

## AUTHOR CORRECTION

# Correction for Dinis et al., Deep Sequencing Reveals Potential Antigenic Variants at Low Frequencies in Influenza A Virus-Infected Humans

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Volume 90, no. 7, p. 3355–3365, 2016. Page 3356, column 2, “Template preparation” paragraph, lines 7 and 8: “H3N2-F (AGCAAAA GCAGGGGATAATTTC) and H3N2-R (AGTAGAAACAAGGGTGTTC)” should read “H3N2-F (GGTTTCGCTAAAAACT TCC) and H3N2-R (GCAAATGTTGCACCTAATGTTG).”

Page 3356, column 2, “Template preparation” paragraph, lines 8 to 10: “H1N1pdm-F (ATATACGCGTAGCGAAAGCAGGGGAA) and H1N1pdm-R (ATATACGCGTAGAAACAAGGTGT)” should read “H1N1pdm-F (AGCAAAAGCAGGGAAACAA) and H1N1pdm-R (AGTAGAAACAAGGGTGTTC).”

**Citation** Dinis JM, Florek NW, Fatola OO, Moncla LH, Mutschler JP, Charlier OK, Meece JK, Belongia EA, Friedrich TC. 2016. Correction for Dinis et al., Deep sequencing reveals potential antigenic variants at low frequencies in influenza A virus-infected humans. *J Virol* 90:8029. doi:10.1128/JVI.01041-16.

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