

Alper Kucukural, PhD

AI · DATA SCIENCE · COMPUTATIONAL BIOLOGY LEADER

Co-founder & CTO of Via Scientific and Associate Professor at UMass Chan Medical School. Builder of enterprise multi-omics and AI platforms in daily use by thousands of scientists worldwide.

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● PROFESSIONAL PROFILE

Senior technology leader with 10+ years across **venture-backed biotech and academic medicine**. I build reproducible AI and analytics platforms used in biomedical research and biopharma decision-making. Co-founder and CTO of Via Scientific (Cambridge, MA). Associate Professor at UMass Chan Medical School. Author or co-author of widely used open-source tools including I-TASSER, DolphinNext, DEBrowser, GUIDEseq, and ASPeak, with **13,500+ citations across 35+ publications**. First-author on DolphinNext, DEBrowser, and ASPeak; co-author on studies published in Nature, Cell, Science, Nature Protocols, Nature Communications, and Nature Structural and Molecular Biology.

● QUANTIFIED IMPACT

13.5K+ scholar citations	h-26 h-index · i10 = 33	35+ peer-reviewed publications	7.8K+ citations on I-TASSER paper alone
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● PROFESSIONAL EXPERIENCE

Co-founder & Chief Technology Officer Via Scientific, Inc., Cambridge, MA

2023 to Present

Lead technology strategy, architecture, and engineering for **Via Foundry**, the multi-omics and AI analytics platform commercialized from UMass Chan. Venture-backed, with institutional investors and advisors from pharma and enterprise AI.

- Defined the AI/ML platform strategy across data ingestion, pipeline orchestration, model training, deployment, and drift monitoring. The reference architecture from that work is what the team ships against today.
- Recruited and led a cross-functional team of AI engineers, software engineers, and computational scientists; shaped technical standards, the hiring bar, and roadmap cadence.
- Evaluated and integrated third-party AI solutions (LLM providers, vector stores, agent frameworks, cloud AI services) against in-house builds on technical, regulatory, and security merit.
- Owned reliability, reproducibility, and security for a customer-facing platform supporting regulated biomedical workflows; versioned, auditable pipelines by design.
- Partnered with investors and advisors (Melissa J. Moore, former CSO of Moderna; Rob Hickey, former EVP Engineering at DataRobot; Shah Nawaz, former VP Digital Transformation at Regeneron) on platform strategy and business execution.

Associate Professor, Program in Molecular Medicine UMass Chan Medical School, Worcester, MA

2020 to Present

Faculty in the Program in Molecular Medicine and Department of Genomics and Computational Biology. Research on AI for multi-omics, reproducible analytics, and RNA therapeutics.

- Co-directed the UMass Chan Bioinformatics Core supporting **80+ labs and 240+ scientists**; set standards for reproducibility, usability, and reliability across institutional workflows.
- Delivered institution-scale platforms (DolphinNext, DEBrowser, GUIDEseq) that became shared infrastructure and the technical basis for Via Foundry.
- Published as senior author on DolphinNext (*BMC Genomics*, 2020) and on the ABRF Functional Annotation Routines paper (*J. Biomolecular Techniques*, 2023).
- Designed and led NGS and bioinformatics training programs and bootcamps that scaled institutional capability.
- Invited speaker, session chair, and reviewer across ABRF, Nextflow, OSU RNA Biology, and editorial panels including BMC Genomics.

Assistant Professor & Bioinformatics Core Lead UMass Chan Medical School · Worcester, MA

Feb 2015 to 2020

Promoted into the faculty track. Designed and built the NGS analytics stack that later became Via Foundry; standardized RNA-Seq, scRNA-Seq, ChIP-Seq, ATAC-Seq, and GATK variant-calling pipelines, and established reproducibility practices across the institution.

Bioinformatician III

Jun 2013 to Jan 2015

UMass Chan Medical School · Bioinformatics Core · Worcester, MA

Built the reusable pipeline platform and training programs at the Bioinformatics Core that supported hundreds of concurrent researchers across UMass Medical School.

