# Mengshu Xu, PhD

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Principal Scientist, Computational Biology
Experience: 7 years of industry experience in drug discovery
Education: PhD in Molecular Genetics & Postdoctoral training in Bioinformatics and Cancer Biology

As Bioinformatics Lead for Immuno-Oncology and Oncology projects, my duties include target discovery, comprehensive target gene/protein expression analyses, multi-omics data integration and developing biomarkers. I have significant expertise in single-cell RNA seq and specialized methodologies like TCR & CITE scRNA seq. I excel at picking up new methodologies and bioinformatics workflows, and consistently delivering impactful results under tight deadlines. My major strength comes from my bench science background, which enables me to design rigorous and feasible experiments, extract biologically meaningful insights from data, and effectively communicate results to non-computational audiences

## COMPUTATIONAL BIOLOGY EXPERTISE

- Programming: R (Advanced), Python/Perl (Intermediate), Unix/Bash environments
- Predictive modeling and Machine Learning (Professional development, DataCamp and Rstudio::conf 2019)
- RNA Analysis: Bulk/scRNA-seq (DESeq2, edgeR, Seurat, Monocle, Scanpy), cell annotation, pseudotime analysis
- DNA genomics: NGS pipelines, SNV, SV, Indel and CNA calling from tumor and germline samples
- Applications: Target ID, MOA elucidation, biomarker development, ADC/TAA identification
- Resources: Cancer genomics (TCGA, GENIE, CPTAC, CCLE, GTEx, 1000 Genomes, dbSNP, HapMap)
- Infrastructure: Cloud computing (AWS, SevenBridges, DNANexus, Slurm, Nextflow)

## WORK EXPERIENCE

### Consultant, Computational Biologist

**Adept Computation Biology** | San Antonio, TX | June 2025 –

- Provide specialized computational biology consulting services to biotechnology companies, delivering data-driven insights to support drug discovery and development initiatives
- Key Clients include:
  K2 Therapeutics | San Francisco, CA
  Immunome Inc | Bothell, WA
  Synthex Labs | San Francisco, CA
  Stealth-mode start-up | New York, NY

### Principal Scientist, Bioinformatics

**Gilead Sciences** | Foster City, CA | 2021 – May 2025, Manager: Min Wang

- Led bioinformatics for 2 oncology projects from research through IND filing and clinical trials, respectively
- Served as bioinformatics lead for 30+ immune oncology and 4 tumor intrinsic pipeline projects, demonstrating strong multitasking and collaboration skills
- Uncovered key immunogenicity mechanisms through MHC-I peptide Mass spec sequencing analysis, revealing crucial insights into tumor cell neo-antigen presentation with findings slated for publication
- Developed a standardized annotation framework for scRNA tumor immune datasets and supervised annotation efforts, creating high-value internal data resources now utilized daily across research teams
- Integrated mouse syngeneic model scRNA data into a comprehensive reference tool, accelerating cross-study comparisons and rational model selection based on pathway activation signatures and markers
- Published and presented research at SITC on CD47 expression patterns across cancer types, establishing important correlations with phagocytic macrophage content in the tumor microenvironment

### Computational Scientist II (2020-2021) | Computational Scientist I (2018-2020)

**RAPT Therapeutics** (Formerly FLX Bio) | South San Francisco, CA | Manager: Gene Cutler

- Led computational biology strategy for three preclinical immune-oncology projects and a key academic collaboration

- Implemented data-driven in vivo model selection: leveraged RNA expression profiles from syngeneic tumor models to successfully predict responder models, which were confirmed through subsequent in vivo experiments
- Established the 10X Chromium single-cell RNA sequencing platform for internal use at RAPT, incorporating advanced CITE-seq and sample hashing methodologies and trained bench scientists on protocol execution
- Conducted collaborative research with Dr. James Talmadge's lab at U Nebraska, implementing scRNA sequencing by setting up the 10X platform on-site. Profiled cancer patient immune cells and characterized immune suppressive myeloid cell populations
- Initiated and directed two strategic biomarker discovery project across RAPT disease areas (inflammation and IO), mentoring a Computational Biology Intern to successful project execution and career advancement

## WORK EXPERIENCE CONTINUED…

### Postdoctoral Fellow

**University of California, San Francisco** | 2015 – 2018 | Supervisor: Iwei Yeh

Identified *SPRED1* (RAS negative regulator) mutations in melanoma through genomic analysis of clinical samples, expanding the known melanoma pathogenic mutation landscape. (Co-first author, *Science* 2018)

### Postdoctoral Fellow

**University of Toronto** | Toronto, Canada | 2014 – 2015 | Supervisor: Marc Meneghini

Studied the role of oncogene and chromatin factor, JARID1, in cancer metabolism (2nd author, *Scientific Reports* 2016)

## EDUCATION

### PhD in Molecular Genetics, University of Toronto 2007-2014

Supervisor: Marc Meneghini

Thesis: Developmental Control Throughout the Budding Yeast Life Cycle by Jhd2, a JARID family Histone H3 Lysine-4 Demethylase. (First author, *Developmental Cell* 2012)

### Honours Bachelor of Science, with High Distinction 2003-2007

Specialization in Molecular Genetics and Microbiology, University of Toronto, Canada

## PUBLICATIONS

1. Nick van Buuren*, Mengshu Xu*, et al. 2025. CD47 Expression Correlates with Phagocytic Tumor-Associated Macrophage abundance in Solid Tumors. *Under Review at JITC*
2. Jeffrey Jackson, … Mengshu Xu et al. 2022. Potent GCN2 Inhibitor Capable of Reversing MDSC-Driven T Cell Suppression Demonstrates In Vivo Efficacy as a Single Agent and in Combination with Anti-Angiogenesis Therapy. 65(19). *J Med Chem*
3. Aparna Jorapur, Lisa Marshall, Scott Jacobson, Mengshu Xu et al. 2022. EBV+ tumors exploit tumor cell-intrinsic and -extrinsic mechanisms to produce regulatory T cell-recruiting chemokines CCL17 and CCL22. 18(1): e1010200. *PLoS Pathogens*
4. Iwei Yeh, Eric Jorgenson, Ling Shen, Mengshu Xu et al. 2019. Targeted Genomic Profiling of Acral Melanoma. 111(10):1068-1077. *J Natl Cancer Inst*
5. Julian Ablain*, Mengshu Xu* et al. 2018. Human tumor genomics and zebrafish modeling identify SPRED1 loss as a driver of mucosal melanoma.362(6418):eaau6509. *Science*
6. Joshua Webster, … , Mengshu Xu et al. 2018. The tumor suppressor BAP1 cooperates with BRAFV600E to promote tumor formation in cutaneous melanoma.32(2).*Pigment Cell & Melanoma Research*
7. Maria Soloveychik, Mengshu Xu, et al. 2016. Mitochondrial control through nutritionally regulated global histone H3 lysine-4 demethylation.6(1):37942. *Scientific Reports*
8. Ryan Schott, Johannes Müller, Clement Yang, Nihar Bhattacharyya, Natalie Chan, Mengshu Xu et al. 2016. Evolutionary transformation of rod photoreceptors in the all-cone retina of a diurnal garter snake.113(2). *PNAS*
9. Mengshu Xu et al. 2012. Timing of transcriptional quiescence during gametogenesis is controlled by global histone H3K4 demethylation.23(5). *Developmental Cell*

Underlined: First Author | *authors contributed equally to the work

## CITIZENSHIP

US & Canadian dual Citizen