CURRICULUM VITAE

Jeffrey H. Chuang, Ph. D.

Contact Information

The Jackson Laboratory for Genomic Medicine
10 Discovery Drive
Farmington, CT 06030-2352
jeff.chuang@jax.org
860-837-2473
Orcid ID: 0000-0002-3298-2358
chuanglab.org

Professional appointments

4/2022-: Deputy Director, The Jackson Laboratory Cancer Center, Farmington, CT.
4/2021-: Professor, Jackson Laboratory for Genomic Medicine, Farmington, CT.
9/2012 – 4/2021: Associate Professor, Jackson Laboratory for Genomic Medicine, Farmington, CT.
2/2014 - : Affiliate Professor, University of Connecticut Health Center, Department of Genetics and Developmental Biology, Farmington, CT.
2/2020 - : Affiliate Professor, University of Connecticut, Computer Science and Engineering Department, Storrs, CT.
8/2014 - : Member, University of Connecticut Institute for Systems Genomics, Farmington, CT.
2005 – 8/2012: Assistant Professor. Department of Biology, Boston College, Chestnut Hill, MA.
2001 - 2005: Postdoctoral fellow. Department of Biochemistry and Biophysics, University of California, San Francisco, CA. Advisor: Hao Li.

EDUCATION

Ph. D. Massachusetts Institute of Technology (1996-2001) in Physics. Thesis title: Energy and Topology of Heteropolymers. Advisors: Alexander Grosberg, Toyoichi Tanaka and Mehran Kardar
B.A. Harvard University (1992-1996) in Chemistry and Physics *summa cum laude.*

Individual Fellowships and Awards

National Science Foundation Postdoctoral Fellowship in Interdisciplinary Informatics, UCSF (2003-2005).
National Institutes of Health Biochemistry Postdoctoral Training Grant Recipient, UCSF (2001-2002).
National Science Foundation Graduate Fellowship, MIT (1997-1999).
American Association for the Advancement of Science Mass Media Fellowship (1997).
Karl Taylor Compton Graduate Fellowship for Theoretical Physics, MIT (1996-1997).
Phi Beta Kappa, Harvard University (1996).
National Science Scholar (1992-1996).
International Chemistry Olympiad, USA Team (1992).

MAJOR LEADERSHIP ACTIVITIES

The Jackson Laboratory Cancer Center. Since 2022, I have served as Deputy Director of the NCI-Designated JAX Cancer Center, which has 37 full and 25 affiliate members. I work closely with the Cancer Center Director on all aspects of Cancer Center management, including strategic planning, leadership, and operational decisions. Major activities include long-term planning of center research directions, development of relationships and collaborations with external institutes and cancer centers, evaluation and decision-making for JAXCC-sponsored research grants, management and mentoring of PIs at all levels, writing and planning for large-scale grants, and coordination of JAX Cancer Center activities with JAX institutional goals.

NCI Patient Derived Xenograft Network. Since 2017, I have been PI for the U24 coordinating center of the NCI PDX Network. In this role, I manage the interactions and activities of a consortium that includes our U24, 6 multi-PI U54 teams, the NCI Patient-Derived Models Repository, and senior NCI personnel. Consortium members include groups at major academic institutes including MD Anderson, Dana Farber, Baylor College of Medicine, Huntsman Cancer Institute, Washington University, the University of Pennsylvania, the Wistar Institute, UC Davis, and Virginia Commonwealth University. The goals of our consortium are to conduct basic cancer research using patient-derived cancer models as well as to perform pre-clinical testing studies leading to cancer clinical trials. These projects have yielded 10 clinical trial letters of intent as well as major publications (e.g. Woo et al Nature Genetics 2021) involving international collaborations across the U.S., Europe, and Asia.

PROFESSIONAL SERVICE

Ad-hoc Journal Reviewer. Bioinformatics, BMC Cancer, BMC Genomics, BMC Genetics, Cancer Research, Cell Reports Medicine, Cell Reports Methods, Communications Biology, Diagnostic Pathology, Genome Research, Genome Biology, G3, Genome Biology and Evolution, iScience, Journal of Cellular Biochemistry, Journal of Chemical Physics, Journal of Chromatography B, Lancet Digital Health, Molecular Biology and Evolution, Nature, Nature Cancer, Nature Communications, Nature Genetics, NPJ Breast Cancer, Nucleic Acids Research, Physical Review E, PLoS Biology, PLoS Computational Biology, PLoS Genetics, PLoS ONE, Science Advances, Scientific Reports.
Editorial Board Member. Scientific Reports (2019-2023).

