Email	l.a.kelley@imperial.ac.uk
Description	P18843
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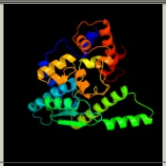
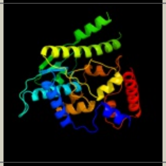
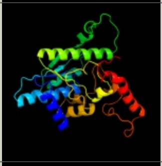
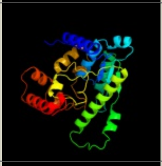
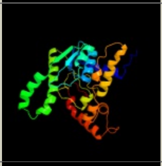
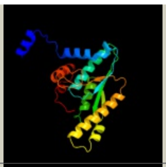
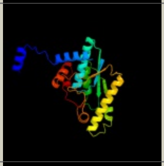
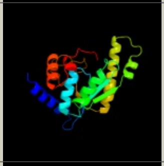
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1wxia1	Alignment		100.0	100	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
2	d1kqpa_	Alignment		100.0	54	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
3	c3dpiA_	Alignment		100.0	44	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nad+ synthetase; **PDBTitle:** crystal structure of nad+ synthetase from burkholderia pseudomallei
4	c3q4gA_	Alignment		100.0	49	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nad synthetase from vibrio cholerae
5	c2e18B_	Alignment		100.0	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of project ph0182 from pyrococcus horikoshii ot3
6	c3fiuD_	Alignment		100.0	32	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis
7	c3dlaD_	Alignment		100.0	22	**PDB header:**ligase **Chain:** D: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** x-ray crystal structure of glutamine-dependent nad+ synthetase from2 mycobacterium tuberculosis bound to naad+ and don
8	c3n05B_	Alignment		100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** crystal structure of nh3-dependent nad+ synthetase from streptomyces2 avermitilis
9	c3ilvA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamine-dependent nad(+) synthetase; **PDBTitle:** crystal structure of a glutamine-dependent nad(+) synthetase2 from cytophaga hutchinsonii
10	d1xnga1	Alignment		100.0	27	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
11	c3p52B_	Alignment		100.0	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** nh3-dependent nad synthetase from campylobacter jejuni subsp. jejuni2 nctc 11168 in complex with the nitrate ion

12	c1gpmD_	Alignment		100.0	17	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
13	c2vxoB_	Alignment		100.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
14	c3uowB_	Alignment		100.0	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
15	c3tqiB_	Alignment		100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
16	c2ywcC_	Alignment		100.0	18	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
17	c2dplA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b; **PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3
18	d1gpma1	Alignment		99.9	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
19	c2hmaA_	Alignment		99.9	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable trna (5-methylaminomethyl-2-thiouridylate)- **PDBTitle:** the crystal structure of trna (5-methylaminomethyl-2-thiouridylate)-2 methyltransferase trmu from streptococcus pneumoniae
20	c2derA_	Alignment		99.8	18	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**trna-specific 2-thiouridylase mnma; **PDBTitle:** cocrystal structure of an rna sulfuration enzyme mnma and2 trna-glu in the initial trna binding state
21	c2c5sA_	Alignment	not modelled	99.7	16	**PDB header:**rna-binding protein **Chain:** A: **PDB Molecule:**probable thiamine biosynthesis protein thii; **PDBTitle:** crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
22	d2c5sa1	Alignment	not modelled	99.7	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
23	d1wy5a1	Alignment	not modelled	99.6	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
24	d1j20a1	Alignment	not modelled	99.6	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
25	d1vl2a1	Alignment	not modelled	99.6	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
26	c3bl5E_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**queuosine biosynthesis protein quec; **PDBTitle:** crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
27	c3k32D_	Alignment	not modelled	99.5	12	**PDB header:**transferase **Chain:** D: **PDB Molecule:**uncharacterized protein mj0690; **PDBTitle:** crystal structure of predicted subunit of trna2 methyltransferase from methanocaldococcus jannaschii dsm
28	d1k92a1	Alignment	not modelled	99.4	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases

29	c2e21A_	Alignment	not modelled	99.4	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
30	d2pg3a1	Alignment	not modelled	99.3	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
31	c1kh2D_	Alignment	not modelled	99.3	13	**PDB header:**ligase **Chain:** D: **PDB Molecule:**argininosuccinate synthetase; **PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp
32	c2nz2A_	Alignment	not modelled	99.3	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of human argininosuccinate synthase in complex with2 aspartate and citrulline
