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Virology | Author Correction

Correction for Domingo et al., “Puzzles, challenges, and information reservoir of SARS-CoV-2 quasispecies”

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Volume 97, no. 12, e01511-23, 2023, https://doi.org/10.1128/jvi.01511-23. Page 7: A calculation mistake was made in the first paragraph of the section titled “The space of the possible: an unexploited resource?” The first two sentences should read as follows. “The theoretical sequence space available to any virus is an unimaginably large number (2). In the case of SARS-CoV-2 with a genome length of about 29,900 nucleotides, considering all possible point mutations, the theoretical sequence space is of $4^{29,900}$ different genomes (4 being the number of nucleotides at any position; possible rare, non-standard nucleotides, are ignored); $4^{29,900}$ is $1.6 \times 10^{18,064}$, an unimaginably vast number.”

This error does not impact the conclusions of the article.

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