Grant review panels

2025. Ad-hoc reviewer for NCI Cancer Immunoprevention Network Special Emphasis Panel April 2025.
2025. Ad-hoc reviewer for NIH Loan Repayment Program study section March 2025.
2024. Ad-hoc reviewer for NIH BDMA study section October 2024.
2023. Ad-hoc reviewer for NCI P01 Program Project Special Emphasis Panel October 2023.
2023. Ad-hoc reviewer for NCI Cancer Systems Biology Grant March 2023.
2022. Ad-hoc reviewer for NCI Cancer Systems Biology Grant March 2022.
2022. Ad-hoc reviewer for FWF Austrian Science Fund, January 2022.
2021. Ad-hoc reviewer for NCI Cancer Center Support Grant April 2021, October 2021.
2020. Ad-hoc reviewer for NCI P01 Program Project Applications Special Emphasis Panel, February 2020, October 2020.
2019. Ad-hoc reviewer for Boston Children's Hospital
2019. Ad-hoc reviewer for NCI Cancer Genetics study section, June 2019.
2018. Ad-hoc reviewer for NCI Informatics Technologies for Cancer Research Special Emphasis Panel.
2018. Ad-hoc reviewer for NIH Biodata Management and Analysis (BDMA) study section.
2018. Ad-hoc review for Breast Cancer Now.

2017. Reviewer for National Cancer Institute Moonshot Initiative: R33 Integration and Validation of Emerging Technologies for Cancer Research.
2017. Ad-hoc reviewer for Genome Quebec -- Large-Scale Applied Research Project Competition: Genomics and Precision Health
2017. Reviewer for National Cancer Institute Special Emphasis Panel: U01 Cancer Target Discovery and Development Network.
2016. Ad-hoc reviewer for Netherlands Organisation for Scientific Research (NWO).
2016. Ad-hoc reviewer for U.S. Department of Veterans Affairs
2010. Panel Reviewer for NSF Postdoctoral Fellowship in Biological Informatics
2007. Ad-hoc reviewer for National Science Foundation DBI: Biological Databases and Informatics Cluster
2007. Ad-hoc reviewer for National Science Foundation MCB: Genes and Genome Systems Cluster
2007. Ad-hoc reviewer for NSF-sponsored Bioinformatics Education module at Oakland University

Conference organization
2025. PDXNet Consortium-wide Annual Meeting, Chicago, IL, organizer.
2025. JAX Cancer Evolution workshop, virtual, co-organizer.
2024. JAX Tissue AI workshop, virtual, organizer.
2024. PDXNet Consortium-wide Annual Meeting, San Diego, CA, co-organizer.
2023. PDXNet Consortium-wide Annual Meeting, online, co-organizer.
2022. PDXNet Consortium-wide Annual Meeting, online, co-organizer.
2022. NCI 3D Models of Cancer Workshop, Farmington, CT, co-organizer.
2021. JAX/Yale Cancer Centers Joint Microenvironment Workshop, co-organizer.
2021. PDXNet Consortium-wide Annual Meeting, online, co-organizer.
2020. PDXNet Consortium-wide Annual Meeting, online, co-organizer.
2019. PDXNet Consortium-wide Annual Meeting, Atlanta, GA, co-organizer.
2019. PDXNet Moonshot Fall Meeting, Rockville, MD, co-organizer.
2018. PDXNet Consortium-wide Annual Meeting, Chicago, IL, organizer.
2015. JAX-BIDMC Workshop on RNA Biology, faculty co-organizer.
2013. JAX-UCONN/BECAT/UCHC Joint Workshop on Computational Biology and Bioinformatics, conference co-organizer.
2009. Society of Molecular Biology and Evolution Conference, symposium organizer and session chair (Molecular Evolution of Functional Noncoding Sequences).
2007. New England Association of Parasitologists Meeting, conference co-organizer.
2007. Society of Molecular Biology and Evolution Conference, session chair (Methods in Comparative Genomics).
2006. Boston Area Pathogen and Vector Encounter, conference co-organizer.
2004. Biopathways Consortium at ISMB. Network evolution and regulatory networks, panel discussion member.

Professional Associations (various times)**.** New York Genome Center: Scientific and Clinical Steering Committee. American Society for Human Genetics, American Association for Cancer Research, Human Genome Organization, International Society for Computational Biology, Society for Molecular Biology and Evolution, American Association for the Advancement of Science, Genetics Society of America, Sigma Xi Research Honor Society, American Physical Society.

OTHER SERVICE – JACKSON LABORATORY FOR GENOMIC MEDICINE

The Jackson Laboratory Cancer Center (JAXCC)

Member (2013-). Principle investigator specializing in patient derived xenograft data analysis, tumor heterogeneity, and tumor microenvironmental analysis.

Computational Sciences Project Co-Lead (2016-). Advisor for organization of computational analysis capabilities.

