



# Ken Lau, PhD

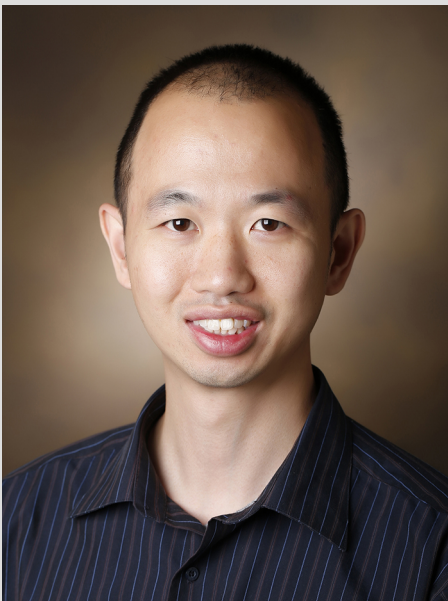
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@KenLauLab



## Biosketch

Ken was born in Hong Kong and grew up in Toronto, Canada. He was the first student in the Proteomics and Bioinformatics graduate program at the University of Toronto. He joined the faculty at Vanderbilt after a successful four-and-a-half-year postdoctoral fellow at MIT and Massachusetts General Hospital, a Harvard teaching hospital. Ken received a Damon Runyon Research Fellowship, as well as an Innovator Award from the American Association of Cancer Research.

## Key Publications

"Unsupervised trajectory analysis of single-cell RNA-seq and imaging data reveals alternative tuft cell origins in the gut," *Cell Systems*, 6(1), 37-51, 2018

"Impaired coordination between signaling pathways is revealed in human colorectal cancer using single-cell mass cytometry of archival tissue blocks," *Science Signaling*, 9(449), rs11, 2016

"Cytometry-based single cell analysis of intact epithelial signaling reveals MAPK activation divergent from TNF- $\alpha$ -induced apoptosis *in vivo*," *Molecular Systems Biology*, 11(10):835, 2015

## "Big data modeling of cell-microbe social networks"

The Lau lab considers every one of the 30 plus trillion cells in the body to be unique, thus, **utilizes state-of-the art technologies to profile tissues at the single-cell resolution**. Resulting "big data" consisting of **thousands of data points and dimensions** are analyzed by **data science-driven computational techniques** to determine:

- how altering different cell types in the gut influences the **cell-microbiome ecosystem of Inflammatory Bowel Disease**
- how interactions between the gut microbiome and epithelial cells contribute to **benign colonic polyps progressing to colon cancer**
- how the **origins of colon cancer stem cells** affect the progression of cancer and responses to therapies
- how different **mutations affecting the same pathway** can lead to different outcomes depending on the cellular ecosystem

