Christian K. Roy, PhD

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- Greater Boston Area, MA
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- Website
- LinkedIn
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With over 20 years of expertise in pharmaceuticals, biotech, and academic research, I specialize in leveraging large-scale datasets to optimize clinical trial insights, execution, and outcomes. Thriving in collaborative environments, my strategic leadership and technical proficiency have consistently driven innovation across global organizations while delivering high-quality patient outcomes. As a results-driven professional with a deep passion for data science and translational research, I am committed to advancing data-driven solutions that enable informed decision-making and foster impactful collaborative environments.

Core Competencies

- RNA Biology, Oncology, Immunotherapy
- Multi-Omics Data Integration
- Translational Biomarker Development
- Computational Oncology & Cell/Gene Therapy
- Cloud Infrastructure & Pipeline Automation (AWS, Nextflow)
- Predictive Modeling & Data Visualization
- Team Leadership & Cross-Functional Collaboration
- Clinical Trial Data Management & EDC Tools
- Scientific Communication & Stakeholder Engagement

Experience

Affini-T Therapeutics (Watertown, MA)

Associate Director: Precision and Translational Medicine and Computational Biology
December 2021 – Present

- Led multidisciplinary initiatives at a cell and gene therapy start-up, successfully driving translational and computational strategies supporting AFNT-211, a multi-site single-arm TCR-T clinical trial in solid tumors.
- Led a diverse Computational team of 1 FTE, 3 contractors, 2 associated Discovery scientists, 2 academic consultants, and multiple vendors.
- Integrated and harmonized complex multi-source clinical, translational, and manufacturing data types, including EDC, CMC, ctDNA, PK/PD, flow cytometry, scRNA-seq, and cytokines.
- Designed and maintained interactive dashboards that increased trial data accessibility, stakeholder engagement, and decision making.
- Developed statistical models to predict responses based on enrollment criteria and improve patient trial response rates.
- Conducted site visits engaging clinical investigators, leading to increased in enrollment rates and enhanced site feedback incorporation.
- Contributed patient population analysis based on preclinical experiments for inclusion in IND filings.
- Created a novel patient population estimation algorithm based on HLA and mutation frequencies (see Roy2025 for HLA component).
- Leveraged public and proprietary datasets to assess HLA Loss of Heterozygosity impacts on therapy efficacy (see Poster).

- Architected and maintained a multi-account AWS cloud infrastructure supporting both Discovery and Clinical programs.
- Championed deployment of computational workflow management systems enabling scalable, reproducible analysis pipelines.
- Supported Discovery and Prelinical activities from 2021–2024, and after a RIF, insured continuity and knowledge retention.
- Led efforts in TCR sequencing analysis and novel target identification (oncogene antigens, private neoantigens, ncRNAs, cryptic peptides).

Takeda Oncology (Cambridge, MA)

Principal Scientist: Discovery Translational Science and Computational Oncology
October 2017 – December 2021

- Directed Computational Oncology support for multiple cell therapy discovery projects.
- Collaborated closely with cell therapy teams to design and analyze preclinical translational experiments, informing clinical strategy.
- Led pilot evaluations of spatial transcriptomics platforms, informing technology adoption across Discovery.
- Managed three direct reports, fostering skill development and productivity improvements.
- Spearheaded optimization of cell therapy combinations involving armoring, target selection, platform delivery, and patient population stratification (Project "Square").
- Identified novel cell therapy targets with an emphasis on clinical relevance and competitive landscape.
- Played key role in interview panels and onboarding, enhancing team cohesion and technical ramp-up.
- Integrated public and proprietary genomic and proteomic datasets to identify tumor-associated antigens uniquely overexpressed in lung cancer.
- Supported GI-DDU scientists with RNA-Seq and scRNA-Seq dataset analyses and external therapeutic platform designs.
- Developed, validated, and disseminated single-cell RNA-seq pipelines, enabling reproducible data analysis across platforms.
- Founded and led internal working group focused on scRNA-seq technology awareness and best practices.
- Revitalized scientific computing environments, facilitating cloud migration and elastic resource scaling.
- Oversaw NGS outsourcing operations for multiple teams, ensuring cost efficiency and data quality.

- Core team member piloting Apple MacBooks deployment across Discovery, supporting IT transition.