Program Co-Leader (2020-3). Research program development specializing in tumor heterogeneity, the tumor microenvironment, and data analysis.

Cancer Advanced Technology (CATch) Project Leader (2021-). This $1.2 million project organizes JAXCC capabilities in computational biology, advanced imaging technologies, and cancer models to establish, innovate, and strengthen approaches for spatial omics analysis.

Deputy Director, (2022-). I work closely with the JAXCC Director in all Cancer Center activities, including long-term planning of research directions, development of external relationships, decision-making for sponsored research grants, management and mentoring of PIs at all levels, writing and planning of large-scale grants, and coordination of JAXCC activities with JAX institutional goals.

JAX Computational Sciences / Data Science. Faculty advisor to Computational Sciences / Data Science (2015-). Research Data Management / Data Center Planning Committees (2013-2018). Co-organizer, Computational Community Retreat (2019). Interviewer for many computational scientist and software engineer candidates (2012-). Advisor for re-organization of JAX Data Science (2023-4). Faculty Dyad for Data Analytics Core (2025-).

JAX Scientific Advisory Council. Elected member of faculty group advising senior leadership on faculty concerns (2016-2018, 2025-). Co-led faculty evaluations of JAX Computational Sciences and Graduate Admissions. JAX-GM SAC FAC Chair (2020-2021)

JAX-GM Graduate Admissions. Chair, (2014-2018). Coordinated with UCHC and JAX education office to expand and develop graduate program. Member of UCHC Genetics and Genome Sciences Graduate Committee. Member of UCHC MD/PhD Admissions Committee. Interviewer for graduate student admissions (2014-).

JAX Postdoc/Predoc Training Committee (2012-2018). Helped design new JAX postdoc scholars program. Reviewed applications. Committee chair (2016-2018). JAX/UCHC Postdoc Research Day: Speak4Science Judging Panel (2022).

JAX Ramping Up Research Committee. (2020-2022). JAX-GM faculty representative for Covid-19-related planning and re-organization.

JAX PDX Governance Team. (2019-2021) Committee for planning and evaluation of JAX PDX activities.

JAX Bioinformatics Training Working Group. Committee to design new bioinformatics curriculum (2018-2019). Helped design UCONN Computational Biology Special Topics Course (2018-2020). JAX Machine Learning Interest Group, council member (2016-2018). Data Science training group (2021-22).

JAX Special Search Committees / Interviewer: JAX Vice-President for Education Search Committee (2017-2018). JAX Chief Information Officer Search Committee (2018-2019). JAX Chief Data Science Officer Search Committee (2022-2023). JAX Chief Scientific Officer Interviewer (2022-2023).

Faculty Search Committees. Host for numerous faculty searches for JAX-GM (2012-2018). Additional review of multiple JAX bioinformatics candidates. Guest member for UCHC Developmental Biology and Genetics search committee (2014). Computational/Systems Genomics search committee (2014-2015). JAX cancer domain review committee (2016-). JAX faculty search committee (2020-2023).

University of Connecticut Institute for Systems Genomics (2014-2021). Scientific steering committee.

Research Grant Review Committee. Standing reviewer for research grant applications (2014). Ad hoc reviewer (2015-).

JGM Genomics Journal Club (2013-2014). Initiated and managed the first journal club at JGM.

Website Committee (2012-15). Input for JAX website redesign and vendor selection.

OTHER SERVICE - BOSTON COLLEGE (selected)

Biology Graduate Committee (2005-2012). Reviewed applications to the Ph.D. and Masters programs in biology, including all bioinformatics applicants. Co-designed bioinformatics and biology admissions materials. Graduate Student Technology Grant co-organizer. Biology Department Research Retreat Co-organizer (2007).

Bioinformatics Curriculum Development Committee (2005-2012). Managed course requirements for undergraduate and graduate students studying bioinformatics. Led overhaul of graduate requirements in 2009. Partnered with Computer Science and Math faculty to revise the undergraduate bioinformatics concentration in 2009 and 2010.

Academic Technology Fund (2006–2012). Biology department committee chair. Managed procurement of core resources and computer equipment for faculty and staff. Faculty Technology Contact (2006-2012). Member of committee to re-organize university technology consultants (2008). Boston College High Performance Computing Committee (2007 – 2012), Biology representative for management of the university-wide computing cluster.

Biology Department Computational Management: Co-manager of Jason Persampieri, scientific programmer (2006-2008). Co-manager of Tony Schreiner, Ph.D., UNIX system administrator (2006-2012).

Bioinformatics Faculty Search Committee. Member for searches in 2007, 2010. Ad-hoc for Chemistry Department (2008).