33	d1ni5a1	Alignment	not modelled	99.3	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PP-loop ATPase
34	c1vl2C_	Alignment	not modelled	99.3	18	**PDB header:**ligase **Chain:** C: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of argininosuccinate synthase (tm1780) from2 thermotoga maritima at 1.65 a resolution
35	c3a2kB_	Alignment	not modelled	99.2	16	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**trna(ile)-lysidine synthase; **PDBTitle:** crystal structure of tils complexed with trna
36	c1k97A_	Alignment	not modelled	99.1	10	**PDB header:**ligase **Chain:** A: **PDB Molecule:**argininosuccinate synthase; **PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline
37	d1sura_	Alignment	not modelled	99.0	9	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
38	d1q15a1	Alignment	not modelled	98.9	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
39	d1vbka1	Alignment	not modelled	98.8	10	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ThiI-like
40	c1ni5A_	Alignment	not modelled	98.8	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**putative cell cycle protein mesj; **PDBTitle:** structure of the mesj pp-atpase from escherichia coli
41	c1q15A_	Alignment	not modelled	98.8	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**cara; **PDBTitle:** carbapenam synthetase
42	d1jgta1	Alignment	not modelled	98.7	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
43	c2o8vA_	Alignment	not modelled	98.7	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** paps reductase in a covalent complex with thioredoxin c35a
44	c1zunA_	Alignment	not modelled	98.7	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase subunit 2; **PDBTitle:** crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
45	c2goyC_	Alignment	not modelled	98.6	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**adenosine phosphosulfate reductase; **PDBTitle:** crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
46	d1ct9a1	Alignment	not modelled	98.6	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
47	d1zuna1	Alignment	not modelled	98.6	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**PAPS reductase-like
48	c1ct9D_	Alignment	not modelled	98.4	11	**PDB header:**ligase **Chain:** D: **PDB Molecule:**asparagine synthetase b; **PDBTitle:** crystal structure of asparagine synthetase b from2 escherichia coli
49	c1m1zB_	Alignment	not modelled	98.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**beta-lactam synthetase; **PDBTitle:** beta-lactam synthetase apo enzyme
50	c2oq2B_	Alignment	not modelled	98.0	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**phosphoadenosine phosphosulfate reductase; **PDBTitle:** crystal structure of yeast paps reductase with pap, a product complex
51	d1ru8a_	Alignment	not modelled	97.7	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
52	c1vbkA_	Alignment	not modelled	97.3	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1313; **PDBTitle:** crystal structure of ph1313 from pyrococcus horikoshii ot3
53	c2wsiA_	Alignment	not modelled	97.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fad synthetase; **PDBTitle:** crystal structure of yeast fad synthetase (fad1) in complex2 with fad
54	c3g59A_	Alignment	not modelled	97.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fmn adenylyltransferase; **PDBTitle:** crystal structure of candida glabrata fmn2 adenylyltransferase in complex with atp
						Fold: Adenine nucleotide alpha hydrolase-like

55	d2d13a1	Alignment	not modelled	94.6	17	**Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**N-type ATP pyrophosphatases
56	d1rz3a_	Alignment	not modelled	78.2	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
57	c1y89B_	Alignment	not modelled	59.2	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**devb protein; **PDBTitle:** crystal structure of devb protein
58	c3c8uA_	Alignment	not modelled	56.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
59	c3oc6A_	Alignment	not modelled	51.2	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
60	c3lwdA_	Alignment	not modelled	50.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
61	c3e15D_	Alignment	not modelled	50.2	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** 6-phosphogluconolactonase from plasmodium vivax
62	c3lhiA_	Alignment	not modelled	46.8	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative 6-phosphogluconolactonase; **PDBTitle:** crystal structure of putative 6-2 phosphogluconolactonase(yp_207848.1) from neisseria3 gonorrhoeae fa 1090 at 1.33 a resolution
63	d2ap1a2	Alignment	not modelled	38.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**ROK
64	d1fsfa_	Alignment	not modelled	37.4	18	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
