吴逵

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研究方向：癌症多组学大数据系统研究，基于单细胞组学/时空组学的癌症演化生态学，癌症精准医学应用新技术。

丹麦哥本哈根大学分子生物医学博士学位，基因组学研究员，中国科学院大学研究生导师，深圳市高层次专业人才。担任广东省人类疾病基因组重点实验室主任，深圳市单细胞组学重点实验室学术带头人，中科院基础医学与肿瘤研究所兼职研究员，广东省精准医学应用学会结直肠癌分会副主任委员，广东省临床医学学会精准医疗专业委员会常务委员，中国医药生物技术协会精准医疗分会委员。

带领团队主要围绕癌症系统生物学研究开展科研与技术攻关，完成包括肺癌、肝癌、结直肠癌、乳腺癌、淋巴瘤等多种癌症的多组学图谱解析，在癌症组学特征、分子标志物、免疫逃逸机制等方向取得多项科研成果。利用单细胞组学/时空组学技术，研究癌症免疫微环境与异质性演化，构建癌症数字化病理图谱。基于癌症多组学大数据积累，针对癌症早期预测和新型免疫治疗应用等进行关键技术研发。

迄今在 Nature, Cell, Cancer Discovery, Journal of Hepatology, Gut, Nature Communications, Cell Reports 等期刊发表科研论文 60 余篇，申请发明专利 31 项，主持或作为课题骨干参与国家、省、市各级科研经费项目 10 项，获广东省自然科学一等奖（2019）。

代表性论文：

(1) Y. Lin, L. Peng, L. Dong, D. Liu, ..., J. Fan*, **K. Wu***, Q. Gao*. Geospatial immune heterogeneity reflects the diverse tumor-immune interactions in intrahepatic cholangiocarcinoma. ***Cancer Discovery***, https://doi.org/10.1158/2159-8290.CD-21-1640 (2022). (*通讯作者)

(2) W. Ren, X. Wang, M. Yang, ..., **K. Wu***, H. Zhang*, Q. Pan-Hammarström*. Distinct clinical and genetic features of hepatitis B virus–associated follicular lymphoma in Chinese patients. ***Blood Advances***, 6 (9): 2731–2744 (2022). (*通讯作者)

(3) X. Ye, L. Wang, M. Nie, …, **K. Wu***, Q. Pan-Hammarström*. A single-cell atlas of diffuse large B cell lymphoma. ***Cell Reports***, 39: 110713 (2022). (*通讯作者)

(4) H. Zhou, G. Li, J. Yin, ..., D. Zhou*, L. Wang*, **K. Wu***. Neoadjuvant chemotherapy alters peripheral and tumour-infiltrating immune cells in breast cancer revealed by single-cell RNA sequencing. ***Clinical and Translational Medicine***, 11 (12): e621 (2021). (*通讯作者)

(5) X. Ye, W. Ren, D. Liu, X. Li, …H. Zhang*, **K. Wu***, Q. Pan-Hammarström*. Genome-wide mutational signatures revealed distinct developmental paths for human B cell lymphomas. ***Journal of Experimental Medicine***, 218 (2): e20200573 (2021). (*通讯作者)

(6) H. Liang, F. Li, S. Qiao, X. Zhou, G. Xie, X. Zhao, Y. Zhang*, **K. Wu***. Whole-genome sequencing of cell-free DNA yields genome-wide read distribution patterns to track tissue of origin in cancer patients. ***Clinical and Translational Medicine***, 10 (6): e177 (2020). (*通讯作者)

(7) Y. Chen, J. Yin, W. Li, H. Li, D. Chen, C. Zhang, … **K. Wu***, D. Kuang*, G. Li*, N. Liu*, J. Ma*. Single-cell transcriptomics reveals regulators underlying immune cell diversity and immune subtypes associated with prognosis in nasopharyngeal carcinoma. ***Cell Research***, 30: 1024-1042 (2020). (*co-senior authors)

(8) L. Dong, L. Peng, L. Ma, D. Liu, … J. Fan, **K. Wu***, Q. Gao*. Heterogeneous immunogenomic features and distinct escape mechanisms in multifocal hepatocellular carcinoma. ***Journal of Hepatology***, 72 (5): 896-908 (2020). (*通讯作者)

(9) X. Hong, S. Qiao, F. Li, …Y. Zhao, **K. Wu***, W. Wu*. Whole-genome sequencing reveals distinct genetic bases for insulinomas and non-functional pancreatic neuroendocrine tumours: leading to a new classification system. ***Gut***, 69: 877-887 (2020). (*通讯作者)

(10) S. Hong#, D. Liu#, S. Luo#, W. Fang#, …, **K. Wu***, Li Zhang*. The Genomic Landscape of Epstein-Barr virus (EBV)-associated pulmonary lymphoepithelioma-like carcinoma. ***Nature Communications***, 10: 3108 (2019). (*通讯作者)

(11) **K. Wu**#, X. Zhang#, F. Li#, D. Xiao#, Y. Hou#, S. Zhu#, *et al.*. Frequent Alterations in Cytoskeleton Remodelling Genes in Primary and Metastatic Lung Adenocarcinomas. ***Nature Communications***, 6: 10131 (2015). (#第一作者)

