Corrigendum

Immune and artificial selection in the haemagglutinin (H) glycoprotein of measles virus

Christopher H. Woelk, Li Jin, Edward C. Holmes and David W. G. Brown


Page 2469, right hand column, line 29. The amino acid substitutions referred to were transposed; the correct version of the text is given below.

Low-affinity CD46-binding isolates can be converted to the high-affinity CD46-binding phenotype by a substitution of Tyr instead of Asn at position 481 (Hsu *et al.*, 1998). Likewise, a substitution of Gly instead of Ser at site 546 has been shown to confer both the properties of CD46 binding and haemadsorption to isolates that were previously defective for these traits (Li *et al.*, 1999).

Corrigendum

Non Fc receptor-mediated infection of human macrophages by dengue virus serotype 2

M. M. Bertha Moreno-Altamirano, F. Javier Sánchez-García and M. Lourdes Muñoz


Fig. 3. The original legend was incorrect; the correct version is given below.

*Fig. 3.* DEN-2 VOPB assays. Cell membrane proteins from human macrophages (lane 1), PMA-differentiated U-937 cells (lane 2) and undifferentiated U-937 cells (lane 3) were separated by 12% SDS–PAGE and transferred to nitrocellulose. Nitrocellulose sheets were layered with DEN-2 and then incubated with the anti-E protein mAb 2C5.1 and rabbit anti-mouse IgG–PO pAbs. Nitrocellulose sheets were treated with ECL reagent and autoradiographed.
Corrigendum

Generation of infectious and transmissible virions from a GB virus B full-length consensus clone in tamarins

Andrea Sbardellati, Elisa Scarselli, Ernst Verschoor, Amedeo De Tomassi, Domenico Lazzaro and Cinzia Traboni


Page 2441, Table 1. Comparison of GBV-B genomic sequences (*cont.*). The data in the table for the 3′-UTR contain a number of errors. The correct version of that part of the table is given below.

<table>
<thead>
<tr>
<th>Genomic region*</th>
<th>Position of nt (aa)</th>
<th>Nucleotide</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Simons et al.</td>
<td>FL-1</td>
</tr>
<tr>
<td>3′-UTR (9038–end)</td>
<td>9061</td>
<td>T</td>
</tr>
<tr>
<td>Poly(U) length</td>
<td>27</td>
<td>21</td>
</tr>
<tr>
<td>9136–9137†</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>9310‡</td>
<td>NA</td>
<td>NA</td>
</tr>
<tr>
<td>3′Y sequence</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

* Amino acid residue positions of putative protein boundaries are shown in parentheses.
† From nt 9137 the numbering is increased by one unit with respect to that of the U22304 sequence.
‡ Position of FL-3 sequence (AJ2779479).
NA, Not applicable.