Ohana Biosciences/VL34 Inc **(Cambridge, MA)**

Senior Scientist, Computational Biology
October 2016 – October 2017

- Provided foundational scientific analysis culminating in publication in Science.
- Designed and implemented AWS-based collaborative computing environments for large-scale genomics.
- Performed exome sequencing of key commercial dairy bulls to identify novel tissue-specific protein isoforms.
- Developed scalable pipelines for transcript reconstruction and whole chromosome haplotype phasing across species.
- Led multi-species genomic analyses interpreting whole genome, exome, and single-cell sequencing.
- Assembled tissue- and cell-type-specific transcriptomes integrating publicly available datasets.
- Integrated RNA-Seq data from >15 distinct bovine tissues to generate comprehensive gene and transcript annotations.
- Fostered relationships with dairy farmers innovating in cattle genetics, integrating phenotype and genotype datasets.
- Developed candidate evaluation portals integrating multi-omic data to optimize candidate selection efficiency.

Takeda Oncology **(Cambridge, MA)**

Scientist 2, Computational Biologist
October 2014 – October 2016

- Advanced oncology small molecule drug development using HTS data from public and in-house sources.
- Conducted comprehensive bioinformatic assessments covering expression profiles, indication suitability, mutations, and other omic features.
- Identified early translational strategies applying tool molecule responses across hundreds of cell lines.

- Selected translationally appropriate *in vitro* and *in vivo* models for target validation.
- Conducted genome-wide screening for antibody drug conjugate targets.
- Analyzed treatment-induced differential gene expression in models.
- Enhanced department-wide computational biology capabilities with command-line and cloud computing adoption.

Voyager Therapeutics (Cambridge, MA)

Consultant, Computational Biology Vector Design Group
June 2014 – October 2014

- Built AWS cloud-based computational biology HTS analysis environment.
- Directed AAV vector design leveraging public small RNA-Seq datasets.
- Analyzed and interpreted company-generated HTS data.

Graduate School (Worcester, MA)

Graduate Student
See Education for details. September 2007 – June 2014

Genzyme (Framingham, MA)

Research Associate, Bioanalytical Development Group
April 2004 – September 2007

- Developed GLP/GMP biochemical assays for recombinant protein clinical trials.
- Engineered HPLC assays for protein glycosylation quantification.
- Developed qPCR assays to monitor viral contamination in production cell lines.

Research Intern, Bioanalytical Development Group
Summer 2003

- Supported preclinical and clinical research via IEF assays and ELISAs.

Achillion Pharmaceuticals (New Haven, CT)

Research Internship
Summer 2002

- Conducted ELISAs and cell culture supporting small molecule screening.

Education

University of Massachusetts Medical School (Worcester, MA)

- Graduate School of Biomedical Sciences
- RNA Therapeutics Institute and Howard Hughes Medical Institute
- Doctor of Philosophy, Biochemistry and Molecular Pharmacology
- Advisors: Melissa J. Moore & Phillip D. Zamore
- September 2007 – May 2014
- Developed novel ligation-based assays for long RNAs (1,000–10,000 nt) (eLife 2015)
- Characterized piRNA-producing lncRNAs using multi-omic HTS data (Molecular Cell 2013)

Worcester Polytechnic Institute (Worcester, MA)

- Bachelor of Science with High Distinction
- September 2000 – May 2004
- Major: Biology & Biotechnology, Minor: Management

Patents, Publications, Software

You can also browse my ORCID profile

- **Regional Distribution of HLA Frequencies in the USA: Implications for TCR-Based Therapies** *Journal for ImmunoTherapy of Cancer* (April 2025)
  Christian K. Roy, Tomasz Sewastianik, Ileana Saenz, Gregory J. Opiteck, Sean Stagg, Martin Maiers, Dirk Nagorsen
- **CensusHLA**: R Package in support of Roy 2025 JITC
  Available from: Zenodo and GitHub
- **Allele-Specific HLA LOH Impacts Survival of Colorectal and Non-Small Cell Lung Cancer Patients** (submitted)
  Journal for ImmunoTherapy of Cancer (~2025)
  Tomasz Sewastianik, **Christian Roy**, Michael Gormally, Meagan Montesion, Patrick Halvey, Aastha Jindal, Hubert Lam, Adam Schoenfeld, Christopher Klebanoff, Gregory Opiteck, Dirk Nagorsen
- **Human NLRC4 Expression Promotes Cancer Survival and Associates with Type I Interferon Signaling and Immune Infiltration**
  Journal of Clinical Investigation (2024)
  Charlotte Domblides, Steven Crampton, Hong Liu, Juliet M. Bartleson, Annie Nguyen, Claudia Champagne, Emily E. Landy, et al.
- **Widespread Haploid-Biased Gene Expression Enables Sperm-Level Natural Selection**
  Science (March 2021)
  Kunal Bhutani, Katherine Stansifer, Simina Ticau, Lazar Bojic, Chloe Villani, Joanna Slisz, Claudia Cremers, **Christian Roy**, Jerry Donovan, Brian Fiske, Robin Friedman
- **Subsets of Mononuclear Phagocytes Are Enriched in the Inflamed Colons of Patients with IBD**
  BMC Immunology (November 2019)
  Hong Liu, Suryasarathi Dasgupta, Yu Fu, Brandi Bailey, **Christian Roy**, Eric Lightcap, Benjamin Faustin
- **Assessing Long-Distance RNA Sequence Connectivity via RNA-Templated DNA-DNA Ligation**
  eLife (April 2015)
  Christian K. Roy, Sarah Olson, Brenton R. Graveley, Phillip D. Zamore, Melissa J. Moore
- **Deducing Exon Connectivity by RNA-Templated DNA Ligation/Sequencing**
  Patent US8975019 B2 (March 2015)
  Phillip D. Zamore, Melissa J. Moore, **Christian K. Roy**

