Li Chuin Chong

Current Appointments TWINCORE Centre for Experimental and Clinical Infection Research c/o

Helmholtz Centre for Infection Research (HZI) | Hannover, DE

Institute for Experimental Virology

Doctoral Researcher

Apr 2022 - Present

Education

Hannover Medical School | Hannover Biomedical Research School, Germany

Ph.D., Biomedical Data Science

Apr 2022 - Present

Supervisory committee: Chris Lauber (main), Stefan Seitz, Alice Mc Hardy, Daniel P. Depledge

Perdana University | School of Data Sciences, Malaysia

M.Sc. by Research, Bioinformatics

2020

- Dissertation: Mapping the minimal set of the viral peptidome
- Awarded with Distinction
- Supervisory committee: Asif M. Khan (main), Sy Bing Choi, Kenneth Ban Hon Kim

Universiti Putra Malaysia | Faculty of Medicine and Health Sciences, Malaysia

B.Sc., Biomedical Sciences

2018

- Dissertation: Expression, purification and characterisation of the protruding domain of Macrobrachium rosenbergii nodavirus capsid protein
- Supervisory committee: Kok Lian Ho, Abdah MD Akim

Professional Experience

Visiting Research Fellow

Sep 2023 - Present

GISAID EpiArbo™

Visiting Trainee

Oct - Nov 2023

Division of Virus Associated Carcinogenesis (F170), German Cancer Research Center (DKFZ), Germany

Research Intern May 2020 - Dec 2021

Faculty of Medical Technology, Mahidol University, Thailand

International Visiting Researcher

Feb - Sep 2021

Beykoz Institute of Life Sciences and Biotechnology (BILSAB), Bezmialem Vakif University, Turkey

Research Assistant Sep - Dec 2020

Faculty of Dentistry, University of Malaya, Malaysia & Cancer Research Malaysia

Publications

Charon, J., Olendraite, I., Forgia, M., **Chong, L. C.**, Hillary, L. S., Roux, S., ... Neri, U. (2024). Consensus statement from the first RdRp summit: Advancing RNA virus discovery at scale across communities. *Frontiers in Virology*. doi:https://doi.org/10.3389/fviro.2024.1371958.

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- **Chong, L. C.**, & Lauber, C. (2023). Viroid-like RNA-dependent RNA polymerase-encoding ambiviruses are abundant in complex fungi. *Frontiers in Microbiology*, *14*. doi:https://doi.org/10.3389/fmicb.2023.1144003 [Citations = 2].
- Tajuddin, S., Khan, A. M., **Chong, L. C.**, Wong, C. L., Tan, J. S., Salwany, M. Y. I., ... Tan, W. S. (2023). Genomic analysis and biological characterization of a novel *Schitoviridae* phage infecting *Vibrio alginolyticus*. *Applied Microbiology and Biotechnology*, *107*, 749–768. doi:https://doi.org/10.1007/s00253-022-12312-3 [Citations = 5].
- Yu, T., **Chong, L. C.**, Nantasenamat, C., Anuwongcharoen, N., & Piacham, T. (2023). Machine learning approaches to study the structure-activity relationships of Lpxc inhibitors. *EXCLI Journal*, *22*, 975–991. doi:https://doi.org/10.17179/excli2023-6356.
- **Chong, L. C.**, & Khan, A. M. (2022). UNIQmin, an alignment-free tool to study viral sequence diversity across taxonomic lineages: A case study of monkeypox virus. *bioRxiv*. doi:https://doi.org/10.1101/2022.08.09.503271 [Citations = 3].
- **Chong, L. C.**, & Khan, A. M. (2022). Historical milestone in 42 years of viral sequencing Impetus for a community-driven sequencing of global priority pathogens. *Frontiers in Microbiology*, *13*. doi:https://doi.org/10.3389/fmicb.2022.1020148.
- **Chong, L. C.**, & Khan, A. M. (2022). Negligible peptidome diversity of SARS-CoV-2 and its higher taxonomic ranks. *bioRxiv*. doi:https://doi.org/10.1101/2022.10.31.513750 [Citations = 1].
- Nguyen, Q. V., **Chong, L. C.**, Hor, Y. Y., Lew, L. C., Irfan, A. R., & Choi, S. B. (2022). Role of probiotics in the management of COVID-19: A computational perspective. *Nutrients*, *14*(*2*), 274. doi:https://doi.org/10.3390/nu14020274 [Citations = 45].
- Wang, J., Youkharibache, P., Marchler-Bauer, A., Lanczycki, C., Zhang, D., Lu, S., ... Ge, Y. (2022). iCn3D: From web-based 3D viewer to structural analysis tool in batch mode. *Frontiers in Molecular Biosciences*, 9. doi:https://doi.org/10.3389/fmolb.2022.831740 [Citations = 29].
- **Chong, L. C.**, Lim, W. L., Ban, K. H. K., & Khan, A. M. (2021). An alignment-independent approach for the study of viral sequence diversity at any given rank of taxonomy lineage. *Biology*, *10(9)*, 853. doi:https://doi.org/10.3390/biology10090853 [Citations = 3].
- **Chong, LC**, Gayatri, G., Lim, J. M., Yeo, W. W. Y., & Choi, S. B. (2021). Drug discovery of spinal muscular atrophy (SMA) in computational perspective: A comprehensive review. *International Journal of Molecular Sciences*, 22(16), 8962. doi:https://doi.org/10.3390/ijms22168962 [Citations = 10].
- Tan, S., Sjaugi, M. F., Fong, S. C., **Chong, L. C.**, Abd Raman, H. S., Nik Mohamed, N. E., ... Khan, A. M. (2021). Avian influenza H7N9 virus adaption to human hosts. *Viruses*, *13*(*5*), 871. doi:https://doi.org/10.3390/v13050871 [Citations = 4].

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- **TMGH-Global COVID-19 Collaborative**. (2021). Perceived stress of quarantine and isolation during COVID-19 pandemic: A global survey. *Frontiers in Psychiatry*, *12*, 651. doi:https://doi.org/10.3389/fpsyt.2021.656664 [Citations = 48].
- **TMGH-Global COVID-19 Collaborative**. (2021). Psychological impacts and post-traumatic stress disorder among people under COVID-19 quarantine and isolation: A global survey. *International Journal of Environmental Research and Public Health*, *18*(*11*), 5719. doi:https://doi.org/10.3390/ijerph18115719 [Citations = 30].
- **Chong, L. C.**, Hagilaa, G., Yong, C. Y., Tan, W. S., & Ho, K. L. (2019). Expression, purification and characterisation of the dimeric protruding domain of *Macrobrachium rosenbergii* nodavirus capsid protein expressed in *Escherichia coli*. *PLoS ONE*, *14*(2), e0211740. doi:https://doi.org/10.1371/journal.pone.0211740 [Citations = 9].
- **Chong, L. C.**, & Khan, A. M. (2019). Identification of serotype-specific, highly conserved dengue virus sequences: Implications for vaccine design. *BMC Genomics*, 20(Suppl 9), 921. doi:https://doi.org/10.1186/s12864-019-6311-z [Citations = 17].

Book Chapters

Chong, L. C., & Khan, A. M. (2019). Vaccine target discovery. Encyclopedia of Bioinformatics and Computational Biology. doi:10.1016/B978-0-12-809633-8.20100-3 [Citations = 23].

Software

UNIQmin: An alignment-independent tool for the study of pathogen sequence diversity at any given rank of taxonomy lineage

♣ PyPi • 🗘 UNIQmin

Role: Developer (main) and maintainer

vDiveR: A graphical user interface (GUI)-based web application hosted on R Shiny for the visualization of various diversity dynamics

Role: Domain expert

Presentations

Invited talks

Unravelling the virosphere: Insights from viral discovery and sequence diversity analysis

17 Jun 2023

• Guest Lecture series of Indonesian Medical Education and Research Institute (IMERI)

Contributed talks

A near-full compression of SARS-CoV-2 peptidome using UNIQmin

12-21 Sep 2022

- 21st European Conference on Computational Biology (ECCB2022), Stiges, Barcelona
- GOBLET Fund & Malaysia Trust Fund Travel Fellowship Award

Identification of highly conserved, serotype-specific dengue virus sequences: Implications for vaccine design

10-12 Sep 2019

- 18th International Conference on Bioinformatics (InCoB 2019), Jakarta, Indonesia
- APBioNET Travel Fellowship Award

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Posters

Identification of RNA viruses and host reservoirs with high spillover risk

17-21 Oct 2022

• EMBL-EBI: Bioinformatics approach to viruses (virtual)

UNIQmin, an alignment-independent tool for the study of viral sequence diversity at any given rank of taxonomy lineage: HPC solutions for big-data performance boost 30 Aug-3 Sep 2021

