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BIG DATA, GENOMICS AND OUTBREAKS

Hybrid de novo Whole-Genome Assembly and Annotation of SARS-CoV-2 Virus from Nosocomial Infection in Pahang, Malaysia

**ABSTRACT** 

## Hybrid de novo Whole-Genome Assembly c Nosocomial Infection i

Ummu Afeera Zainulabid, Norhidayah Kamaruc Aini Syahida Mat Yassin, How



SARS-CoV-2 virus is highly contagious and spreads easily that it is difficult to detect in elucidating the pattern of infection for contact tracing purposes. The advent of high-throughput sequencing techniques has improved diagnosis in detection the viral lineages especially involving sporadic infection. The combination of short- and longreads greatly improved the assembly of the SARS-CoV-2 genome and marked as a new approach to correct erroneous frame-shifts from single sequencing effort.



## POSTER PRESENTATION

View the poster presentation below.

0:00 2:00

## **SPEAKERS**

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