- **Putting the Pieces Together: Exons and piRNAs**
  UMMS Dissertation (May 2014)
  Christian K. Roy
  Available on Github
- **An Ancient Transcription Factor Initiates the Burst of piRNA Production during Early Meiosis in Mouse Testes**
  Molecular Cell (April 2013)
  X.Z. Li*, **Christian K. Roy***, X. Dong, E. Bolcun-Filas, J. Wang, B.W. Han, J. Xu, Melissa J. Moore, J.C. Schimenti, Z. Weng, Phillip D. Zamore (*Equal contribution)
- **Defining piRNA Primary Transcripts**
  Cell Cycle (May 2013)
  X.Z. Li, **Christian K. Roy**, Melissa J. Moore, Phillip D. Zamore
- **UPF1 Is Crucial for the Infectivity of Human Immunodeficiency Virus Type 1 Progeny Virions**
  Journal of Virology (August 2013)
  A.K.P. Serquiña, R.D. Suman, E. Popova, O.A. Ojelabi, **Christian K. Roy**, H.G. Göttlinger

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Presentations

Conference / Event (Date)	Work Presented	Link
American Society for Histocompatibility and Immunogenetics (ASHI) Annual Meeting, Anaheim, CA (2024)	*Poster*: Integrating US Census Demographic Data with HLA Frequencies to Accelerate Targeted Cell Therapy Patient Enrollment	Poster
American Society of Gene and Cell Therapy (ASGCT) Annual Meeting, Baltimore (2024)	*Poster*: Loss of Heterozygosity is Low for Specific HLA Alleles in Cancer Patients with Driver Mutations	Poster
Gordon Conference: The Biology Of Post-Transcriptional Gene Regulation, Newport, RI (2014)	*Short Talk*: Assessing long-distance RNA sequence connectivity via RNA-templated DNA-DNA ligation	

Conference / Event (Date)	Work Presented	Link
17th Annual Meeting of the RNA Society, Ann Arbor, MI (2012)	*Poster*: "SeqZip—A versatile methodology for analyzing long RNAs" **Winner** - Nature Reviews Molecular Cell Biology Poster Prize	Poster
Gordon Conference: The Biology Of Post-Transcriptional Gene Regulation, Newport, RI (2010)	*Poster*: "A novel technique to discover connectivity between distant alternatively spliced exons"	
UMass Medical School RNA Club, Worcester, MA (2009)	*Presentation*: "Uncovering connectivity between distant alternatively spliced exons"	

Skills

Translational

- Multi-omics data integration and translational biomarker development
- Modeling and prediction to improve clinical trial outcomes
- Assay contracting, vendor management, and clinical site relationship management
- Electronic Data Capture database analysis (e.g., Medidata Rave)

Computational

- Cloud computing on Amazon Web Services (AWS)
- Advanced R programming with experience in complete Posit Suite (Workbench/Rstudio; Package Manager; Connect)
- High-throughput sequencing data analysis and pipeline automation (`nextflow`, `snakemake`)
- Version control and collaborative development (`git`, GitHub Enterprise)
- Software containerization and deployment (`docker`, AWS EKS)
- Single-cell RNA-seq processing and analysis (`Seurat`, Bioturing, cellxgene)
- UNIX/Linux/GNU environments (`bash`, `perl`, `R`, `sql*`, some `python`)
- Data visualization and reporting (`quarto`, `knitr`, `shiny`, `spotfire`)

Bench

- Molecular biology and biochemical laboratory techniques
- HTS library construction
- Cell culture and spectrophotometry
- High-performance liquid chromatography (HPLC)
- Nucleic acid radioactive manipulation
