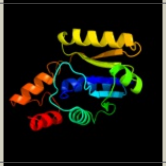
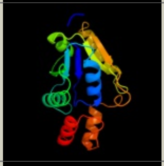
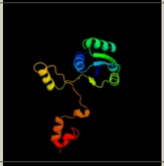
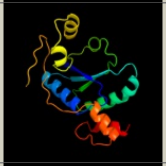
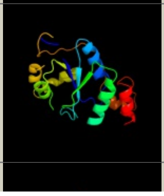
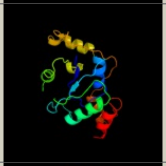
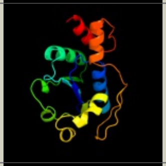
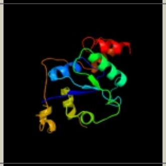
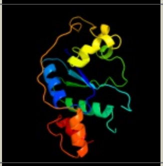
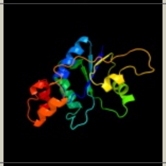
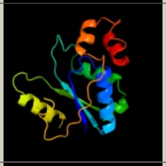
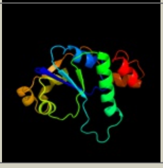
Email	l.a.kelley@imperial.ac.uk
Description	P0A6I6
Date	Thu Jan 5 11:03:13 GMT 2012
Unique Job ID	a7c24054c12530cd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qjca_	Alignment		100.0	100	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
2	d1o6ba_	Alignment		100.0	42	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
3	d1tfua_	Alignment		100.0	43	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
4	d1vlha_	Alignment		100.0	49	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
5	c3ikzA_	Alignment		100.0	46	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of phosphopantetheine adenylyltransferase from2 burkholderia pseudomallei
6	c3f3mA_	Alignment		100.0	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** six crystal structures of two phosphopantetheine2 adenylyltransferases reveal an alternative ligand binding3 mode and an associated structural change
7	d1od6a_	Alignment		100.0	48	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
8	c3nd5D_	Alignment		100.0	45	**PDB header:**transferase **Chain:** D: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of phosphopantetheine adenylyltransferase (ppat)2 from enterococcus faecalis
9	c3nv7A_	Alignment		100.0	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** crystal structure of h.pylori phosphopantetheine adenylyltransferase2 mutant i4v/n76y
10	d1kama_	Alignment		100.0	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
11	d1k4ma_	Alignment		100.0	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase

12	c2h29A_	Alignment		100.0	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable nicotinate-nucleotide **PDBTitle:** crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from staphylococcus aureus: product3 bound form 1
13	d1kr2a_	Alignment		100.0	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
14	c3e27B_	Alignment		100.0	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nicotinate (nicotinamide) nucleotide **PDBTitle:** nicotinic acid mononucleotide (namn) adenylyltransferase2 from bacillus anthracis: product complex
15	d1nuua_	Alignment		100.0	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
16	c1yunB_	Alignment		100.0	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable nicotinate-nucleotide **PDBTitle:** crystal structure of nicotinic acid mononucleotide2 adenylyltransferase from pseudomonas aeruginosa
17	d1ej2a_	Alignment		100.0	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
18	d1f9aa_	Alignment		100.0	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
19	c2qjoB_	Alignment		100.0	16	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**bifunctional nmn adenylyltransferase/nudix hydrolase; **PDBTitle:** crystal structure of a bifunctional nmn adenylyltransferase/adp ribose2 pyrophosphatase (nadm) complexed with adprp and nad from3 synechocystis sp.
