle:** structure of 5'-methylthionadenosine/s-adenosylhomocysteine2 nucleosidase from s. pneumoniae with a transition-state3 inhibitor mt-imma
23	d1jysa_	Alignment	not modelled	100.0	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
24	c2h8gA_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine nucleosidase; **PDBTitle:** 5'-methylthioadenosine nucleosidase from arabidopsis2 thaliana
25	c3bsfB_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**at4g34840; **PDBTitle:** crystal structure of the mta/sah nucleosidase
26	c3ozbF_	Alignment	not modelled	99.9	13	**PDB header:**transferase **Chain:** F: **PDB Molecule:**methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-methylthioinosine phosphorylase from2 psedomonas aeruginosa in complex with hypoxanthine
27	c1wtaA_	Alignment	not modelled	99.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5'-methylthioadenosine phosphorylase; **PDBTitle:** crystal structure of 5'-deoxy-5'-methylthioadenosine from aeropyrum2 pernix (r32 form)
28	d1g2oa_	Alignment	not modelled	99.9	12	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
						Fold: Phosphorylase/hydrolase-like

29	d1v4na_	Alignment	not modelled	99.9	13	**Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
30	c3khsB_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** crystal structure of grouper iridovirus purine nucleoside2 phosphorylase
31	d1vmka_	Alignment	not modelled	99.8	9	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
32	c2p4sA_	Alignment	not modelled	99.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
33	d1cb0a_	Alignment	not modelled	99.8	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
34	c1yr3A_	Alignment	not modelled	99.8	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**xanthosine phosphorylase; **PDBTitle:** escherichia coli purine nucleoside phosphorylase ii, the2 product of the xapa gene
35	d1qe5a_	Alignment	not modelled	99.8	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
36	c1tcvB_	Alignment	not modelled	99.8	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**purine-nucleoside phosphorylase; **PDBTitle:** crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate
37	c3la8A_	Alignment	not modelled	99.8	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative purine nucleoside phosphorylase; **PDBTitle:** the crystal structure of smu.1229 from streptococcus mutans ua159
38	d3bgsa1	Alignment	not modelled	99.8	15	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
39	d3pnpa_	Alignment	not modelled	99.8	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Purine and uridine phosphorylases **Family:**Purine and uridine phosphorylases
40	c3ggsA_	Alignment	not modelled	99.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**purine nucleoside phosphorylase; **PDBTitle:** human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
41	d1ixka_	Alignment	not modelled	74.3	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
42	d1sv6a_	Alignment	not modelled	66.4	20	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
43	c3lywA_	Alignment	not modelled	60.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ybbr family protein; **PDBTitle:** crystal structure of ybbr family protein dhaf_0833 from2 desulfitobacterium hafniense dcb-2. northeast structural3 genomics consortium target id dhr29b
44	c3m4xA_	Alignment	not modelled	53.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**nol1/nop2/sun family protein; **PDBTitle:** structure of a ribosomal methyltransferase
45	c2yxlA_	Alignment	not modelled	48.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**450aa long hypothetical fmu protein; **PDBTitle:** crystal structure of ph0851
46	c2eb5D_	Alignment	not modelled	44.0	14	**PDB header:**lyase **Chain:** D: **PDB Molecule:**2-oxo-hept-3-ene-1,7-dioate hydratase; **PDBTitle:** crystal structure of hpcg complexed with oxalate
47	d1nr9a_	Alignment	not modelled	42.9	14	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
48	d1sgva2	Alignment	not modelled	41.2	23	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase II TruB
49	d1gtta2	Alignment	not modelled	40.8	18	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
50	d2es9a1	Alignment	not modelled	37.9	40	**Fold:**YoaC-like **Superfamily:**YoaC-like **Family:**YoaC-like
51	d1gpua3	Alignment	not modelled	37.6	16	**Fold:**TK C-terminal domain-like **Superfamily:**TK C-terminal domain-like **Family:**Transketolase C-terminal domain-like
52	c3r6oA_	Alignment	not modelled	37.1	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2-hydroxyhepta-2,4-diene-1, 7-dioateisomerase; **PDBTitle:** crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioateisomerase from mycobacterium abscessus
53	c2dfuB_	Alignment	not modelled	36.7	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; **PDBTitle:** crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
54	c1ojhK_	Alignment	not modelled	36.6	47	**PDB header:**protein binding **Chain:** K: **PDB Molecule:**nbla; **PDBTitle:** crystal structure of nbla from pcc 7120