- Designed and implemented reusable, robust, production-grade bioinformatics pipelines for NGS, microarray, genomics, proteomics, and chemogenomics data supporting hundreds of concurrent users.
- Integrated computational methods and pipelines with high-performance computing clusters; designed hardware configurations to optimize software performance and scalability.

- Partnered directly with PIs on research projects, including scoping the collaboration, researching the underlying science, implementing the appropriate bioinformatics solutions, and delivering to project timelines.
- Installed, maintained, and configured sequencing data analysis interfaces and portals including Galaxy, GenePattern, and Genome Space for the UMass Medical School community.
- Developed rapid prototypes, custom scripts, and novel algorithms with integrated visualization applications where existing software packages were not available or adequate.
- Built custom databases and web portals for managing raw and processed experimental data.
- Documented computational analysis procedures and authored summary reports suitable for inclusion in manuscripts and grant applications.
- Led bioinformatics training and workshops for analysis pipelines and in-house software applications; coordinated with biostatisticians, IT, and interdepartmental project teams.
- Participated in oral presentation of project findings and abstracts, including periodic project status meetings and final project deliverables.

Bioinformatician

Aug 2009 to Jun 2013

UMass Chan Medical School · Moore and Zamore Labs · Worcester, MA

Worked on post-transcriptional gene regulation in eukaryotes via RNA mechanisms under the supervision of Prof. Melissa J. Moore and Prof. Phillip D. Zamore. Built the NGS software and algorithms that later became DolphinNext, DEBrowser, and ASPeak.

- Developed bioinformatics software to analyze data from SOLEXA and SOLID next-generation sequencing platforms, including analysis and visualization tooling.
- Designed algorithms to eliminate noise in sequencing data and call peaks robustly; accounted for noise sources including experimental method and genome-mappability bias. Foundational work for ASPeak (*Bioinformatics*, 2013).
- Engineered custom per-project user interfaces so scientists could easily reach, summarize, analyze, and visualize data with different algorithms and approaches.
- Installed and maintained UCSC Genome Browser mirrors; built data-conversion pipelines for UCSC and Galaxy formats (wiggle plots, BED, SNP visualization and analysis).
- Developed pattern-search algorithms using machine-learning methods.

Postdoctoral Fellow, Computational Structural Biology

2008 to 2009

University of Kansas · Yang Zhang Lab · Lawrence, KS

Co-developed **I-TASSER**, the unified platform for automated protein structure and function prediction. Co-author on the *Nature Protocols* (2010) method paper, cited **7,800+ times** and still a reference in computational structural biology and early drug-design workflows.

MAJOR PLATFORMS & TOOLS

Via Foundry

Enterprise multi-omics & AI analytics platform. Exclusively licensed from UMass Chan. Serves biotech, pharma, and academic research teams worldwide.

DolphinNext

Distributed pipeline platform for high-throughput genomics. GUI-based Nextflow authoring, reproducible execution, HPC and cloud. *BMC Genomics*, 2020.

DEBrowser

Interactive differential expression analytics, Bioconductor-distributed. First-author method paper. *BMC Genomics*, 2019.

I-TASSER

Unified automated protein structure and function prediction. Co-author. *Nature Protocols*, 2010 (7,800+ citations).

GUIDEseq

Bioconductor package for CRISPR-Cas off-target analysis from GUIDE-Seq data. *BMC Genomics*, 2017.

ASPeak

Abundance-sensitive peak-detection algorithm for RIP-Seq. First author. *Bioinformatics*, 2013.

TECHNICAL STACK

AI / LLMS	Claude · Claude Code · GPT · Gemini · Vertex · Llama · Generative AI · Agentic workflows · Machine Learning · Deep Learning
ML FRAMEWORKS	PyTorch · scikit-learn · MLflow · Hugging Face · LangChain
DEVELOPER TOOLING	CLI · SDK · MCP server development · VSCode extension · Claude Code plugin development
LANGUAGES & DATA	Python · Perl · R · Shiny · SQL · TypeScript · Node.js · Pandas · Nextflow · Snakemake · Prisma · PostgreSQL · MongoDB · Zarr · TileDB
INFRASTRUCTURE	Linux · AWS · Azure OpenAI · Databricks · Docker · Kubernetes · Apache · Nginx
DELIVERY	Agile / SDLC · JIRA · Confluence · GitHub · CI/CD · MLOps
COLLABORATION & UX	UX/UI sensibility · executive stakeholder communication

EDUCATION

PhD · Biological Sciences and Bioengineering

Sabanci University, Istanbul · 2004 to 2009. Dissertation on graph-theoretic discrimination of native protein folds.

MS · Systems Analysis (Engineering Management)

Istanbul Technical University · 2000 to 2004.

BS · Mathematics Engineering

Istanbul Technical University · 1995 to 2000.

Postdoc · Computational Structural Biology

University of Kansas · Yang Zhang Lab · 2008 to 2009.

● INVITED TALKS & SERVICE

- ♦ **Center for RNA Biology Seminar, The Ohio State University.** "Via Foundry: Accelerating Scientific Discovery through Cutting-Edge Multi-Omics Solutions." Co-presented with Melissa J. Moore · May 2024.
- ♦ **Nextflow Camp.** Invited speaker on DolphinNext · 2019.
- ♦ **ABRF Genomic Bioinformatics Research Group (GBIRG).** Member; co-author on the 2023 ABRF functional annotation study.
- ♦ **Workflow Session Chair, ABRF Annual Meeting** · 2023.
- ♦ **Keynote · Penn State Life Sciences Symposium** · 2026 (invited).
- ♦ Editorial and peer review for BMC Genomics and other life-sciences journals.

● SELECTED PEER-REVIEWED PUBLICATIONS

1. tRNA-derived RNA processing in sperm transmits non-genetically inherited phenotypes to offspring in *C. elegans*. *Nature Communications*, 2026 (online ahead of print). DOI: 10.1038/s41467-026-70029-7.
2. Worm Perturb-Seq: massively parallel whole-animal RNAi and RNA-seq (preprint). *bioRxiv*, 2025. DOI: 10.1101/2025.02.02.636107.
3. CRISPR-induced exon skipping of beta-catenin reveals tumorigenic mutants driving distinct subtypes of liver cancer. *Journal of Pathology*, 2023, 259(4), 415-427.
4. Functional Annotation Routines Used by ABRF Bioinformatics Core Facilities. *Journal of Biomolecular Techniques*, 2023, 34(1).
5. AAV-delivered suppressor tRNA overcomes a nonsense mutation in mice. *Nature*, 2022, 604, 343-348.
6. A Translational Model for Venous Thromboembolism: MicroRNA Expression in Hibernating Black Bears. *Journal of Surgical Research*, 2021, 257, 203-212.
7. Reduced Neurog3 Gene Dosage Shifts Enteroendocrine Progenitor Towards Goblet Cell Lineage in the Mouse Intestine. *Cellular and Molecular Gastroenterology and Hepatology*, 2021, 11, 433-448.
8. Dietary suppression of MHC class II expression in intestinal epithelial cells enhances intestinal tumorigenesis. *Cell Stem Cell*, 2021, 28, 1922-1935.
9. Type I IFN-Driven Immune Cell Dysregulation in Rat Autoimmune Diabetes. *ImmunoHorizons*, 2021, 5, 855-869.
10. Evolutionarily conserved pachytene piRNA loci are highly divergent among modern humans. *Nature Ecology and Evolution*, 2020, 4, 156-168.
11. HIV-1-induced cytokines deplete homeostatic innate lymphoid cells and expand TCF7-dependent memory NK cells. *Nature Immunology*, 2020, 21, 274-286.
12. Recovery of viable endocrine-specific cells and transcriptomes from human pancreatic islet-engrafted mice. *FASEB Journal*, 2020, 34, 1901-1911.
13. Genomic Characterization of Endothelial Enhancers Reveals a Multifunctional Role for NR2F2 in Regulation of Arteriovenous Gene Expression. *Circulation Research*, 2020, 126, 875-888.
14. **DolphinNext: a distributed data processing platform for high-throughput genomics.** *BMC Genomics*, 2020, 21, 310. (Senior author)
15. An atlas of cell types in the mouse epididymis and vas deferens. *eLife*, 2020, 9.
16. An improved zebrafish transcriptome annotation for sensitive and comprehensive detection of cell type-specific genes. *eLife*, 2020, 9.
17. Bioinformatics Core Survey Highlights the Challenges Facing Data Analysis Facilities. *Journal of Biomolecular Techniques*, 2020, 31.
18. Diverse repertoire of human adipocyte subtypes develops from transcriptionally distinct mesenchymal progenitor cells. *PNAS*, 2019, 116, 17970-17979.
19. **DEBrowser: interactive differential expression analysis and visualization tool for count data.** *BMC Genomics*, 2019, 20, 6. (First author)
20. CRISPR-SONIC: targeted somatic oncogene knock-in enables rapid *in vivo* cancer modeling. *Genome Medicine*, 2019, 11, 21.
21. HLA Class II Antigen Processing and Presentation Pathway Components Demonstrated by Transcriptome and Protein Analyses of Islet β -Cells From Donors With Type 1 Diabetes. *Diabetes*, 2019, 68, 988-1001.
22. Comparative Analysis of Immune Cells Reveals a Conserved Regulatory Lexicon. *Cell Systems*, 2018, 6, 381-394.
23. GUIDEseq: a bioconductor package to analyze GUIDE-Seq datasets for CRISPR-Cas nucleases. *BMC Genomics*, 2017, 18, 379.
24. Ebola Virus Glycoprotein with Increased Infectivity Dominated the 2013-2016 Epidemic. *Cell*, 2016, 167, 1088-1098.
25. Platelet functional and transcriptional changes induced by intralipid infusion. *Thrombosis and Haemostasis*, 2016, 115, 1147-1156.
26. Comparison of RNA isolation and associated methods for extracellular RNA detection by high-throughput quantitative polymerase chain reaction. *Analytical Biochemistry*, 2016, 501, 66-74.
27. Genetic and Epigenetic Variation, but Not Diet, Shape the Sperm Methylome. *Developmental Cell*, 2015, 35, 750-758.
28. Simultaneous generation of many RNA-seq libraries in a single reaction. *Nature Methods*, 2015, 12, 323-325.
29. Novel Observations From Next-Generation RNA Sequencing of Highly Purified Human Adult and Fetal Islet Cell Subsets. *Diabetes*, 2015, 64, 3172-3181.
30. Staufen1 senses overall transcript secondary structure to regulate translation. *Nature Structural and Molecular Biology*, 2014, 21, 26-35.
31. **ASPeak: an abundance-sensitive peak detection algorithm for RIP-Seq.** *Bioinformatics*, 2013, 29, 2485-2486. (First author)
32. The Cellular EJC Interactome Reveals Higher-Order mRNP Structure and an EJC-SR Protein Nexus. *Cell*, 2012, 151, 750-764.
33. Identification of Neuronal RNA Targets of TDP-43-containing Ribonucleoprotein Complexes. *Journal of Biological Chemistry*, 2011, 286, 1204-1215.
34. **I-TASSER: a unified platform for automated protein structure and function prediction.** *Nature Protocols*, 2010, 5, 725-738. (Co-author · 7,800+ citations)
35. mRNAs with a complex: The long-term consequences of a nuclear upbringing. *FASEB Journal*, 2010, 24, 68.1.