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学习经历。

麻省综合医院 (Massachusetts General Hosptial)

美国

美国

2020.12 - 2025-02

2020.12 - 2025-02

美国

2020.12 - 至今 新加坡

2020.4 - 2020.11

新加坡

2019.4 - 2020.4

新加坡

2015 - 2019 新加坡

2010 - 2014

麻省综合医院 (Massachusetts General Hosptial) 博士后研究员

博德研究所 (Broad Institute)

博士后研究员

新加坡基因组研究所 (Genome Institute of Singapore)

博士后研究员 (II)

新加坡基因组研究所 (Genome Institute of Singapore)

博士后研究员(I)

新加坡国立大学 (NUS)

博士, 计算机科学

新加坡国立大学 (NUS)

学士,计算生物学

研究方向。

功能宏基因组,肠道菌群与宿主互作,时空微生物组

学术成果___

代表论文

- 1. T. Mayassi[#], C. Li[#], ..., R. Xavier. Spatial restricted immune and microbiota-driven adaptation of the gut. Nature. (2024, IF2024: 48.5)
- 2. C. Li[#], M. Stražar[#], ..., R. Xavier. Gut microbiome and metabolome profiling in Framingham Heart Study reveals cholesterol-metabolizing bacteria linked with lower cardiovascular risk. Cell. (2024, IF2024: 45.5).
- 3. H. Hu[#], Y. Tan[#], C. Li[#], ..., L. Dai. StrainPanDA: linked reconstruction of strain composition and gene content profiles via pangenome-based decomposition of metagenomic data. iMeta. (2022, IF2022: 23.8).
- 4. C. Li^{#,\$}, T. V. Av-Shalom, J. W. G. Tan, J. S. Kwah, K. R. Chng, N. Nagarajan\$. BEEM- Static: Accurate inference of ecological interactions from cross-sectional metagenomic data. **PLOS Computational Biology** (2021, IF2021:
- 5. A. S. L. Tay[#], **C. Li**[#], T. Nandi[#], ..., N. Nagarajan. Skin microbiome dermotypes in atopic dermatitis are linked to host immunity and microbial virulence. The Journal of Allergy and Clinical Immunology (2022, IF2022:
- 6. K. R. Chng[#], **C. Li**[#], D. Bertrand[#], ..., N. Nagarajan. Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nature Medicine (2020, IF2020: 36.1)
- 7. C. Li[#], K. R. Chng, T. V. Av-Shalom, ..., N. Nagarajan. An expectation-maximization algorithm enables accurate ecological modeling using longitudinal microbiome sequencing data. Microbiome (2019, IF2019: 10.5)
- 8. C. Li#, K. R. Chng#, E. J. H. Boey, ..., N. Nagarajan. INC-Seq: Accurate single molecule reads using nanopore sequencing. GigaScience (2016, IF2016: 9.2)

其他论文

- 1. A. Ravikrishnan, I. Wijaya, ..., C. Li, ..., N. Nagarajan. Gut metagenomes of Asian octogenarians reveal a metabolic shift and distinct microbial species associated with aging phenotypes. Nature Communication (2024, IF2024: 15.7)
- 2. T. Nakata, C. Li, ..., D. Graham, R. Xavier. Genetic vulnerability to healing reveals a spatially resolved epithelial restitution program. Science Translational Medicine. (2023, IF2023: 14.6).
- 3. F. Meyer, A. Fritz, ..., C. Li, ..., A. C. McHardy. Critical Assessment of Metagenome Interpretation the second round of challenges. Nature Methods. (2022, IF2022: 48.0).

- 4. D. Danko, et al. A global metagenomic map of urban microbiomes and antimicrobial resistance. **Cell** (2021, IF2021: 41.58) (as MetaSUB consortium member)
- 5. J. G. A. Aw, S. W. Lim, J. X. Wang, ..., **C. Li**, ..., N. Nagarajan, Y. Wan. Direct RNA sequencing reveals structural differences between transcript isoforms. **Nature Biotechnology** (2021, IF2021: 54.9)
- 6. Y. Tan, H. Hu, C. Li, X. Luo, Y. Tan, L. Dai. Research progress and applications of strain analysis based on metagenomic data. 生物工程学报 (2020, IF2020: 3.0)
- 7. T. Nandi, I. R. Lee, T. Ghosh, ..., **C. Li**, ..., N. Nagarajan. Gut microbiome recovery after antibiotic usage is mediated by specific bacterial species. **Nature Ecology and Evolution** (2020, IF2020: 13.6)
- 8. D. Bertrand, J. Shaw, M. Narayan, A. H. Q. Ng, ..., **C. Li**, ..., N. Nagarajan. Nanopore sequencing enables high-resolution analysis of resistance determinants and mobile elements in the human gut microbiome. **Nature Biotechnology** (2019, IF2019: 36.6)
- 9. D. Bertrand, S. Drissler, B. Chia, ..., **C. Li**, ..., N. Nagarajan. ConsensusDriver improves upon individual algorithms for predicting driver alterations in different cancer types and individual patients A Toolbox For Precision Oncology. **Cancer Research** (2017, IF2017: 9.1)
- 10. Y. O. Zhu, P. P. K. Aw, P. F. de Sessions, ..., **C. Li**, ..., M. Hibberd. Single-virion sequenc- ing of lamivudine-treated HBV populations reveal population evolution dynamics and demographic history. **BMC Genomics** (2017, IF2017: 3.7)
- 11. K. M. K. Lim, **C. Li**, K. R. Chng, N. Nagarajan. @MInter: Automated text-mining of microbial interactions. **Bioinformatics** (2016, IF2016: 6.1)
- 12. K. R. Chng, S. H. Chan, ..., **C. Li**, ..., N. Nagarajan. Tissue microbiome profiling identifies an enrichment of specific enteric bacteria in Opisthorchis viverrini associated cholangiocar-cinoma. **EBioMedicine** (2016, IF2016: 6.2)
- 13. K. R. Chng, A. S. L. Tay, **C. Li**, ..., N. Nagarajan. Whole metagenome profiling reveals skin microbiome dependent susceptibility to atopic dermatitis flares. **Nature Microbiology** (2016, IF2016: 14.2)
- 14. **C. Li**[#], K. R. Chng, K. M. K. Lim, N. Nagarajan. Predicting Microbial Interactions through Computational Approaches. **Methods** (2016, IF2016: 3.9)
- 15. G. Wu, H. Zhao, **C. Li**, ..., N. Nagarajan. Genus-wide comparative genomics of Malassezia delineates its phylogeny, physiology, and niche adaptation on human skin. **PLOS Genetics** (2015, IF2015: 6.2)
- #: (共同) 第一作者; \$: (共同) 通讯作者

获奖经历_

- •哈佛华人生命科学年度杰出研究奖, 2024 (Harvard Chinese Life Science Annual Distinguished Research Award)
- GIS 研究生突出成就奖, 2018 (GIS Graduate Student Prize)
- NUS 教学卓悦奖, 2018 (Honor List of Student Tutors)
- 计算生物专业最佳毕业设计, 2014 (Lijen Industrial Development Medal)
- 理学院计算机方向最优学生, 2011 (Lim Soo Peng Book Prize)

受邀报告_

Gut Microbiome and Metabolome Characterization Reveals Cholesterol-metabolizing Bacteria Associated with Lower Cardiovascular Risk. Gut Microbiota for Health World Summit, 2025, Washington, D. C. System Biology Modeling with Compositional Microbiome Data Reveals Personalized Gut Microbial Dynamics and Keystone Species. International Human Microbiome Congress 2018, Ireland