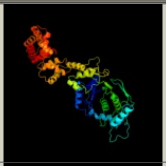
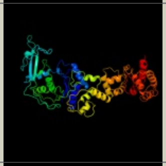
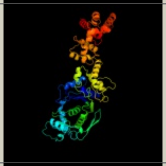
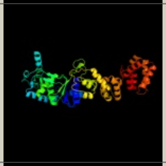
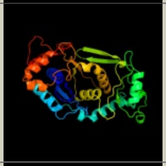
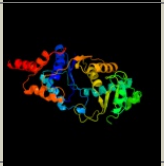
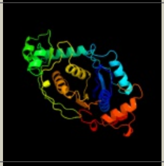
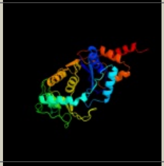
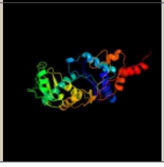
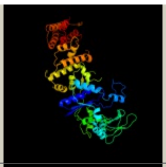
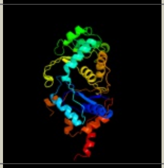
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P04805
Date	Thu Jan 5 10:58:21 GMT 2012
Unique Job ID	7d0698c85c8d0f6f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2cfoA_	Alignment		100.0	41	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** non-discriminating glutamyl-trna synthetase from2 thermosynechococcus elongatus in complex with glu
2	c3al0C_	Alignment		100.0	36	**PDB header:**ligase/rna **Chain:** C: **PDB Molecule:**glutamyl-trna(gln) amidotransferase subunit c, glutamyl- **PDBTitle:** crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
3	c2ja2A_	Alignment		100.0	37	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** mycobacterium tuberculosis glutamyl-trna synthetase
4	c3afhA_	Alignment		100.0	36	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase 2; **PDBTitle:** crystal structure of thermotoga maritima nondiscriminating glutamyl-2 trna synthetase in complex with a glutamyl-amp analog
5	c1g59A_	Alignment		100.0	37	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** glutamyl-trna synthetase complexed with trna(glu).
6	c2o5rA_	Alignment		100.0	40	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase 1; **PDBTitle:** crystal structure of glutamyl-trna synthetase 1 (ec 6.1.1.17)2 (glutamate-trna ligase 1) (glurs 1) (tm1351) from thermotoga maritima3 at 2.5 a resolution
7	d1j09a2	Alignment		100.0	41	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
8	d1gtra2	Alignment		100.0	23	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
9	d1nzja_	Alignment		100.0	36	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
10	c2hz7A_	Alignment		100.0	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans
11	c1exdA_	Alignment		100.0	23	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of a tight-binding glutamine trna bound2 to glutamine aminoacyl trna synthetase

12	c1irxA_	Alignment		100.0	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of class i lysyl-trna synthetase
13	c3aiiA_	Alignment		100.0	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
14	d1f7ua2	Alignment		100.0	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
15	c1u0bB_	Alignment		100.0	15	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**cysteinyl trna; **PDBTitle:** crystal structure of cysteinyl-trna synthetase binary2 complex with trnacys
16	d1li5a2	Alignment		100.0	16	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
17	d2d5ba2	Alignment		100.0	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
18	c3sp1B_	Alignment		100.0	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** crystal structure of cysteinyl-trna synthetase (cyss) from borrelia2 burgdorferi
19	d1irxa2	Alignment		100.0	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
20	d1pfva2	Alignment		100.0	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
21	d1j09a1	Alignment	not modelled	100.0	29	**Fold:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Superfamily:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Family:**C-terminal domain of glutamyl-tRNA synthetase (GluRS)
22	c3tqoA_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cysteinyl-trna synthetase; **PDBTitle:** structure of the cysteinyl-trna synthetase (cyss) from coxiella2 burnetii.
23	c3c8zB_	Alignment	not modelled	99.9	19	**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
24	c3fnrA_	Alignment	not modelled	99.9	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of putative arginyl t-rna synthetase from2 campylobacter jejuni;
25	c2x1lC_	Alignment	not modelled	99.9	13	**PDB header:**ligase **Chain:** C: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of mycobacterium smegmatis methionyl-trna2 synthetase in complex with methionine and adenosine
26	c1woyA_	Alignment	not modelled	99.9	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** crystal structure of methionyl trna synthetase y225f mutant2 from thermus thermophilus
27	c2ct8A_	Alignment	not modelled	99.9	16	**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
28	d1ivsa4	Alignment	not modelled	99.9	18	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase

						Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
29	d1rqga2	Alignment	not modelled	99.9	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
30	c1pfuA_	Alignment	not modelled	99.9	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from escherichia coli complexed2 with methionine phosphinate
31	c3kflA_	Alignment	not modelled	99.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** leishmania major methionyl-trna synthetase in complex with2 methionyladenylate and pyrophosphate
32	d1ilea3	Alignment	not modelled	99.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
33	d1ffya3	Alignment	not modelled	99.8	19	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
34	c1rqgA_	Alignment	not modelled	99.8	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**methionyl-trna synthetase; **PDBTitle:** methionyl-trna synthetase from pyrococcus abyssi
35	d1irxa1	Alignment	not modelled	99.8	12	**Fold:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Superfamily:**An anticodon-binding domain of class I aminoacyl-tRNA synthetases **Family:**C-terminal domain of class I lysyl-tRNA synthetase
36	d1iq0a2	Alignment	not modelled	99.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
37	d1h3na3	Alignment	not modelled	99.8	22	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
38	c2zufA_	Alignment	not modelled	99.7	22	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii arginyl-trna2 synthetase complexed with trna(arg)
39	c1gaxB_	Alignment	not modelled	99.7	24	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**valyl-trna synthetase; **PDBTitle:** crystal structure of thermus thermophilus valyl-trna2 synthetase complexed with trna(val) and valyl-adenylate3 analogue
40	c1ileA_	Alignment	not modelled	99.7	23	**PDB header:**aminoacyl-trna synthetase **Chain:** A: **PDB Molecule:**isoleucyl-trna synthetase; **PDBTitle:** isoleucyl-trna synthetase
41	c1iq0A_	Alignment	not modelled	99.6	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** thermus thermophilus arginyl-trna synthetase
42	c1qu2A_	Alignment	not modelled	99.6	20	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**isoleucyl-trna synthetase; **PDBTitle:** insights into editing from an ile-trna synthetase structure2 with trna(ile) and mupirocin
43	c1f7uA_	Alignment	not modelled	99.6	22	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**arginyl-trna synthetase; **PDBTitle:** crystal structure of the arginyl-trna synthetase complexed with the2 trna(arg) and l-arg
44	c1wz2B_	Alignment	not modelled	99.6	28	**PDB header:**ligase/rna **Chain:** B: **PDB Molecule:**leucyl-trna synthetase; **PDBTitle:** the crystal structure of leucyl-trna synthetase and trna(leucine)2 complex
45	c1wkbA_	Alignment	not modelled	99.5	29	**PDB header:**ligase **Chain:** A: **PDB Molecule:**leucyl-trna synthetase; **PDBTitle:** crystal structure of leucyl-trna synthetase from the2 archaeon pyrococcus horikoshii reveals a novel editing3 domain orientation
46	c1obhA_	Alignment	not modelled	99.3	27	**PDB header:**synthetase **Chain:** A: **PDB Molecule:**leucyl-trna synthetase; **PDBTitle:** leucyl-trna synthetase from thermus thermophilus complexed2 with a pre-transfer editing substrate analogue in both3 synthetic active site and editing site
47	c2g36A_	Alignment	not modelled	99.0	23	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase (ec 6.1.1.2)2 (tryptophan-trna ligase)(trprs) (tm0492) from thermotoga maritima at3 2.50 a resolution
48	c2cybA_	Alignment	not modelled	98.8	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with2 l-tyrosine from archaeoglobus fulgidus
49	c2j5bA_	Alignment	not modelled	98.8	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of the tyrosyl trna synthetase from acanthamoeba2 polyphaga mimivirus complexed with tyrosynol
50	c2el7A_	Alignment	not modelled	98.6	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from thermus2 thermophilus
51	c2cyaA_	Alignment	not modelled	98.5	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase from aeropyrum pernix
52	c3jxeB_	Alignment	not modelled	98.5	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
53	c3hzrD_	Alignment	not modelled	98.5	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase homolog from entamoeba histolytica

54	c3focB_	Alignment	not modelled	98.5	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from giardia lamblia
55	c3a05A_	Alignment	not modelled	98.4	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 hyperthermophilic archaeon, aeropyrum pernix k1 complex3 with tryptophan
56	c3m5wB_	Alignment	not modelled	98.3	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from2 campylobacter jejuni
57	c3prhB_	Alignment	not modelled	98.3	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase val144pro mutant from b. subtilis
58	c2yy5C_	Alignment	not modelled	98.1	16	**PDB header:**ligase **Chain:** C: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from mycoplasma2 pneumoniae
59	c2quiB_	Alignment	not modelled	98.1	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structures of human tryptophanyl-trna synthetase in2 complex with tryptophanamide and atp
60	c3p0jD_	Alignment	not modelled	98.1	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** leishmania major tyrosyl-trna synthetase in complex with tyrosinol,2 triclinic crystal form 1
61	d1i6la_	Alignment	not modelled	98.1	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
62	c1yi8C_	Alignment	not modelled	98.0	20	**PDB header:**ligase **Chain:** C: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl trrna synthetase ii from deinococcus2 radiodurans in complex with l-trp
