

TABLE 1 tRNA synthetase interactions (distance &lt;3.5 Å)

tRNA		AspRS	
U1	OP	<b>Lys 293*</b>	Nζ
	OP	Asn 328	Nδ
	O4	<i>Asn 330</i>	N
A72	OP	<b>Lys 428</b>	Nζ
	N6	<i>Asn 330</i>	O
G73	OP	<i>Thr 424</i>	Oγ
	OP	<i>Ser 423</i>	Oγ
	O6†	<i>Thr 331</i>	Oγ
	N1†	<i>Ser 329</i>	Oγ
	N2†	Asn 328	O
C74	N2†	<b>Glu 327</b>	Oε
	N3†	<i>Ser 329</i>	Oγ
	N4†	<i>His 334</i>	Nε
C67	OP	<i>Lys 553</i>	Nζ
U11	O2'	<i>Asp 210</i>	Oδ
U12	OP	<i>Thr 230</i>	Oγ
	OP	<b>Asn 227</b>	N
G27	O2'	Glu 202	Oε
G30	OP	<b>Lys 155</b>	Nζ
Ψ32	N3	Gln 120	O
U33	O4	<i>Thr 124</i>	Oγ
G34	N7	<i>Lys 142</i>	Nζ
	N2	<b>Glu 188</b>	Oε
U35	O4'	Gln 121	Nε
	N3	<b>Gln 138</b>	Oε
	O2	<b>Arg 119</b>	Nη
	—	<b>Phe 127</b>	Stacking
C36	O4'	<b>Arg 119</b>	Nη
	O2	<i>Ser 181</i>	Oγ
	O2	Lys 180	N
	N4	Pro 178	O
m1G37	OP	Lys 180	Nζ
C38	OP	Asn 117	Nδ
	N4	Gln 120	O
	N3	Gln 121	Oε

Interactions within the active site (nucleotides C75 and A76) are not included. Residues in bold are highly conserved in all AspRS, whereas those in italics are conserved in eukaryotes only. In tRNA, phosphate oxygens are named OP, atoms with primes belong to the ribose, all others to the base.

\* This residue belongs to the other subunit.

† The conformations are different in the two subunits. In the map of the binary complex the active sites are different in the two subunits. In subunit B, although the crystals were grown in the absence of ATP in the mother liquor, a clear electron density is visible in which an AMP model can be fitted. In the other subunit, this site is partially occupied by the terminal adenosine of tRNA as a result of a conformational change which extends up to the first base pair of the acceptor stem. In subunit B, where the CCA end of tRNA occupies its functional location, A76 is stacked on Phe 304 with its ribose group above and close to the β phosphate of ATP. The ATP binding site essentially comprises the class II conserved Glu 327 and Phe 338 (stacked on the purine ring) and the glycine-rich strand of motif 3 (Gly 526–Gly 528) which interacts with the ribose-phosphate groups. The invariant residues of motifs 2 and 3 bind to the α-phosphate (Arg 325) and to the ribose (Arg 531). Addition of ATP to the crystals leads to fully symmetrical dimers. A detailed analysis of the structure-function relationship in the active site will be published (J.C. *et al.*, manuscript in preparation).

II aaRS. Subgroup specificity is then obtained by the addition of a module at the N-terminal end. Another module, not conserved in prokaryotic AspRS, is inserted after the conserved motif 2 of class II and plays an important role in the specific recognition of tRNA. An additional recognition element interacting with the minor groove of the acceptor stem may be present in some class II enzymes, for example in the *E. coli* AlaRS system where the main tRNA identity determinant is the third base pair of the acceptor stem<sup>23,24</sup>. The insertion peptide after motif 2 could also act as a minor groove recognition module. □

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## CORRECTION

### Lead isotope evidence for young trace element enrichment in the oceanic upper mantle

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WE have been unable to precisely reproduce some of the lead isotope data for Madeira lavas reported in the above paper. In the light of further analyses the correct compositions are as follows:

Sample number	<sup>206</sup> Pb/ <sup>204</sup> Pb	<sup>207</sup> Pb/ <sup>204</sup> Pb	<sup>208</sup> Pb/ <sup>204</sup> Pb
MD4	19.159	15.533	38.825
MD10	19.182	15.535	38.864
MD32	19.097	15.559	38.946
MD40	19.143	15.573	38.864
MD64	19.038	15.556	38.753

The <sup>207</sup>Pb/<sup>204</sup>Pb, <sup>87</sup>Sr/<sup>86</sup>Sr and <sup>143</sup>Nd/<sup>144</sup>Nd ratios still plot within the field of Atlantic MORB, whereas the <sup>206</sup>Pb/<sup>204</sup>Pb and <sup>208</sup>Pb/<sup>204</sup>Pb ratios are relatively high for MORB. Therefore, although the revised Pb isotopic compositions plot closer to other OIB, the overall interpretation is unchanged. □