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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Reply to a letter to the editor

Dear Editor-in-Chief, Life Sciences Journal

Thanks for giving me a chance to reply to the letter you received about my paper entitled: "Ribavirin, Remdesivir, Sofosbuvir, Galidesivir, and Tenofovir against SARS-CoV-2 RNA dependent RNA polymerase (RdRp): A molecular docking study". 117592.

First, I'd like to thank Professor Erik De Clercq for coming across my paper. It is my pleasure that a pioneer AIDS fighter reads and comments on my work.

SARS-CoV-2, the current pandemic health crisis, motivated me to conduct research work aiming at wide screening and suggestion of possible fast solutions to pave the way for further laboratory and clinical studies to proceed in order to offer reliable treatment options to front line physicians. Drug repurposing is a successful strategy that was used before to tackle such emerging infectious diseases [1,2]. The computational work has been enormously enhanced in the last three decades and become a second hand for drug designers [3,4]. Thanks to the computational power that helped to accelerate the drug development journey efficiently by saving time, effort, and money.

As this paper is purely computational, it is clearly mentioned in the abstract and the conclusion that "*The results **suggest** the effectiveness of Ribavirin, Remdesivir, Sofosbuvir, Galidesivir, and Tenofovir as potent drugs against SARS-CoV-2 since they tightly bind to its RdRp*". The sufficient binding to the viral polymerase may counteract its RNA replication as the mentioned nucleotide inhibitors are competing with the natural NTPs as reported in previous studies [5,6] including Prof Erik De Clercq's chapter [7]. Still, it is a recommendation, as mentioned in the paper, and sure, experimental validation is a must. Fortunately, clinical trials are currently being carried on some of the suggested drugs, and hopefully, one of them will be, soon, approved by FDA against SARS-CoV-2 [8,9].

The guanosine derivative (IDX-184), Setrobuvir, and YAK are chemical compounds, not drugs, and not approved by the FDA. Although they show outstanding binding affinity to SARS-CoV-2 *in silico*, still *in vitro* and *in vivo* testing are required to check their safety and effectiveness as possible inhibitors. I mentioned in the abstract that "*The **drugs** mentioned above can tightly bind to the RdRp of the SARS-CoV-2 strain and thus may be used to treat the disease. No toxicity measurements are required for these drugs since they were previously tested prior to their approval by the FDA.*", here I am referring to the drugs that are listed earlier (Ribavirin, Remdesivir, Sofosbuvir, Galidesivir, and Tenofovir), and not the chemical compounds (IDX-184, Setrobuvir, and YAK).

I would believe that everyone agrees that although computers would not solely treat any disease, yet they can help save lives by accelerating the drug design step for combating the emerging pandemic COVID-19.

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Abdo A. Elfiky*
Biophysics Department, Faculty of Science, Cairo University, Giza, Egypt
The International Center for Theoretical Physics (ICTP), Trieste, Italy
E-mail address: abdo@sci.cu.edu.eg.

* The International Center for Theoretical Physics (ICTP), Trieste, Italy.

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