55	d1ojha_	Alignment	not modelled	35.0	47	**Fold:**NblA-like **Superfamily:**NblA-like **Family:**NblA-like
56	c1sqgA_	Alignment	not modelled	34.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sun protein; **PDBTitle:** the crystal structure of the e. coli fmu apoenzyme at 1.652 a resolution
57	d1gtta1	Alignment	not modelled	33.8	21	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
58	c3g7gG_	Alignment	not modelled	32.5	19	**PDB header:**structural genomics, unknown function **Chain:** G: **PDB Molecule:**upf0311 protein ca_c3321; **PDBTitle:** crystal structure of the protein with unknown function from2 clostridium acetobutylicum atcc 824
59	d1nkqa_	Alignment	not modelled	31.1	29	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
60	d1qcza_	Alignment	not modelled	30.1	20	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
61	c1a4iB_	Alignment	not modelled	30.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase / **PDBTitle:** human tetrahydrofolate dehydrogenase / cyclohydrolase
62	d2cl5a1	Alignment	not modelled	26.5	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**COMT-like
63	d1b0aa1	Alignment	not modelled	25.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
64	c3qdfA_	Alignment	not modelled	25.3	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; **PDBTitle:** crystal structure of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from mycobacterium marinum
65	c3c5oD_	Alignment	not modelled	25.1	17	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**upf0311 protein rpa1785; **PDBTitle:** crystal structure of the conserved protein of unknown function rpa17852 from rhodopseudomonas palustris
66	c1wzoC_	Alignment	not modelled	24.7	14	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**hpce; **PDBTitle:** crystal structure of the hpce from thermus thermophilus hb8
67	c3p2oA_	Alignment	not modelled	23.7	16	**PDB header:**oxidoreductase, hydrolase **Chain:** A: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
68	d1sawa_	Alignment	not modelled	22.9	13	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
69	d1a4ia1	Alignment	not modelled	22.8	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
70	d1p9ea_	Alignment	not modelled	22.4	24	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Methyl parathion hydrolase
71	c1p9eA_	Alignment	not modelled	22.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methyl parathion hydrolase; **PDBTitle:** crystal structure analysis of methyl parathion hydrolase from2 pseudomonas sp wbc-3
72	c2h31A_	Alignment	not modelled	21.9	15	**PDB header:**ligase, lyase **Chain:** A: **PDB Molecule:**multifunctional protein ade2; **PDBTitle:** crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
73	d1sqga2	Alignment	not modelled	21.9	17	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**NOL1/NOP2/sun
74	d1o4va_	Alignment	not modelled	21.6	22	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
75	c3p2oB_	Alignment	not modelled	21.5	16	**PDB header:**oxidoreductase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional protein fold; **PDBTitle:** crystal structure of fold bifunctional protein from campylobacter2 jejuni
76	c3eshB_	Alignment	not modelled	21.2	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein similar to metal-dependent hydrolase; **PDBTitle:** crystal structure of a probable metal-dependent hydrolase2 from staphylococcus aureus. northeast structural genomics3 target zr314
77	c3m6wA_	Alignment	not modelled	19.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rrna methylase; **PDBTitle:** multi-site-specific 16s rrna methyltransferase rsmf from thermus2 thermophilus in space group p21212 in complex with s-adenosyl-l-3 methionine
78	c2q1dX_	Alignment	not modelled	18.3	13	**PDB header:**lyase **Chain:** X: **PDB Molecule:**2-keto-3-deoxy-d-arabinonate dehydratase; **PDBTitle:** 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and2 2,5-dioxopentanoate
						PDB header:structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif;

79	c2k5jB_	Alignment	not modelled	17.8	20	**PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
80	c3l53F_	Alignment	not modelled	17.6	18	**PDB header:**structural genomics, unknown function **Chain:** F: **PDB Molecule:**putative fumarylacetoacetate isomerase/hydrolase; **PDBTitle:** crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica
81	d1sr9a3	Alignment	not modelled	17.6	23	**Fold:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Superfamily:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain **Family:**2-isopropylmalate synthase LeuA, allosteric (dimerisation) domain
82	c3peiA_	Alignment	not modelled	16.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** crystal structure of cytosol aminopeptidase from francisella2 tularensis
83	d1xmpa_	Alignment	not modelled	15.6	22	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
84	c1zmrA_	Alignment	not modelled	15.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of the e. coli phosphoglycerate kinase
85	d1n08a_	Alignment	not modelled	15.0	28	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin kinase-like **Family:**ATP-dependent riboflavin kinase-like
86	c2gfqC_	Alignment	not modelled	14.9	24	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**upf0204 protein ph0006; **PDBTitle:** structure of protein of unknown function ph0006 from pyrococcus2 horikoshii
87	d2ja9a1	Alignment	not modelled	14.9	36	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
88	d1vqod1	Alignment	not modelled	14.5	26	**Fold:**RL5-like **Superfamily:**RL5-like **Family:**Ribosomal protein L5
89	c2x4lA_	Alignment	not modelled	14.0	16	**PDB header:**transport **Chain:** A: **PDB Molecule:**ferric-siderophore receptor protein; **PDBTitle:** crystal structure of dese, a ferric-siderophore receptor2 protein from streptomyces coelicolor
90	c3rggD_	Alignment	not modelled	12.6	15	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
91	c2equA_	Alignment	not modelled	12.4	33	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1
92	d1oh1a_	Alignment	not modelled	12.2	43	**Fold:**Streptavidin-like **Superfamily:**beta-Barrel protease inhibitors **Family:**Staphostatin
93	d1bl0a2	Alignment	not modelled	12.0	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**AraC type transcriptional activator
94	d2nn6g1	Alignment	not modelled	11.8	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
95	d1hyoa2	Alignment	not modelled	11.8	22	**Fold:**FAH **Superfamily:**FAH **Family:**FAH
96	c3f6hA_	Alignment	not modelled	11.6	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**alpha-isopropylmalate synthase; **PDBTitle:** crystal structure of the regulatory domain of licms in2 complexed with isoleucine - type iii
97	d1b12a_	Alignment	not modelled	11.5	29	**Fold:**LexA/Signal peptidase **Superfamily:**LexA/Signal peptidase **Family:**Type 1 signal peptidase
98	c3trhI_	Alignment	not modelled	11.5	20	**PDB header:**lyase **Chain:** I: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase **PDBTitle:** structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
99	c1dfwA_	Alignment	not modelled	11.3	57	**PDB header:**immune system **Chain:** A: **PDB Molecule:**lung surfactant protein b; **PDBTitle:** conformational mapping of the n-terminal segment of2 surfactant protein b in lipid using 13c-enhanced fourier3 transform infrared spectroscopy (ftir)