

Ruoqing Feng

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EDUCATIONAL BACKGROUND & WORKING EXPERIENCE

German Center for Neurodegenerative Diseases (LMU-GSN)

PhD Student in the lab of Prof. Mikael Simons.

03/2023 – Present

Shenzhen Institute of Advanced Technology, Chinese Academy of Sciences

Research Assistant in Bioinformatics

06/2022 – 02/2023

Southern University of Science and Technology

Master of Science in Biology

09/2019 – 06/2022

Southern University of Science and Technology

Bachelor of Science in Bioinformatics

09/2015 – 06/2019

PUBLICATIONS

Feng, R., Spieth, L., Liu, L., Simons, M., et al. Single-cell spatial transcriptomic profiling defines a pathogenic inflammatory niche in chronic active multiple sclerosis lesions. *Immunity*. 2025 Dec 9;58(12):2989-3005.e10. (first author)

Wu, Z*, Wang, Z*, Wang, H*, **Feng, R***, Ginhoux, F., Li, H., et al. Spatial-temporal dynamics of human macrophage specification during development. *Cell*. 2022. Volume 186, Issue 20, 4454 - 4471.e19. (co-first author)

Groh, J., **Feng, Ruo.**, Simons, M., et al. Microglia activation orchestrates CXCL10-mediated CD8+ T cell recruitment to promote aging-related white matter degeneration. *Nature Neuroscience*. 2025 Jun;28(6):1160-1173.

Kedia, S., Ji, H., **Feng, R.**, Simons, M., et al. T cell mediated microglia activation triggers myelin pathology in a model of amyloidosis. *Nature Neuroscience*. 2024 Aug;27(8):1468-1474.

Zhao, Y., Sun, J., Li, Y., Li, Z., Xie, Y., **Feng, R.**, Zhao, J., & Hu, Y. (2021). The strand-biased transcription of SARS-CoV-2 and unbalanced inhibition by remdesivir. *IScience*, 24(8), 102857.

RESEARCH EXPERIENCE

A single cell resolved spatial transcriptomics atlas of human multiple sclerosis lesion

11/2020 – Present

- High-resolution spatial transcriptomics reveals hallmarks of chronic active MS lesions
- CD8+ T cell niches are enriched with lipid-associated, inflamed microglia
- IFN- γ promotes the storage of myelin-derived cholesterol in microglia
- Inhibition of cholesterol efflux in microglia drives inflammatory processes in EAE

A single cell RNA-seq atlas of the human developing immune system

11/2020 – 10/2023

- Created a spatial-temporally resolved scRNA-seq atlas (29w+ cells) of the developing human immune system, with a focused interrogation of macrophages
- Characterized the proangiogenic macrophage subtype, and demonstrated that this subtype promotes angiogenesis, resides in the perivascular space across prenatal organs, and is of yolk-sac origin
- Found microglia was outside the central nervous system, in the fetal epidermis. Microglia colonize the developing epidermis prior to Langerhans cells and then gradually dismiss

SKILLS

NGS data preparation; alignment; counting; differential expression analysis & enrichment analysis, scRNA-seq/scATAC-seq data preparation; single cell clustering (Seurat, scanpy & metacell); annotation; TF analysis; velocity analysis; trajectory analysis (monocle, dynonverse, etc.).