

## Correction

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## Geographic distribution of hepatitis C virus genotypes in Brazil

The correct GenBank Accession Numbers are given below.

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#### Sequence analysis

Reverse and forward strand sequences were aligned and a consensus sequence was obtained for each case. The consensus sequence was then compared with the sequences of all HCV genotypes from the database. The alignment included 311 5'UTR sequences, of which 98 were from genotype 1, 38 from genotype 2, 76 from genotype 3, 66 from genotype 4, 24 from genotype 5, and 9 from genotype 6. This alignment was obtained from Smith et al. (12). For this purpose, the EditSeq and MegAlign programs from the DNASTAR package (LaserGene Inc., Madison, WI, USA) were used. One sequence from each genotype is shown in Figure 1 and the features used to identify the genotypes are highlighted. Sequences from Brazilian patients were deposited in GenBank under the accession numbers AY306229-AY306686, AY309974-**AY310119**, and AY310921-AY311334.

For html or pdf file, see:

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