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EDITORIAL

Special issue editorial: Methods to facilitate SARS-CoV-2 and COVID-19 research

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This special issue of *Journal of Biological Methods* presents methods related to SARS-CoV-2 research in responding to the current global COVID-19 pandemic.

Keywords: COVID-19, SARS-CoV-2, pandemic, minION nanopore sequencing, MTiOpenScreen

The outbreak of COVID-19 pandemic has greatly impacted the lives around the globe in countless ways. After nearly two years of battling with the coronavirus SARS-CoV-2, significant research progress has been made in our understanding and ability to combat this pathogen. In this special issue, we aim to present current methods to facilitate the different areas of COVID-19 research. With the emergence of new viral variants, it is critical that we expand the toolbox to characterize the virus, develop more efficacious vaccine, repurpose existing drugs, and discover novel therapeutics for COVID-19 treatments as the virus continues to evolve.

The special issue is launched with two articles on technology platforms: A cost-effective high throughput sequencing platform of SARS-CoV-2 viral genomes for rapid tracking the spread of viral variants and an open tool virtual drug screening platform for small molecule inhibitors of SARS-CoV-2 viral proteins.

Pater *et al*. [1]. provide a detailed "how to" guide for high throughput sequencing of SARS-CoV-2 virus genomes, from patient samples to visualized phylogenetic trees, using an affordable minION nanopore sequencing instrument. Detailed protocols for setting the bioinformatics pipeline and deposition in global databases like GISAID are included in supplemental working protocols. Although many pieces to the protocol, including ARTIC primer sets and minION bioinformatic tools, could previously be found in the literature, a complete published protocol from start to finish was lacking. Tips and tricks are included at each step, along with the rationale for optimization when needed. These include correction of a notorious ARTIC v3 amplicon dropout *via* primer spike-in, testing of multiple reagents, real-time base calling and data analysis, and multiple quality control steps. This method should be especially helpful for smaller laboratories or those without access to other sequencing platforms. The utility of their protocol was demonstrated by the sequencing of over 4000 complete, high-quality SARS-CoV-2 genomes across the U.S. state of Illinois over the course of the pandemic, resulting in phylogenetic trees and geographic map views to track the regional introduction and spread of SARS-CoV-2 variants.

Chen *et al*. [2] present a primer for how to dock small molecules to the main protease of the SARS-CoV-2 virus, known as M^{pro} or $3CL^{pro}$. Small molecule drugs that can slow or stop the COVID-19-causing virus during replication in host cells are highly sought after. Using this methodology, relatively new researchers can model small molecule docking to proteins and perform virtual screens for preliminary leads. Virtual screening is facilitated by an open tool, MTiOpenScreen, and protein structure preparation, virtual screening on the webserver and how to access screen results are explained. They also provide examples of real results and how to analyze them, as well as offer tips and hints throughout. This protocol provides an entry level, low-cost platform for discovering protein-binding molecules, especially for the M^{pro} protease of SARS-CoV-2.

We hope you will find these articles informative. On behalf of the editorial staff and colleagues, we thank all the authors and reviewers for your contributions to this special issue. Articles are published on a rolling basis, and we encourage scientists working on any aspect of SARS-CoV-2 to continue to submit to this special issue.

References

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About our Guest Editor

Dr. Keith Gagnon is an Associate Professor at Southern Illinois University School of Medicine in Carbondale. His lab is interested in studying neurological repeat expansion disorders and RNA-guided enzymes including design of CRISPR-based proteins for therapeutic applications. Dr. Gagnon joined the Editorial Board of JBM in 2019.

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About our Deputy Editor

Dr. Vera Huang is a trained molecular biologist and cancer biologist. In addition to her editor role, Vera has over 8 years of experience in biopharma industry and drug discovery in small molecules, biologics, and nucleic acid based therapetuics. Vera joined the editorial team of Journal of Biological Methods in 2013.