65	c3ch4B_	Alignment	not modelled	36.8	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphomevalonate kinase; **PDBTitle:** the crystal structure of human phosphomavelonate kinase at2 1.8 a resolution
66	c2bkxB_	Alignment	not modelled	33.7	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily
67	d1qgpa_	Alignment	not modelled	32.4	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
68	d1qbjc_	Alignment	not modelled	32.2	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
69	c1usdA_	Alignment	not modelled	30.7	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** human vasp tetramerisation domain l352m
70	c2zbtB_	Alignment	not modelled	30.3	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** crystal structure of pyridoxine biosynthesis protein from thermus2 thermophilus hb8
71	d2gxba1	Alignment	not modelled	29.8	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
72	c1pbtA_	Alignment	not modelled	29.1	11	**PDB header:**hydrolase, oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
73	c3nwpA_	Alignment	not modelled	28.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
74	c1wyoA_	Alignment	not modelled	28.3	16	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**microtubule-associated protein rp/eb family **PDBTitle:** solution structure of the ch domain of human microtubule-2 associated protein rp/eb family member 3
75	d2gnpa1	Alignment	not modelled	28.0	12	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**SorC sugar-binding domain-like
76	d1pjqa3	Alignment	not modelled	27.4	29	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
77	c3grfA_	Alignment	not modelled	26.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
78	d1vl1a_	Alignment	not modelled	26.6	10	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
79	d1ne7a_	Alignment	not modelled	25.3	12	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**NagB-like
80	c2p2gD_	Alignment	not modelled	24.9	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine carbamoyltransferase; **PDBTitle:** crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form

81	c3zquA_	Alignment	not modelled	24.1	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
82	c1fvoB_	Alignment	not modelled	23.1	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ornithine transcarbamylase; **PDBTitle:** crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
83	d2eyqa4	Alignment	not modelled	22.0	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
84	c3cssA_	Alignment	not modelled	21.6	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from leishmania2 guyanensis
85	d1g66a_	Alignment	not modelled	21.2	23	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Cutinase-like
86	c3kv1A_	Alignment	not modelled	20.7	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional repressor; **PDBTitle:** crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
87	d1saza1	Alignment	not modelled	20.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
88	c2qjxA_	Alignment	not modelled	19.7	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein bim1; **PDBTitle:** structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
89	c2nv2U_	Alignment	not modelled	19.6	16	**PDB header:**lyase/transferase **Chain:** U: **PDB Molecule:**pyridoxal biosynthesis lyase pdxs; **PDBTitle:** structure of the plp synthase complex pdx1/2 (yaad/e) from bacillus2 subtilis
90	d3cx5a1	Alignment	not modelled	19.3	13	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**MPP-like
91	c2ejbA_	Alignment	not modelled	19.2	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
92	d2qjza1	Alignment	not modelled	19.2	17	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
93	c3icoA_	Alignment	not modelled	19.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**6-phosphogluconolactonase; **PDBTitle:** crystal structure of 6-phosphogluconolactonase from2 mycobacterium tuberculosis
94	d1v5ka_	Alignment	not modelled	18.5	17	**Fold:**CH domain-like **Superfamily:**Calponin-homology domain, CH-domain **Family:**Calponin-homology domain, CH-domain
95	c3sdsA_	Alignment	not modelled	18.2	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ornithine carbamoyltransferase, mitochondrial; **PDBTitle:** crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
96	c2ri0B_	Alignment	not modelled	18.1	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans
97	d1cexa_	Alignment	not modelled	17.8	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Cutinase-like
98	c3hn6D_	Alignment	not modelled	17.3	12	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**glucosamine-6-phosphate deaminase; **PDBTitle:** crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
99	d1otha1	Alignment	not modelled	16.6	14	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase