Curriculum Vitae

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Executive Summary

- Bioinformatics, Computational Biology, and Data Science leader with 15 years of experience in translational research, clinical studies, and product development.
- Specialized in multi-omics data analysis, biomarker discovery, NGS and non-NGS pipelines, and AI/ML applications in precision medicine.
- Experienced in leading cross-functional teams and collaborating with pharma, biotech, and academia.
- Providing bioinformatics and data analysis consulting services via archerzbio.com.

Professional Experience

Self-Employed Consultant | ArcherzBio | Foster City, CA | 2024–Present
• Provide consulting services in bioinformatics method development and scientific data analysis for translational and clinical studies.

Serimmune Inc. | Associate Director / Sr. Manager, Bioinformatics and Data Science | 2019–2024
• Led 30+ antibody biomarker discovery projects across infectious disease, autoimmune disorders, cancer, and vaccines.
• Led epitope profiling for Moderna COVID-19 vaccine and Long COVID studies.
• Built scalable pipelines and data warehouse on Google Cloud.
• Contributed to multiple high-impact publications (Nature, Frontiers in Immunology, Clinical Cancer Research, Communications Biology, etc).

Illumina Inc. | Manager / Scientist, Bioinformatics | 2014–2019
• Bioinformatics lead for BaseSpace™ Cohort Analyzer and Correlation Engine integrating genomics, transcriptomics, proteomics, and clinical data.
• Migrated pipelines to AWS, reducing costs and improving scalability.
• Validated BaseSpace™ Variant Interpreter from pre-alpha to beta release.

NextBio Inc. (Acquired by Illumina Inc.) | Bioinformatics Scientist | 2012–2013
• Developed pipelines for gene expression, CNV, methylation, and GWAS datasets.
• Standardized and normalized large-scale drug response and GWAS data for translational research.

University of Cincinnati / Cincinnati Children's Hospital | Graduate Research Assistant | 2007–2012

- Knowledge discovery and pattern recognition in multi-omics molecular data.
- Molecular network analysis and biomarker discovery.

Education

Stanford Graduate School of Business | LEAD Corporate Innovation & Leadership (2025)
University of Cincinnati | Ph.D. Computer Science & Engineering (2012)
Huazhong University of Science & Technology | B.E. Electronics & Information Engineering (2006)

Publications

Journal Articles

- Bastos VC, Greene KA, Tabachnikova A, Bhattacharjee B, Sjögren P, Bertilson B, Reifert J, Zhang M, Kamath K, Shon J. (2025). Cerebrospinal fluid immune phenotyping reveals distinct immunotypes of myalgic encephalomyelitis/chronic fatigue syndrome. The Journal of Immunology. vkaf087.
- Girard B, Baum-Jones E, Best RL, Campbell TW, Coupart J, Dangerfield K, Dhal A, Jhatro M, Martinez B, Reifert J, Zhang M, et al. (2024). Profiling antibody epitopes induced by mRNA-1273 vaccination and boosters. Frontiers in Immunology. 15:1285278.
- Klein J, Wood J, Jaycox JR, Dhodapkar RM, Lu P, Gehlhausen JR, Tabachnikova A, Greene K, Tabacof L, Malik AA, Zhang M, et al. (2023). Distinguishing features of long COVID identified through immune profiling. Nature. 623(7985):139-148.
- Hoerner CR, Jhatro M, Waitz R, Kamath K, Zhang M, Dhal A, Shon J, Fan AC. (2022). Utilizing the autoantibody immune response to tumor antigens for kidney cancer early detection. ASCO Annual Meeting Proceedings.
- Dorff T, Hirasawa Y, Acoba J, Pagano I, Tamura D, Pal S, Zhang M, Waitz R, Dhal A, Haynes W, et al. (2021). Phase Ib study of patients with metastatic castrate-resistant prostate cancer treated with sequencing regimens of atezolizumab and sipuleucel-T. Journal for Immunotherapy of Cancer. 9(8):e002931.
- Haynes WA, Kamath K, Bozekowski J, Baum-Jones E, Campbell M, Casanovas-Massana A, Zhang M, et al. (2021). High-resolution epitope mapping and characterization of SARS-CoV-2 antibodies in large cohorts. Communications Biology. 4:1317.
- Chen WS, Haynes WA, Waitz R, Kamath K, Vega-Crespo A, Shrestha R, Zhang M, et al. (2020). Autoantibody landscape in patients with advanced prostate cancer. Clinical Cancer Research. 26(23):6204-6214.
- Green JV, Orsborn KI, Zhang M, Tan QKG, Greis KD, Porollo A, Andes DR, Lu LJ, Hostetter MK. (2013). Heparin-binding motifs and biofilm formation by Candida albicans. Journal of Infectious Diseases. 208(10):1695-1704.

- Zhang M, Su S, Bhatnagar RK, Hassett DJ, Lu LJ. (2012). Prediction and analysis of the protein interactome in Pseudomonas aeruginosa. PLoS One. 7(7):e41202.
- Feng X, Krishnan K, Richie DL, Aimanianda V, Hartl L, Grahl N, Powers-Fletcher MV, Zhang M, Fuller KK, Nierman WC, et al. (2011). HacA-independent functions of ER stress sensor IreA in Aspergillus fumigatus. PLoS Pathogens. 7(10):e1002330.
- Ren J, Jegga AG, Zhang M, Deng J, Liu J, Gordon CB, Aronow BJ, Lu LJ, Zhang B, Ma J. (2011). A Drosophila model of SCA17 reveals RBP-J/Su(H) role. Human Molecular Genetics. 20(17):3424-3436.
- Zhang M, Zhu C, Jacomy A, Lu LJ, Jegga AG. (2011). The orphan disease networks. AJHG. 88(6):755-766.
- Sardana D, Zhu C, Zhang M, Gudivada RC, Yang L, Jegga AG. (2011). Drug repositioning for orphan diseases. Brief Bioinformatics. 12(4):346-356.
- Deng J, Deng L, Su S, Zhang M, Lin X, Wei L, Minai A, Hassett DJ, Lu LJ. (2011). Predictability of essential genes across organisms. Nucleic Acids Research. 39(3):795-807.
- Zhang M, Lu LJ. (2010). Validity of network analysis by protein stratification. BMC Bioinformatics. 11:466.
- Xu Y, Zhang M, Wang Y, Kadambi P, Dave V, Lu LJ, Whitsett J. (2010). Mapping transcriptional networks controlling surfactant homeostasis. BMC Genomics. 11:451.
- Zhu HY, Wang SW, Martin LJ, Liu L, Li YH, Chen R, Wang L, Zhang M, Benson DW. (2009). Role of mitochondrial genome in hypertension. Eur J Hum Genet. 17(11):1501-1506.
- Zhu HY, Wang SW, Liu L, Chen R, Wang L, Gong XL, Zhang M. (2009). Genetic variants in mitochondrial tRNA genes linked to hypertension. Clin Chim Acta. 410(1-2):64-69.

Book Chapters

- Zhang M, Deng J, Tan L, Chen Y, Lu LJ. (2012). Network Analysis in Translational Research. In: Pediatric Biomedical Informatics. Springer.
- Zhang M, Deng J, Fang C, Zhang X, Lu LJ. (2010). Molecular network analysis and applications. In: Knowledge-Based Bioinformatics. Wiley.

Conference Proceedings

- Zhang M, Fang CV, Xu Y, Bhatnagar RK, Lu LJ. (2010). An integrative scoring approach to identify transcriptional regulations controlling lung surfactant homeostasis. IEEE ICDM Workshops:787-792.
- Fang CV, Zhang M, Ralescu AL, Lu LJ. (2010). Curve Profiling Feature: novel compact representation for Drosophila embryonic gene expression pattern mining. IEEE ICDM Workshops:695-702.

Encyclopedia Entries

- Zhang M, Lu LJ. (2013). Biological applications of network modules. In: Encyclopedia of Systems Biology. Springer.
- Zhang M, Lu LJ. (2013). Modules in networks: algorithms and methods. In: Encyclopedia of Systems Biology. Springer.

- Lu LJ, Zhang M. (2013). Protein-Protein Interaction Networks. In: Encyclopedia of Systems Biology. Springer.
- Lu LJ, Zhang M. (2013). Network Clustering. In: Encyclopedia of Systems Biology. Springer.
- Lu LJ, Zhang M. (2013). Heuristic Search. In: Encyclopedia of Systems Biology. Springer.
- Lu LJ, Zhang M. (2013). Edge betweenness centrality. In: Encyclopedia of Systems Biology. Springer.
- Lu LJ, Zhang M. (2013). Interactome. In: Encyclopedia of Systems Biology. Springer.