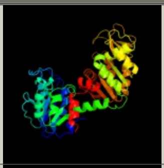
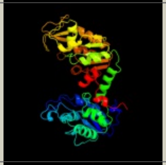
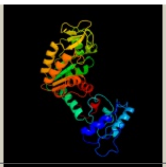
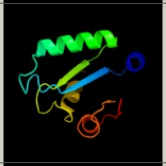
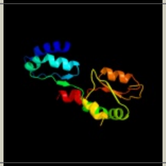
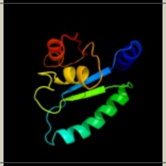
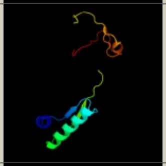
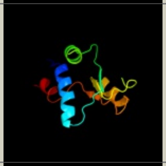
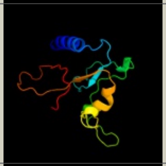
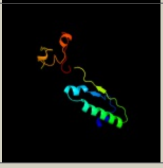
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A799
Date	Thu Jan 5 11:05:09 GMT 2012
Unique Job ID	d403d960e79f4e5d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1zmrA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of the e. coli phosphoglycerate kinase
2	d1phpa_	Alignment		100.0	47	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
3	d1vpea_	Alignment		100.0	46	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
4	c3q3vA_	Alignment		100.0	45	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
5	d16pka_	Alignment		100.0	42	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
6	d1v6sa_	Alignment		100.0	43	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
7	c2cunA_	Alignment		100.0	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
8	d1vjda_	Alignment		100.0	40	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
9	d1qpga_	Alignment		100.0	43	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
10	d1hdia_	Alignment		100.0	39	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
11	d1ltka_	Alignment		100.0	39	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase

12	d1fw8a_	Alignment		100.0	40	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
13	c3zvmA_	Alignment		82.0	21	**PDB header:**hydrolase/transferase/dna **Chain:** A: **PDB Molecule:**bifunctional polynucleotide phosphatase/kinase; **PDBTitle:** the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
14	c2pjuD_	Alignment		80.4	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon2 regulatory protein prpr
15	d1yj5a1	Alignment		76.9	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
16	c1yj5B_	Alignment		73.6	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase catalytic domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
17	c3eoeC_	Alignment		64.9	13	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from toxoplasma gondii, 55.m00007
18	d2pjua1	Alignment		55.4	14	**Fold:**Chelatase-like **Superfamily:**PrpR receptor domain-like **Family:**PrpR receptor domain-like
19	d1c8ba_	Alignment		53.2	23	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**HybD-like **Family:**Germination protease
20	c1pklB_	Alignment		50.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein (pyruvate kinase); **PDBTitle:** the structure of leishmania pyruvate kinase
21	c2wdfA_	Alignment	not modelled	49.9	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfur oxidation protein soxb; **PDBTitle:** termus thermophilus sulfate thiohydrolase soxb
22	c1ecjB_	Alignment	not modelled	47.7	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutamine phosphoribosylpyrophosphate **PDBTitle:** escherichia coli glutamine phosphoribosylpyrophosphate2 (prpp) amidotransferase complexed with 2 amp per tetramer
23	d2btya1	Alignment	not modelled	47.6	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**N-acetyl-l-glutamate kinase
24	c2q5cA_	Alignment	not modelled	46.7	7	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ntrc family transcriptional regulator; **PDBTitle:** crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
25	d1weka_	Alignment	not modelled	43.8	20	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
26	c2qyhD_	Alignment	not modelled	43.3	16	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical conserved protein, gk1056; **PDBTitle:** crystal structure of the hypothetical protein (gk1056) from2 geobacillus kaustophilus hta426
27	c3cxtA_	Alignment	not modelled	42.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase with different specificities; **PDBTitle:** quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
28	c2e28A_	Alignment	not modelled	42.3	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure analysis of pyruvate kinase from

						bacillus2 stearothermophilus
29	d1dqua_	Alignment	not modelled	38.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Phosphoenolpyruvate mutase/Isocitrate lyase-like
30	d1ecfa1	Alignment	not modelled	37.8	27	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
31	d1bj4a_	Alignment	not modelled	36.7	14	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
32	c1e0tD_	Alignment	not modelled	35.7	16	**PDB header:**phosphotransferase **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** r292d mutant of e. coli pyruvate kinase
33	c3e0vB_	Alignment	not modelled	35.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of pyruvate kinase from leishmania mexicana in2 complex with sulphate ions
34	c2r98A_	Alignment	not modelled	35.0	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetylglutamate synthase; **PDBTitle:** crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
35	d1t3ta2	Alignment	not modelled	34.9	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
