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CORRIGENDUM

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Corrigendum

Dominant clade-featured SARS-CoV-2 co-occurring mutations reveal plausible epistasis: An in silico based hypothetical model.

The article[1] to which the corrigendum refers was published in the Journal of Medical Virology 94(3): 1035-1049 (https://onlinelibrary.wiley.com/doi/10.1002/jmv.27416)

On page 1036, the sentence "The virus contains four major structural proteins: spike glycoprotein (S), envelope (E), membrane (M), and nucleocapsid (N) protein, along with 16 nonstructural proteins (NSP1–NSP16) and seven accessory proteins (ORF3a, ORF6, ORF7a, ORF7b, ORF8a, ORF8b, and ORF10)." should be changed to "The virus contains four major structural proteins: spike glycoprotein (S), envelope (E), membrane (M), and nucleocapsid (N) protein, along with 16 nonstructural proteins (NSP1–NSP16) and seven accessory proteins (ORF3a, ORF6, ORF7a, ORF7b, ORF8, ORF9b, ORF9c, and ORF10)."

The authors regret this error.

REFERENCE

1. Alam A, Islam OK, Hasan MS, et al. Dominant clade-featured SARS-CoV-2 co-occurring mutations reveal plausible epistasis: An in silico based hypothetical model. *J Med Virol*. 2022;94:1035-1049. doi:10.1002/jmv.27416