Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

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Correction

Structure, Function, and Antigenicity of the SARS-CoV-2 Spike Glycoprotein

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We recently discovered that the purified ACE2 ectodomain used for affinity determinations encompasses residues 19–741 of macaque ACE2 instead of residues 1–615 of human ACE2. Although the binding interface is conserved, the presence of the endogenous ACE2 dimerization domain affects the affinities reported in Table 1 due to avidity. New measurements were carried out with the human ACE2 ectodomain (residues 19–615), and the corresponding affinities were corrected (Starr, T.N., et al. (2020). Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding. Cell 182, 1295–1310. 10.1016/j.cell.2020.08.012). Note that the relative difference in affinities between SARS-CoV-2 RBD and SARS-CoV RBD are unchanged. None of the other data are affected, and our conclusions remain unchanged. We apologize for any confusion that this error may have caused.