(12) Y. Hou#, **K. Wu#**, X. Shi#, F. Li#, L. Song#, H. Wu#, *et al.*. Comparison of Variations Detection between Whole-Genome Amplification Methods Used in Single-Cell Resequencing. ***GigaScience***, 4: 37 (2015). (#第一作者)

(13) D. Xiao, F. Li, H. Pan, H. Liang, **K. Wu***, and J. He*. Integrative Analysis of Genomic Sequencing Data Reveals Higher Prevalence of LRP1B Mutations in Lung Adenocarcinoma Patients with COPD. ***Scientific Reports***, 7: 2121 (2017). (*通讯作者)

(14) S. Yuan#, **K. Wu#**, *et al.*. Amphioxus SARM Involved in Neural Development May Function as a Suppressor of TLR Signaling. ***Journal of Immunology***, 184: 6874-81 (2010). (#第一作者)

(15) S. Zhao, Z. Zhang, J. Zhan, X. Zhao, X. Chen, L. Xiao, K. Wu, Y. Ma, M. Li, Y. Yang, W. Fang, H. Zhao and L. Zhang. Utility of comprehensive genomic profiling in directing treatment and improving patient outcomes in advanced non-small cell lung cancer. ***BMC Medicine***, 19 (1): 223 (2021).

(16) M. Nie, L. Du, W. Ren, ..., **K. Wu**, F. Zhang and Q. Pan-Hammarström. Genome-wide CRISPR screens reveal synthetic lethal interaction between CREBBP and EP300 in diffuse large B-cell lymphoma. ***Cell Death & Disease***, 12: 419 (2021)

(17) D. Guallar, A. Fuentes-Iglesias, …, **K. Wu**, …J. Wang, and M. Fidalgo. ADAR1-Dependent RNA Editing Promotes MET and iPSC Reprogramming by Alleviating ER Stress. ***Cell Stem Cell***, 27 (2): 300-314 (2020)

(18) PCAWG Transcriptome Core Group, …, **K. Wu**, …PCAWG Consortium. Genomic basis for RNA alterations in cancer. ***Nature***, 578 (7793): 129-136 (2020).

(19) ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium. Pan-cancer analysis of whole genomes. ***Nature***, 578 (7793): 82-93 (2020)

(20) A. Huang, X. Zhao, X. R. Yang, F. Q. Li, X. L. Zhou, **K. Wu**, X. Zhang, Q. M. Sun, Y. Cao, H. M. Zhu, X. D. Wang, H. M. Yang, J. Wang, Z. Y. Tang, Y. Hou, J. Fan, and J. Zhou. Circumventing Intratumoral Heterogeneity to Identify Potential Therapeutic Targets in Hepatocellular Carcinoma. ***Journal of Hepatology***, 67: 293-301 (2017).

(21)Y. Hou, L. Song, P. Zhu, B. Zhang, Y. Tao, X. Xu, F. Li, **K. Wu**, , *et al.*. Single-Cell Exome Sequencing and Monoclonal Evolution of a JAK2-Negative Myeloproliferative Neoplasm. ***Cell***, 148: 73-85 (2012).

(22) X. Xu, Y. Hou, X. Yin, L. Bao, A. Tang, L. Song, F. Li, S. Tsang, **K. Wu**, , *et al.*. Single-Cell Exome Sequencing Reveals Single-Nucleotide Mutation Characteristics of a Kidney Tumor. ***Cell***, 148: 886-95 (2012)

主持或参加科研项目（课题）:

1. 国家自然科学基金委员会，重大研究计划，92259301，胶质瘤演进过程中异质性和免疫微环境可视化智慧诊断，2023-01-01 至 2026-12-31，350 万元，在研，参与
2. 浙江省“尖兵”“领雁”研发攻关计划，2023C03103，单细胞代谢标志物分析仪与试剂研发，2023-01-01 至 2025-12-31，300 万元，在研，子课题负责人
3. 广东省重点领域研发计划，2019B020229002，结直肠癌个体化治疗靶标发现和精准用药临床研究，2019/3-2022/3，500 万，结题，课题骨干
4. 国家重点研发计划“精准医学”专项，2016YFC0905500，肺癌的诊疗规范及应用方案的精准化研究，2016/01-2019/12，670 万，结题，课题骨干
5. 国家重点研发计划“精准医学”专项，2016YFC0904600，以生物组学特征与多模态功能影像为基础的多线束精准放疗方案研究，2016/01-2018/12，1200 万，已结题，课题骨干
6. 深圳市科技计划应用示范项目，KJYY20170412153658082，肿瘤高通量测序基因检测诊疗的应用示范，2017/06-2019/06，300 万元，已结题，主持
7. 深圳市科技计划技术开发项目，CXZZ20150330171838997，基于高通量测序的单细胞分析技术的研发及应用，2015/08-2017/08，200 万元，已结题，主持
8. 深圳市科技计划应用示范项目，KJYY20140530141443717，深圳市乳腺癌高发人群基因筛查技术应用示范，2014/12-2016/12，500 万元，已结题，参与
9. 国家高技术研究发展计划（863 计划），2012AA02A201，与重要疾病相关的基因组学和生物信息学技术，2012/01-2015/12，3167 万，已结题，课题骨干
10. 国家高技术研究发展计划（863 计划），2009AA022707，肺癌和糖尿病全基因遗传变异分析和新遗传标志物的筛选，2009/12-2011/12，1400 万元，已结题，参与