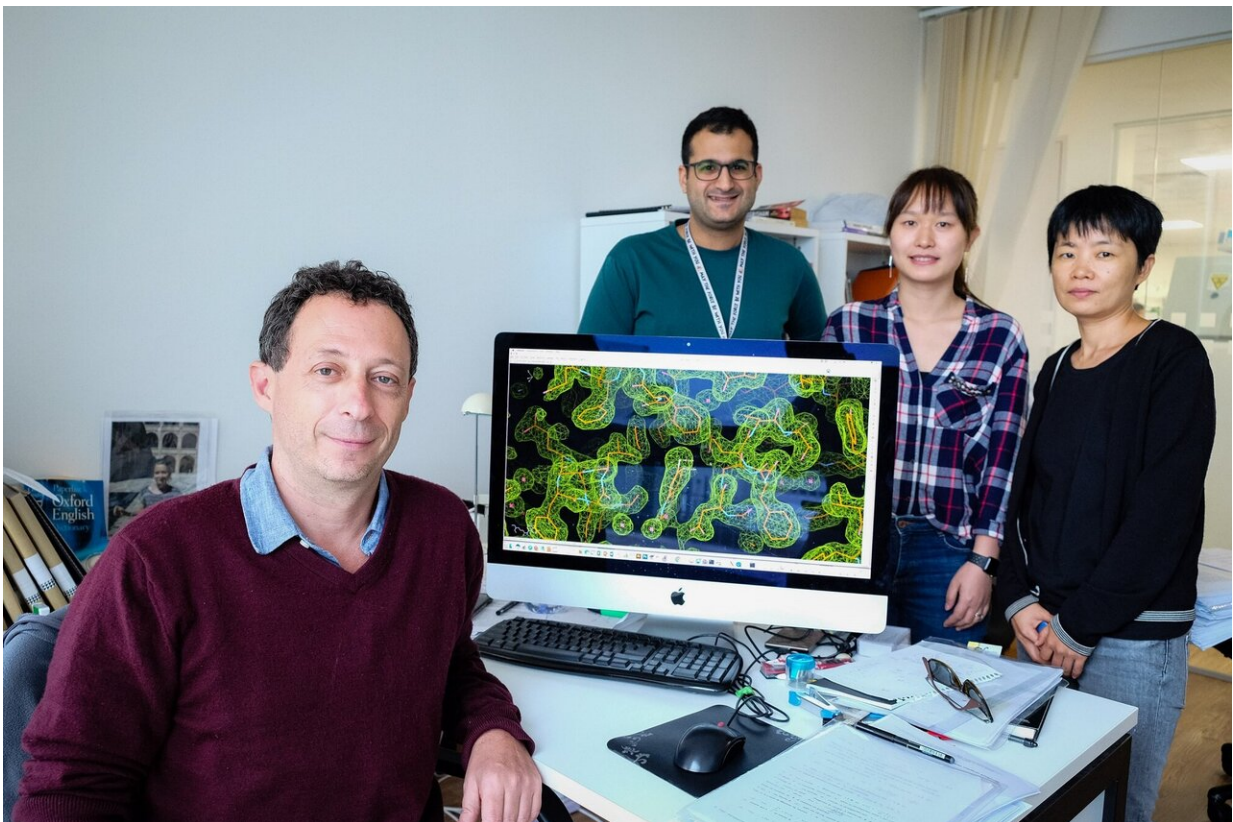


Scientists uncover structure of key pneumonia virus enzyme, suggesting a route for new antiviral treatments

December 9 2019



(left) NTU Assoc Prof Julien Lescar, Dr Abbas El Sahili, PhD student Ms Jia Huan and Dr Xinlei Qian, who imaged and analysed an enzyme that could be key to disabling respiratory syncytial virus (RSV) and human metapneumovirus (HMPV), both which currently have no effective cure or vaccine. Credit: Nanyang Technological University

A team of molecular and structural biologists from Nanyang Technological University, Singapore (NTU Singapore), has found a potential new route to disabling respiratory syncytial virus (RSV) and human metapneumovirus (HMPV) after elucidating the structure of one of its key components.

RSV and HMPV are two closely related viruses causing severe and life-threatening [respiratory diseases](#) such as pneumonia and bronchiolitis in premature babies and infants, the elderly, and anyone with a weak immune system.

According to UNICEF, pneumonia killed a child somewhere in the world every 39 seconds in 2018, but there are no vaccines or effective antiviral therapies against it.

As they infect human cells, HMPV and RSV commandeer the cell's machinery to make copies of themselves. To initiate the process, special proteins released by the virus interact with each other to make distinct protein complexes.

Writing in *Nature*, Dr. Julien Lescar from NTU's School of Biological Sciences and his team report that they have used cryo-[electron microscopy](#) to image the [molecular structure](#) of one of these large complexes, an enzyme called HMPV L:P polymerase.

Cryo-electron microscopy uses an advanced electron-scanning microscope, which can image a cryogenically frozen sample down to the sub-nanometer range. The NTU images captured the enzyme at a resolution of 3.7 Angstrom, or 0.37 nanometers. Based on these two-dimensional pictures, the team then built three-dimensional computer models of the proteins' L:P molecular structures.

Analysis of these model structures revealed key sites for molecules to

interact, offering new targets for designing antiviral molecules against both viruses. Dr. Lescar, a principal investigator at the NTU Institute of Structural Biology, said that with this detailed structural knowledge, researchers can now develop inhibitors that disrupt the enzymatic activities of HPMV L:P protein and potentially block infection by the virus.

"We hope that our work will help researchers in pharma and academia around the world to design much-needed therapies for difficult viral infections that often lead to [antibiotic-resistant bacterial infections](#)," said Dr. Lescar.

Since the HMPV proteins they studied are essentially unchanged through evolution and very similar to those of RSV and other [virus](#) species belonging to the Pneumoviridae family, the scientists hope that inhibitors developed against HPMV could also work against a broad spectrum of viruses involved in respiratory diseases, and inform similar quests against other viral diseases.

Dr. Lescar and colleagues have founded a spin-off company named Epitoire that is actively engaged in designing DNA replication blockers as potential therapies against these viruses, and the company is currently seeking investors and clinicians to support it.

More information: Junhua Pan et al. Structure of the human metapneumovirus polymerase phosphoprotein complex, *Nature* (2019). [DOI: 10.1038/s41586-019-1759-1](https://doi.org/10.1038/s41586-019-1759-1)

Provided by Nanyang Technological University

Citation: Scientists uncover structure of key pneumonia virus enzyme, suggesting a route for new

antiviral treatments (2019, December 9) retrieved 21 June 2024 from
<https://phys.org/news/2019-12-scientists-uncover-key-pneumonia-virus.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.