36	c3dnpA_	Alignment	not modelled	33.2	26	**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
37	d1uala_	Alignment	not modelled	32.7	27	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
38	d1u7za_	Alignment	not modelled	32.3	13	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
39	c3ibgF_	Alignment	not modelled	30.7	20	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**atpase, subunit of the get complex; **PDBTitle:** crystal structure of aspergillus fumigatus get3 with bound2 adp
40	c2wdzD_	Alignment	not modelled	30.0	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**short-chain dehydrogenase/reductase; **PDBTitle:** crystal structure of the short chain dehydrogenase2 galactitol-dehydrogenase (gatdh) of rhodobacter3 sphaeroides in complex with nad+ and 1,2-pentandiol
41	c2v5hB_	Alignment	not modelled	29.7	17	**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
42	c3dfzB_	Alignment	not modelled	29.5	37	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**precorrin-2 dehydrogenase; **PDBTitle:** sirc, precorrin-2 dehydrogenase
43	d1p9pa_	Alignment	not modelled	29.0	24	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**tRNA(m1G37)-methyltransferase TrmD
44	d2z1aa2	Alignment	not modelled	28.9	32	**Fold:**Metallo-dependent phosphatases **Superfamily:**Metallo-dependent phosphatases **Family:**5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain
45	c2j5tF_	Alignment	not modelled	27.3	9	**PDB header:**transferase **Chain:** F: **PDB Molecule:**glutamate 5-kinase; **PDBTitle:** glutamate 5-kinase from escherichia coli complexed with2 glutamate
46	c3jyfB_	Alignment	not modelled	27.2	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**2',3'-cyclic nucleotide 2'-phosphodiesterase/3'- **PDBTitle:** the crystal structure of a 2,3-cyclic nucleotide 2-2 phosphodiesterase/3-nucleotidase bifunctional periplasmic precursor3 protein from klebsiella pneumoniae subsp. pneumoniae mgh 78578
47	d2gv8a2	Alignment	not modelled	27.2	26	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
48	c3dg8B_	Alignment	not modelled	27.0	21	**PDB header:**oxidoreductase, transferase **Chain:** B: **PDB Molecule:**bifunctional dihydrofolate reductase-thymidylate **PDBTitle:** quadruple mutant (n51i+c59r+s108n+i164l) plasmodium2 falciparum dihydrofolate reductase-thymidylate synthase3 (pfdhfr-ts) complexed with rjf670, nadph, and dump
49	c2radB_	Alignment	not modelled	26.8	11	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**succinoglycan biosynthesis protein; **PDBTitle:** crystal structure of the succinoglycan biosynthesis2 protein. northeast structural genomics consortium target3 bcr135
50	c1kyqC_	Alignment	not modelled	26.7	26	**PDB header:**oxidoreductase, lyase **Chain:** C: **PDB Molecule:**siroheme biosynthesis protein met8; **PDBTitle:** met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelatase involved in siroheme synthesis.
51	d3b55a1	Alignment	not modelled	26.6	11	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**EreA-like
52	c2kxhB_	Alignment	not modelled	24.8	56	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**peptide of far upstream element-binding protein 1; **PDBTitle:** solution structure of the first two rrm domains of fir in the complex2 with fbp nbox peptide
						PDB header:oxidoreductase

53	c1zdrB_	Alignment	not modelled	24.7	30	**Chain:** B: **PDB Molecule:**dihydrofolate reductase; **PDBTitle:** dhfr from bacillus stearothermophilus
54	c2oemA_	Alignment	not modelled	24.5	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-diketo-5-methylthiopentyl-1-phosphate enolase; **PDBTitle:** crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketohexane 1-phosphate
55	c3nkdB_	Alignment	not modelled	24.1	21	**PDB header:**immune system **Chain:** B: **PDB Molecule:**crispr-associated protein cas1; **PDBTitle:** structure of crisp-associated protein cas1 from escherichia coli str.2 k-12
56	d1mv8a3	Alignment	not modelled	24.1	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**UDP-glucose/GDP-mannose dehydrogenase C-terminal domain **Family:**UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
57	d1knqa_	Alignment	not modelled	23.8	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Gluconate kinase
58	c3fokH_	Alignment	not modelled	23.8	18	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**uncharacterized protein cgl0159; **PDBTitle:** crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
59	c3kb8A_	Alignment	not modelled	23.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
60	c3ctmH_	Alignment	not modelled	23.0	27	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**carbonyl reductase; **PDBTitle:** crystal structure of a carbonyl reductase from candida2 parapsilosis with anti-prelog stereo-specificity
61	c3gveB_	Alignment	not modelled	22.9	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**yfkn protein; **PDBTitle:** crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
62	d1j3ka_	Alignment	not modelled	22.7	21	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
63	d2tpsa_	Alignment	not modelled	22.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