20	c3h05A_	Alignment		100.0	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein vpa0413; **PDBTitle:** the crystal structure of a putative nicotinate-nucleotide2 adenylyltransferase from vibrio parahaemolyticus
21	c2r5wA_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase, transferase **Chain:** A: **PDB Molecule:**nicotinamide-nucleotide adenylyltransferase; **PDBTitle:** crystal structure of a bifunctional nmn2 adenylyltransferase/adp ribose pyrophosphatase from3 francisella tularensis
22	d1coza_	Alignment	not modelled	99.9	26	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Cytidylyltransferase
23	d1lw7a1	Alignment	not modelled	99.8	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
24	c1lw7A_	Alignment	not modelled	99.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulator nadr; **PDBTitle:** nadr protein from haemophilus influenzae
25	c2b7lD_	Alignment	not modelled	99.8	24	**PDB header:**transferase **Chain:** D: **PDB Molecule:**glycerol-3-phosphate cytidylyltransferase; **PDBTitle:** crystal structure of ctp:glycerol-3-phosphate2 cytidylyltransferase from staphylococcus aureus
26	d1mrza2	Alignment	not modelled	99.7	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
27	c3op1A_	Alignment	not modelled	99.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**macrolide-efflux protein; **PDBTitle:** crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
28	c3glvB_	Alignment	not modelled	99.6	19	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**lipopolysaccharide core biosynthesis protein; **PDBTitle:** crystal structure of the lipopolysaccharide core

						biosynthesis protein2 from thermoplasma volcanium gss1
29	c2x0kB_	Alignment	not modelled	99.6	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribf; **PDBTitle:** crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
30	c3elbA_	Alignment	not modelled	99.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ethanolamine-phosphate cytidylyltransferase; **PDBTitle:** human ctp: phosphoethanolamine cytidylyltransferase in complex with2 cmp
31	c1t6zB_	Alignment	not modelled	99.4	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**riboflavin kinase/fmn adenylyltransferase; **PDBTitle:** crystal structure of riboflavin bound tm379
32	c3gmiA_	Alignment	not modelled	99.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0348 protein mj0951; **PDBTitle:** crystal structure of a protein of unknown function from2 methanocaldococcus jannaschii
33	c3hl4B_	Alignment	not modelled	99.3	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**choline-phosphate cytidylyltransferase a; **PDBTitle:** crystal structure of a mammalian ctp:phosphocholine2 cytidylyltransferase with cdp-choline
34	c3do8B_	Alignment	not modelled	99.2	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** the crystal structure of the protein with unknown function2 from archaeoglobus fulgidus
35	d1jhda2	Alignment	not modelled	98.8	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
36	d1g8fa2	Alignment	not modelled	98.8	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
37	d1v47a2	Alignment	not modelled	98.8	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
38	d1x6va2	Alignment	not modelled	98.8	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
39	c1r6xA_	Alignment	not modelled	98.7	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp:sulfate adenylyltransferase; **PDBTitle:** the crystal structure of a truncated form of yeast atp2 sulfurylase, lacking the c-terminal aps kinase-like domain,3 in complex with sulfate
40	c1jhdA_	Alignment	not modelled	98.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** crystal structure of bacterial atp sulfurylase from the2 riftia pachyptila symbiont
41	c1xnjB_	Alignment	not modelled	98.7	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'-phosphosulfate **PDBTitle:** aps complex of human paps synthetase 1
42	c2qjfB_	Alignment	not modelled	98.7	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'- **PDBTitle:** crystal structure of atp-sulfurylase domain of human paps2 synthetase 1
43	c1g8gB_	Alignment	not modelled	98.7	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** atp sulfurylase from s. cerevisiae: the binary product complex with2 aps
44	c1m8pB_	Alignment	not modelled	98.6	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfate adenylyltransferase; **PDBTitle:** crystal structure of p. chrysogenum atp sulfurylase in the t-state
45	d1m8pa2	Alignment	not modelled	98.6	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**ATP sulfurylase catalytic domain
46	c3cr8C_	Alignment	not modelled	98.6	15	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sulfate adenylyltranferase, adenylylsulfate **PDBTitle:** hexameric aps kinase from thiobacillus denitrificans
47	c3guzB_	Alignment	not modelled	98.4	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
48	c1v47B_	Alignment	not modelled	98.4	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp sulfurylase; **PDBTitle:** crystal structure of atp sulfurylase from thermus2 thermophillus hb8 in complex with aps
49	c2gksB_	Alignment	not modelled	98.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional sat/aps kinase; **PDBTitle:** crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
50	d1v8fa_	Alignment	not modelled	98.0	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
51	c3uk2B_	Alignment	not modelled	97.8	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** the structure of pantothenate synthetase from burkholderia2 thailandensis
52	c2ejcA_	Alignment	not modelled	97.8	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantoate--beta-alanine ligase; **PDBTitle:** crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
53	c3ag5A_	Alignment	not modelled	97.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantothenate synthetase from staphylococcus2 aureus

54	c3n8hA_	Alignment	not modelled	97.7	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
