To the editors:

I am pleased to submit the manuscript entitled “A target and two drugs for SARS-CoV-2 found by paralog search” for your consideration for publication in PLOS ONE.

Because of the urgency caused by the global pandemic caused by the SARS-CoV-2 virus, I would appreciate an accelerated peer review of my methods and results. These in-silico methods have discovered 2 (possibly 3) drugs which may be repurposed to treat infection by the SARS-CoV-2 virus, which could potentially save many lives.

# Summary of contribution to scientific literature

This paper describes a method that uses a pathogen genome itself to discover targets and their associated drugs. The method uses sequence similarity between pathogen genes and known targets. This approach is a completely data driven, mechanism-agnostic method. The principle followed is that sequence and structural conservation are directly related to survival of the pathogen of interest.

The original idea for the workflow discussed in this paper came from observing that the ChEMBL database structure supports relating drug targets, drug molecules, and target component sequences. The database structure might provide an easy way to find targets and drugs for other pathogens if we could find proteins in their genomes that were similar enough to them. What was missing was a table with similarity results for those pathogens, and criteria for filtering the results. This paper provides a method for providing the necessary table and similarity criterion.

Uncertainty about whether existing drugs will effectively bind or interfere with the target proteins is somewhat compensated for by the easy accessibility of the existing drugs, and further bolstered by our understanding of their dosage and safety statistics from existing studies. In this particular case, the similarity of the pathogen gene sequence and the target sequence is so high that target and pathogen gene are practically identical. The drugs identified were validated using SWISSDOCK docking simulations.

# Previous publications on this subject

This is a research article not related to any article that I have previously published.

# Editor recommendations

Please choose an appropriate editor for my manuscript. The article describes the use of a PostgreSQL database with bioinformatic data, R, Perl programming language, and some other bioinformatics tools such as BLASTP. The reviewer should be familiar with the concept of sequence conservation and drug targets.

# Authorship statement

I am the only author of this manuscript, and all figures were produced by me. I have no funding or conflicting interests.

Sincerely,

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