63	c2cycB_	Alignment	not modelled	97.9	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of tyrosyl-trna synthetase complexed with l-tyrosine2 from pyrococcus horikoshii
64	c2janD_	Alignment	not modelled	97.8	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from mycobacterium tuberculosis in2 unliganded state
65	d1h3fa1	Alignment	not modelled	97.8	17	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
66	c2ip1A_	Alignment	not modelled	97.7	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure analysis of s. cerevisiae tryptophanyl trna2 synthetase
67	d1r6ta2	Alignment	not modelled	97.6	11	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
68	c2dlcX_	Alignment	not modelled	97.6	14	**PDB header:**ligase/trna **Chain:** X: **PDB Molecule:**tyrosyl-trna synthetase, cytoplasmic; **PDBTitle:** crystal structure of the ternary complex of yeast tyrosyl-trna2 synthetase
69	c1h3eA_	Alignment	not modelled	97.5	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl-trna synthetase from thermus thermophilus complexed2 with wild-type trnatyr(gua) and with atp and tyrosinol
70	d2ts1a_	Alignment	not modelled	97.3	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
71	c2ts1A_	Alignment	not modelled	97.3	14	**PDB header:**ligase (synthetase) **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** structure of tyrosyl-t/rna synthetase refined at 2.3 angstroms2 resolution. interaction of the enzyme with the tyrosyl adenylate3 intermediate
72	c1jiiA_	Alignment	not modelled	97.3	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of s. aureus tyrrs in complex with sb-219383
73	d1jila_	Alignment	not modelled	97.1	13	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
74	c1x8xA_	Alignment	not modelled	97.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** tyrosyl t-rna synthetase from e.coli complexed with tyrosine
75	c3hv0A_	Alignment	not modelled	96.9	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
76	d1n3la_	Alignment	not modelled	96.7	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
77	c3n9iA_	Alignment	not modelled	96.4	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from yersinia pestis2 co92
78	c3sz3A_	Alignment	not modelled	96.1	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of tryptophanyl-trna synthetase from vibrio cholerae2 with an endogenous tryptophan
79	c1q11A_	Alignment	not modelled	95.8	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of an active fragment of human tyrosyl-

						trna2 synthetase with tyrosinol
80	c2rkjM_	Alignment	not modelled	95.7	17	**PDB header:**ligase/rna **Chain:** M: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** cocrystal structure of a tyrosyl-trna synthetase splicing2 factor with a group i intron rna
81	d1j1ua_	Alignment	not modelled	95.6	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
82	c3i05B_	Alignment	not modelled	95.4	8	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from trypanosoma brucei
83	c1r6uB_	Alignment	not modelled	92.9	10	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of an active fragment of human tryptophanyl-trna2 synthetase with cytokine activity
84	c2pidB_	Alignment	not modelled	53.6	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of human mitochondrial tyrosyl-trna synthetase in2 complex with an adenylate analog
85	d2p10a1	Alignment	not modelled	52.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
86	d1w7ca1	Alignment	not modelled	36.9	17	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
87	c2p10D_	Alignment	not modelled	35.6	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
88	d1d6za1	Alignment	not modelled	35.2	33	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
89	c1n9eA_	Alignment	not modelled	33.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysyl oxidase; **PDBTitle:** crystal structure of pichia pastoris lysyl oxidase pplo
90	c1lw7A_	Alignment	not modelled	33.6	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcriptional regulator nadr; **PDBTitle:** nadr protein from haemophilus influenzae
91	c2pncB_	Alignment	not modelled	33.3	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**copper amine oxidase, liver isozyme; **PDBTitle:** crystal structure of bovine plasma copper-containing amine oxidase in2 complex with clonidine
92	c1w7cA_	Alignment	not modelled	33.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lysyl oxidase; **PDBTitle:** pplo at 1.23 angstroms
93	c1h3oA_	Alignment	not modelled	31.8	13	**PDB header:**transcription/tbp-associated factors **Chain:** A: **PDB Molecule:**transcription initiation factor tfiid 135 kda **PDBTitle:** crystal structure of the human taf4-taf122 (tafii135-tafii20) complex
94	d1h3oa_	Alignment	not modelled	31.8	13	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
95	d1w6ga1	Alignment	not modelled	30.0	33	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
96	c1ui7A_	Alignment	not modelled	29.9	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phenylethylamine oxidase; **PDBTitle:** site-directed mutagenesis of his433 involved in binding of2 copper ion in arthrobacter globiformis amine oxidase
97	c1ksiA_	Alignment	not modelled	29.4	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of a eukaryotic (pea seedling) copper-containing2 amine oxidase at 2.2a resolution
98	c3higB_	Alignment	not modelled	28.9	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**amiloride-sensitive amine oxidase; **PDBTitle:** crystal structure of human diamine oxidase in complex with the2 inhibitor berenil
99	c1d6uB_	Alignment	not modelled	26.8	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of e. coli amine oxidase anaerobically reduced with2 beta-phenylethylamine
100	c3pgbA_	Alignment	not modelled	26.1	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of aspergillus nidulans amine oxidase
101	c1ekmC_	Alignment	not modelled	25.9	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure at 2.5 a resolution of zinc-substituted2 copper amine oxidase of hansenula polymorpha expressed in3 escherichia coli
102	c3loyB_	Alignment	not modelled	25.7	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**copper amine oxidase; **PDBTitle:** crystal structure of a copper-containing benzylamine oxidase from2 hansenula polymorpha
103	d2oqea1	Alignment	not modelled	25.1	28	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain
104	d1w2za1	Alignment	not modelled	24.6	33	**Fold:**Supersandwich **Superfamily:**Amine oxidase catalytic domain **Family:**Amine oxidase catalytic domain