64	c1vcnA_	Alignment	not modelled	22.2	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
65	d1gph11	Alignment	not modelled	21.7	26	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
66	c1yadD_	Alignment	not modelled	21.7	19	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
67	d2ae2a_	Alignment	not modelled	21.6	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
68	d1ra9a_	Alignment	not modelled	21.5	18	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
69	c1gph1_	Alignment	not modelled	20.6	26	**PDB header:**transferase(glutamine amidotransferase) **Chain:** 1: **PDB Molecule:**glutamine phosphoribosyl-pyrophosphate amidotransferase; **PDBTitle:** structure of the allosteric regulatory enzyme of purine biosynthesis
70	d2obba1	Alignment	not modelled	20.3	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**BT0820-like
71	c2v79B_	Alignment	not modelled	20.1	16	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**dna replication protein dnad; **PDBTitle:** crystal structure of the n-terminal domain of dnad from2 bacillus subtilis
72	d1juva_	Alignment	not modelled	20.1	35	**Fold:**Dihydrofolate reductase-like **Superfamily:**Dihydrofolate reductase-like **Family:**Dihydrofolate reductases
73	c3kc2A_	Alignment	not modelled	20.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein ykr070w; **PDBTitle:** crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
74	c2yybA_	Alignment	not modelled	19.6	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ttha1606; **PDBTitle:** crystal structure of ttha1606 from thermus thermophilus hb8
75	c3ek5A_	Alignment	not modelled	19.5	15	**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
76	d1krha2	Alignment	not modelled	19.4	27	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
77	d1kyqa1	Alignment	not modelled	19.4	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Siroheme synthase N-terminal domain-like
						Fold:PRTase-like

78	d1wd5a_	Alignment	not modelled	19.4	23	**Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
79	c2gezE_	Alignment	not modelled	19.2	18	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**l-asparaginase alpha subunit; **PDBTitle:** crystal structure of potassium-independent plant asparaginase
80	d1sm4a2	Alignment	not modelled	19.0	11	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
81	c1l9xA_	Alignment	not modelled	18.9	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
82	d1l9xa_	Alignment	not modelled	18.9	25	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
83	c2iz6A_	Alignment	not modelled	18.8	17	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**molybdenum cofactor carrier protein; **PDBTitle:** structure of the chlamydomonas rheinhardtii moco carrier2 protein
84	c3t07D_	Alignment	not modelled	18.3	17	**PDB header:**transferase/transferase inhibitor **Chain:** D: **PDB Molecule:**pyruvate kinase; **PDBTitle:** crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
85	d1wzca1	Alignment	not modelled	18.3	18	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
86	d2ji7a1	Alignment	not modelled	18.2	13	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Pyruvate oxidase and decarboxylase, middle domain
87	c1ii8B_	Alignment	not modelled	17.9	29	**PDB header:**replication **Chain:** B: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
88	c1f2uD_	Alignment	not modelled	17.9	29	**PDB header:**replication **Chain:** D: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of rad50 abc-atpase
89	d2bmwa2	Alignment	not modelled	17.8	21	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
90	d2b30a1	Alignment	not modelled	17.2	26	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Predicted hydrolases Cof
91	c2hcuA_	Alignment	not modelled	17.2	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
92	c3rihB_	Alignment	not modelled	17.0	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**short chain dehydrogenase or reductase; **PDBTitle:** crystal structure of a putative short chain dehydrogenase or reductase2 from mycobacterium abscessus
93	c2rd5A_	Alignment	not modelled	17.0	14	**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
94	c3pvjB_	Alignment	not modelled	16.9	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutarate-dependent taurine dioxygenase; **PDBTitle:** crystal structure of the fe(ii)/alpha-ketoglutarate dependent taurine2 dioxygenase from pseudomonas putida kt2440
95	d1ma3a_	Alignment	not modelled	16.8	15	**Fold:**DHS-like NAD/FAD-binding domain **Superfamily:**DHS-like NAD/FAD-binding domain **Family:**Sir2 family of transcriptional regulators
96	d1m2xa_	Alignment	not modelled	16.7	11	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Zn metallo-beta-lactamase
97	d1ybda1	Alignment	not modelled	16.4	18	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
98	c2c07A_	Alignment	not modelled	16.1	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-oxoacyl-(acyl-carrier protein) reductase; **PDBTitle:** oxoacyl-acp reductase of plasmodium falciparum
99	d2c07a1	Alignment	not modelled	16.1	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases