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Employment

Feb 2023 ~ Present

Postdoctoral Fellow & Bioinformatics Analyst, Institute of Molecular and Cell Biology (IMCB), Agency for Science, Technology and Research (A*STAR), Singapore

Aug 2022 ~ Jan 2023

Postdoctoral Fellow, Duke-NUS Medical School, National University of Singapore (NUS)

Education

Aug 2017 ~ Jul 2022

Ph.D. in Computational Biology, Duke-NUS Medical School, National University of Singapore

Sep 2013 ~ Jun 2017

B.Sc. in Biological Sciences, School of Life Sciences, Fudan University, China

Professional Skills and Research Overview

Bioinformatics - Cohort analysis of genomic, transcriptomic, and health data to identify disease-associated mutations and risk factors

- Association studies (GWAS, TWAS)
- Comorbidity analysis
- Disease risk factor mining

Bioinformatics - Tumor immune microenvironment profiling

- Single-cell transcriptomics analysis
- Spatial transcriptomics (Stereo-seq, 10X Visium, 10X Xenium)
- Flow cytometry data analysis (Cytex)

Tumor neoantigen discovery

- PacBio Isoseq long-read sequencing for structural variants and aberrant splicing
- Prediction of neoantigen immunogenicity and stability
- HLA typing (NGS-based, WES/WGS inference: OptiType, HLA-HD, etc.)
- sc-VDJ-seq for immune response assessment, T cell clonal tracking, and TCR-T therapy development
- Immunopeptidomics - Mass spectrometry validation of antigen presentation

Research Projects

Spatial Transcriptomics

Project	Key Findings	Status	Related Publications
Immunotherapy response in nasopharyngeal cancer (Stereo-seq)	EBV viral RNA levels predict prognosis for Ipi+Nivo combination therapy	Completed	Pub #1
cDC1 anti-tumor mechanisms (Stereo-seq)	cDC1 depletion increases tumor fibrosis and reduces T cell infiltration	Completed	Pub #4
Spatial distribution of APOBEC mutations in Asian breast cancer (Stereo-seq)	30kb deletion alters APOBEC3A/3B activity ratio	Completed	Pub #6-7
CD8+ T cell suppression factors in TNBC (10X Visium)	IQGAP1, B7H3, etc. negatively correlate with CD8+ T cell abundance	⌘ Ongoing	-

Single-cell Transcriptomics

Project	Key Findings	Status	Related Publications
TP53 mutations in colorectal premalignant lesions	Investigating TP53 mutation effects on colonic tissue homeostasis and tumorigenesis	⌘ Ongoing	-

Genome-Wide Association Studies (GWAS)

Project	Key Findings	Status	Related Publications
SLAS cohort aging study (NCT03405675)	TET2 variants significantly associated with hepatocellular carcinoma risk; clonal hematopoiesis analysis	⌘ Ongoing	-

Mutational Signature Analysis

Project	Key Findings	Status	Related Publications
COSMIC mutational signature database	Participated in discovery and validation of standard mutational signatures	Completed	Pub #13
Mutational signature extraction software development	Developed mSigHdp; led performance benchmarking of multiple software tools	Completed	Pub #10-12

Publications

Spatial Transcriptomics & Tumor Microenvironment

First Author:

1. **Wu, Y.** , Neo, Z. W., Chong, L. Y., Goh, D., Iyer, N. G., Chua, M. L. K., Lee, B., Song, X., Yeong, J.

& Lim, D. W.-T. Using longitudinal spatial-omics to demonstrate in-situ Epstein–Barr virus reduction in responders to immunotherapy treated nasopharyngeal cancer. *J. Clin. Oncol.* 43, 16_suppl (2025). https://doi.org/10.1200/JCO.2025.43.16_suppl.6025 (Conference abstract + Poster, IF: 43.4)

2. Wu, Y. , Wee, F., Chong, L. Y., Neo, Z. W., Lim, J., et al. Single-cell resolution spatial transcriptomics detection of pathogens followed by studying the immune milieu: using virus-associated cancers from different organs as paradigm. *J. Immunother. Cancer* 11 (2023). <https://doi.org/10.1136/jitc-2023-SITC2023.1512> (Conference abstract + Poster, IF: 10.6)

Co-first Author:

3. Wang, Y.* , Wu, Y.* , Zhang, F.* , Periasamy, P.* , You, H., Goh, D., Fincham, R. E. A., Ning, X., Wu, D., Liu, L., Jiang, Y., Qian, Z., Yeong, J. & Zhang, Y. Integrating spatial proteogenomics in cancer research. *Adv. Sci.* (in review, 2025). (Review, IF: 17.5)

Co-author:

4. Vilbois, S., Alfei, F., Tao, H., Chuang, Y.-M., Kieffer, Y., Wu, Y., Zhang, S., Chang, T.-H., Hsueh, P.-C., Wang, Y.-H., Low, J. T., Møller, S. H., Ruiz Buendía, G. A., Drobná, D., Schuster, M., Held, W., Yeong, J. P. S., Mechta-Grigoriou, F., Bénéchet, A. P., Zhou, J., & Ho, P.-C. cDC1s restrain tumor fibrosis to sustain T cell motility and T cell anti-tumor responses. *Nat. Immunol.* (in review, 2025). (IF: 27.6)

5. Liu, Y., Chong, C. Y. L., Wang, Y., Xu, L., Tan, Q. X., Hendrikson, J., Tan, J. W.-S., Ng, G., Guo, W., Wang, Y., Huang, L., Ge, W., Rethineswaran, V. K., Ong, J. Z. L., Quek, Y. E., Ang, A. J. Y., Teo, F., Chen, O. W., Ko, T. K., Kannan, B., Lim, B. Y., Lee, E. C. Y., Guo, Z., Lakshmanan, V., Shannon, N. B., Jegannathan, N., Ryan, C., Neo, Z. W., Chong, L. Y., Ng, A. R. H., Lee, J.-Y. J., Loo, L.-H., Wu, Y., Zhang, S., Nie, L., Zhang, Q., Zeng, L., Lim, T. K. H., Ng, M. C. H., Lee, C. J. Z., Chang, P. E. J., Teh, K. K.-J., Tan, H. K., Nadarajah, R., Yong, T. T., Wang, J., Aggarwal, I. M., Fong, E. L. S., Wu, K. Z., So, J. B. Y., Yeoh, K. G., Wong, J. S. M., Seo, C. J., Cai, M., Chia, C. S., Teh, B. T., Tan, I. B., Yeong, J., Chan, J. Y., Guo, T. & Ong, C.-A. J. Identification of novel paracrine therapeutic targets in peritoneal metastases through integrative proteotranscriptomic analysis of ascites. *Cell* (in review, 2025).

6. Tan, Z. C., Wu, Y., Neo, Z. W., Lau, M. C., Teo, S.-H., Yeong, J. P. S., Chang, S. W. & Pan, J. W. Spatial patterns of APOBEC mutagenesis in the tumour microenvironment of Asian breast cancer. *Nat. Commun.* (in review, 2026). *bioRxiv*: <https://www.biorxiv.org/content/10.64898/2026.01.01.697328v1> (IF: 14.7)

7. Tan, Z. C., Wu, Y., Neo, Z. W., Lau, M. C., Chang, S. W., Yeong, J. P. S., Teo, S.-H. & Pan, J. W. Spatial patterns of APOBEC mutagenesis in the tumor microenvironment of Asian breast cancer. *Cancer Res.* 85 (8_Suppl_1), 151 (2025). <https://doi.org/10.1158/1538-7445.AM2025-151> (Conference abstract + Poster, IF: 16.6)