• 2021 ACM Europe Summer School (virtual)

Mapping the minimal set of the viral peptidome across all major viral taxonomies 25-30 Jul 2021

- 29th Conference on Intelligent Systems for Molecular Biology and 20th European Conference on Computational Biology (ISMB/ECCB 2021; virtual)
- ISMB/ECCB Fellowship Award

UNIQmin: An alignment-independent approach to generate a minimal set of viral peptidome

15-16 May 2021

- International Conference on Bioinformatics, Computational Biology, and Biomedical Science (ICBCBBS 2021; virtual)
- · Best E-Poster Award

Identification of serotype-specific, highly conserved dengue virus sequences: Implications for vaccine design

26-28 Sep 2018

- 17th International Conference on Bioinformatics (InCoB 2018), New Delhi, India
- ISCB Travel Fellowship Award

Grants Intramural Funding

Helmholtz Visiting Researcher Grant (€4,000)

Role: Visiting Trainee

Extramural Funding

PUTI Q1 Grant from Universitas Indonesia (IDR 120 million) 2022

Role: Collaborator

PI: Toar Jean Maurice Lalisang (main) & Linda Erlina (co-)

Malaysian Medical Association (MMA) (MYR 5,000)

2019

2023

Role: Collaborator

PI: Mohammad Asif Khan (main) & Choi Sy Bing (co-)

Honors and Awards

- GOBLET Fund Travel Fellowship for ECCB 2022
- Malaysia Trust Fund Travel Fellowship for ECCB 2022
- ESCV Fellowship for ESCV 2021
- ISCB Fellowship for ISMB/ECCB 2021
- Malaysia Trust Fund for support on publication fee for Chong et al. (2021)
- Best E-Poster Award, ICBCBBS 2021
- APBioNET Travel Fellowship for InCoB 2019
- ISCB Travel Fellowship for InCoB 2018
- Public Service Department National Degree Programme (JPA-PIDN) Scholarship for B.Sc. (Biomedical Sciences) 2015-2018

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Teaching and Service

Graduate Student Supervisor

Supervisor

C+ 1 C: 1 + -	D.C.	(Bioinformatics), I3L, ID	2022-2023
Stennen Siloinario	• K > C	(Bioinformaticg) IXI III	71177=71173

Student Mentor

Tham Hong Yun • Ph.D. (Microbiology), UPM, MY	2018-2024
Sofiah binti Tajuddin • M.Sc. (Microbiology), UPM, MY	2019-2022
Srosha Khanjou • BASc (Medicine), MUIC, TH	2020-2021
Interns at CaRE UPM* • B.Sc. (Biomedical Sciences), UPM, MY	2018
• B.Sc. (Biomedical Sciences), UM, MY	2018

*UPM: Siti Najiha Binti Abu Bakar, Anis Zuhaida Binti Mamnun, Nor Shamira Rosdi, Muhammad Rusydie Mohd Rasid; UM: Aisyah Shamsuddin, Wardah Othman, Nurhusna Abd Samad

Interns at CaRE UPM* • B.Sc. (Biomedical Sciences), UPM, MY 2017

*UPM: Eugene Chua, Ong Si Ying, Teo Yu Yun, Lim Xin, Khor Winnie, Lok Zen Hui, Even Lim

Outreach & Professional Societies

Leadership

- Finance Committee Member, ISCB Student Council (ISCBSC)
 Ambassador, Asia Pacific Bioinformatics Network (APBioNET)
 2023-Present
 2021-2022
- Public Relations & Outreach (PRO) Committee Member, Global Organisation for Bioinformatics Learning, Education & Training (GOBLET) 2019-2021
- Executive Council of Association for Medical and Bio-Informatics Singapore (AMBIS) 2018-2019
- Executive Council of Alumni and Leadership of Biomedical Science Club, UPM 2015

References

Dr. Chris Lauber

Head of Computational Virology
Institute of Experimental Virology,
TWINCORE GmbH
Assistant Professor
RESIST Cluster of Excellence,
Medizinische Hochschule Hannover
(MHH)
Hannover, Germany
chris.lauber@twincore.de

Dr. Mohammad Asif Khan

Professor and Associate Dean
College of Computing and Information
Technology
University of Doha for Science and
Technology (UDST)
Doha, Qatar
asif.khan@udst.edu.qa

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