55	d1ihoa_	Alignment	not modelled	97.7	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
56	c3innB_	Alignment	not modelled	97.5	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution
57	c3mxtA_	Alignment	not modelled	97.3	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from campylobacter2 jejuni
58	d2a84a1	Alignment	not modelled	95.9	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
59	c3dzcA_	Alignment	not modelled	82.5	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
60	c2q4dB_	Alignment	not modelled	51.7	11	**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
61	d2d5ba2	Alignment	not modelled	49.4	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
62	c2ct8A_	Alignment	not modelled	47.0	20	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of aquifex aeolicus methionyl-trna2 synthetase complexed with trna(met) and methionyl-adenylate3 anologue
63	c2dx7B_	Alignment	not modelled	42.1	33	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**aspartate racemase; **PDBTitle:** crystal structure of pyrococcus horikoshii ot3 aspartate racemase2 complex with citric acid
64	d1ydha_	Alignment	not modelled	41.9	11	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
65	d2q4oa1	Alignment	not modelled	41.8	7	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
66	c2q4oA_	Alignment	not modelled	41.8	7	**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
67	d1jfla1	Alignment	not modelled	41.1	33	**Fold:**ATC-like **Superfamily:**Aspartate/glutamate racemase **Family:**Aspartate/glutamate racemase
68	c3hv0A_	Alignment	not modelled	40.5	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
69	c2zskA_	Alignment	not modelled	39.9	44	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**226aa long hypothetical aspartate racemase; **PDBTitle:** crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
70	c3tqoA_	Alignment	not modelled	36.2	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** structure of the cysteinyl-trna synthetase (cyss) from coxiella2 burnetii.
71	c3focB_	Alignment	not modelled	34.4	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from giardia lamblia
72	c1woyA_	Alignment	not modelled	33.7	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
73	c3etjB_	Alignment	not modelled	33.6	6	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
74	d1n3la_	Alignment	not modelled	32.7	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
75	d1q0qa2	Alignment	not modelled	32.2	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
76	c1q11A_	Alignment	not modelled	32.0	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of an active fragment of human tyrosyl-trna2 synthetase with tyrosinol
77	c3dhnA_	Alignment	not modelled	30.8	12	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
						PDB header:hydrolase

78	c2x7vA_	Alignment	not modelled	26.9	7	**Chain:** A: **PDB Molecule:**probable endonuclease 4; **PDBTitle:** crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
79	c2ip1A_	Alignment	not modelled	26.9	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
80	d1vjta1	Alignment	not modelled	25.9	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
81	c3c1oA_	Alignment	not modelled	25.5	60	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eugenol synthase; **PDBTitle:** the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
82	d1y81a1	Alignment	not modelled	22.7	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
83	d1jila_	Alignment	not modelled	22.6	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
84	c3i05B_	Alignment	not modelled	22.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from trypanosoma brucei
85	c3sp1B_	Alignment	not modelled	20.9	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** crystal structure of cysteinyl-trna synthetase (cyss) from borrelia2 burgdorferi
86	c3kpgA_	Alignment	not modelled	19.8	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfide-quinone reductase, putative; **PDBTitle:** crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with decylubiquinone
87	c1gshA_	Alignment	not modelled	18.9	11	**PDB header:**glutathione biosynthesis ligase **Chain:** A: **PDB Molecule:**glutathione biosynthetic ligase; **PDBTitle:** structure of escherichia coli glutathione synthetase at ph 7.5
88	d1hdoa_	Alignment	not modelled	18.9	40	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
89	c1rqgA_	Alignment	not modelled	18.6	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from pyrococcus abyssi
90	c1jiiA_	Alignment	not modelled	17.9	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of s. aureus tyrrs in complex with sb-219383
91	c3c8zB_	Alignment	not modelled	17.3	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** the 1.6 a crystal structure of mshc: the rate limiting2 enzyme in the mycothiol biosynthetic pathway
92	c3hskB_	Alignment	not modelled	16.7	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 with nadp from candida albicans
93	d1li5a2	Alignment	not modelled	16.5	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
94	c3s81A_	Alignment	not modelled	16.3	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aspartate racemase; **PDBTitle:** crystal structure of putative aspartate racemase from salmonella2 typhimurium
95	d1rqga2	Alignment	not modelled	16.3	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
96	d1h3fa1	Alignment	not modelled	15.8	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
97	c1x8xA_	Alignment	not modelled	15.8	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl t-rna synthetase from e.coli complexed with tyrosine
98	d1pqua1	Alignment	not modelled	15.6	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
99	d1jw2a_	Alignment	not modelled	15.0	11	**Fold:**Open three-helical up-and-down bundle **Superfamily:**Hemolysin expression modulating protein HHA **Family:**Hemolysin expression modulating protein HHA