8. Zhang, Y., Lee, R. Y., Tan, C. W., Guo, X., Yim, W. W., Lim, J. C., Wee, F. Y., Wu, Y., Kharbanda, M., Lee, J. J., Ngo, N. T., Leow, W. Q., Loo, L. H., Lim, T. K., Sobota, R. M., Lau, M. C., Davis, M. J., & Yeong, J. Spatial omics techniques and data analysis for cancer immunotherapy applications. *Curr. Opin. Biotechnol.* 87, 103111 (2024). <https://doi.org/10.1016/j.copbio.2024.103111> (Review, IF: 7.0)

9. Lee, R. Y., Wu, Y., Goh, D., Tan, V., Ng, C. W., Lim, J. C. T., Lau, M. C., Yeong J. P. S. Application of Artificial Intelligence to In Vitro Tumor Modeling and Characterization of the Tumor Microenvironment. *Adv. Healthc. Mater.* 12, 2202457 (2023). <https://doi.org/10.1002/adhm.202202457> (Review, IF: 9.6)

Mutational Signature Analysis

First Author:

10. Wu, Y. , Chua, E. H. Z., Ng, A. W. T., Boot, A. & Rozen, S. G. Accuracy of mutational signature software on correlated signatures. *Sci. Rep.* 12, 390 (2022). <https://doi.org/10.1038/s41598-021-04207-6> (IF: 4.3)

Co-first Author:

11. Liu, M.* , Wu, Y.* , Jiang, N., Boot, A. & Rozen, S. G. mSigHdp: hierarchical Dirichlet process

mixture modeling for mutational signature discovery. NAR Genom. Bioinform. 5, lqad005 (2023). <https://doi.org/10.1093/nargab/lqad005> (IF: 5.0)

Co-author:

12. Islam, S. M. A., Díaz-Gay, M., Wu, Y., Barnes, M., Vangara, R., Bergstrom, E. N., He, Y., Vella, M., Wang, J., Teague, J. W., Clapham, P., Moody, S., Senkin, S., Li, Y. R., Riva, L., Zhang, T., Gruber, A. J., Steele, C. D., Otlu, B., Khandekar, A., ... Alexandrov, L. B. Uncovering novel mutational signatures by de novo extraction with SigProfilerExtractor. Cell Genom. 2, 100179 (2022). <https://doi.org/10.1016/j.xgen.2022.100179> (IF: 11.1)

13. Alexandrov, L. B., Kim, J., Haradhvala, N. J., Huang, M. N., Ng, A. W. T., Wu, Y., Boot, A., Covington, K. R., Gordenin, D. A., Bergstrom, E. N., Islam, S. M. A., Lopez-Bigas, N., Klimczak, L. J., McPherson, J. R., Morganella, S., Sabarinathan, R., Wheeler, D. A., Mustonen, V., Getz, G., Rozen, S. G., Stratton, M. R. & P. Consortium. The repertoire of mutational signatures in human cancer. Nature 578, 94-101 (2020). <https://doi.org/10.1038/s41586-020-1943-3> (IF: 55.0)

Proteomics

14. Periasamy, P., Soon, K., Lim, X., Wu, Y., Meng, J., Lim, F., Yeong, J. DETECT – Cost-effective, high-throughput enrichment of low molecular weight proteins in serum proteomics – insights from a CAR-T therapy trial. J. Immunother. Cancer 11 (2023). <https://doi.org/10.1136/jitc-2023-SITC2023.0200> (Conference abstract + Poster, IF: 10.6)

Bioinformatics Tool Development

15. Li, Z., Zhang, F., Wang, Y., Qiu, Y., Wu, Y., Lu, Y., Yang, L., Qu, W. J., Wang, H., Zhou, W. & Tian, W. PhenoPro: a novel toolkit for assisting in the diagnosis of Mendelian disease. Bioinformatics 35, 3559-3566 (2019). <https://doi.org/10.1093/bioinformatics/btz100> (IF: 7.1)