Biology Department External Review (2006-2007). Junior faculty development committee.

Infectious Disease Group (2005-2007). Co-organizer of monthly intradepartmental seminars, paper discussions.

FUNDING HISTORY

Pending Grants

Agency: NIH
Project Title: Summer Undergraduate Research Fellowship in the Molecular Biology and Genomics of Human Cancer
Dates: 07/01/2025 - 06/30/2030
Role: PI

Agency: NIH
Project Title: The Jackson Laboratory Cancer Center Support Grant
Dates: 4/2025-3/2030
Role: Deputy Director

Agency: NIH
Project Title: Comparative spatial omics of cancer microenvironmental structures within and across species (R01)
Dates: 7/2025-6/2030
Role: PI

Agency: NIH
Project Title: Building a spatial transcriptomics infrastructure for isoform profiling in aging pre-neoplastic tissues (R33)
Role: PD/PI (PI, Olga Anczukow, JAX)

Agency: Florida Department of Health
Project Title: Creating a Florida Cancer Immunotherapy Tissue Mapping and Computational Pathology Center for AI-Optimized Patient Outcomes
Dates: 7/2025-6/2026
Role: co-I (PI: Pei-Ling Chen, Moffitt Cancer Center)

Agency: NIH
Project Title: 3D Spatial Biology Quantification of the Metastatic Melanoma Tumor Microenvironment in Response and Resistance to Immunotherapy
Dates: 7/2025-6/2026
Role: co-I (PI: Nick Reder, Alpenglow)

Current Grants

Agency: JAX Director's Innovation Fund
Project Title: Bridging the spatial microenvironment between mouse and human lung tumors
Dates: 4/2025-5/2026
Role: PI (Co-PI: Palucka, JAX)
Total award: $231,630

Agency: JAX Director's Innovation Fund
Project Title: Self-supervised representation learning of whole slide images
Dates: 3/2024-9/2025
Role: PI (Co-PI: Robson, JAX)
Total award: $98,146

Agency: NIH
Title: Data Coordination Center for PDX Net U24CA224067
Dates: 09/01/2023-8/31/2028
Role: PI

Agency: NIH
Project Title: Building a spatial transcriptomics infrastructure for isoform profiling in aging pre-neoplastic tissues (1R21AG080243-01A1)
Dates: 9/1/23-5/31/25
Role: PD/PI (PI, Olga Anczukow, JAX)

Agency: Department of Defense
Project Title: Dissecting the Spatial Molecular Architecture of the Transformed Cutaneous T-Cell Lymphoma Tumor Microenvironment to Target Novel Therapeutic Vulnerabilities (HT9425-23-1-0947)
Dates: 9/30/23-9/29/2025
Role: Co-I (PI, Pei-ling Chen, Moffitt)
Total award: $182,666

Agency: Hevolution
Project Title: Building a spatial transcriptomics infrastructure for isoform profiling in aging epithelial tissues (HF-AGE, AGE-002)
Dates: 1/15/23-1/14/28
Role: PD/PI (PI, Olga Anczukow, JAX)

Agency: NIH
Project Title: The KAPP-Sen Tissue Mapping Center Collaborative (U54 AG075941)
Dates: 9/30/21-8/31/26
Role: Data Analysis Core, co-lead. (PIs: Kuchel, Garovic, Musi, Robson).

Agency: JAX Director's Innovation Fund
Title: Genetic determinations of tumor phenotypes in aged genetically diverse mice
Dates: 3/2023-3/2025 (extended to 2026)
Role: PI (co-PIs Korstanje, Palucka, Robson)
Total award: $248,054

Agency: NIH
Project Title: Pediatric Oncology In Vivo Testing Program Coordinating Center (U24CA263963)
Dates: 08/25/2021-7/31/2026
Role: PD/PI (joint with Prof. Carol Bult, JAX)

Completed Grants

Agency: NIH
Project Title: Automated Classification of Pediatric Soft Tissue Sarcoma from Histopathology Images (CCSG Supplement to P30CA034196)
Dates: 9/23/2023-9/22/2024 (extended to 2025)
Role: Co-I (CCSG PI: Palucka, Project PI: Rubinstein, JAX).

Agency: NIH
Project Title: Cancer Center Support (CORE) Grant
Dates: 4/2020-3/2025
Role: Computational Sciences Shared Resource Core Lead + Administration Core

Agency: JAX Director's Innovation Fund
Title: Spatially resolved gene expression profiling to predict colon cancer outcome
Dates: 6/2022-12/2023
Role: co-I (PI: Rubinstein)

Agency: NIH
Project Title: Summer Undergraduate Research Fellowship in the Molecular Biology and Genomics of Human Cancer (R25CA233420)
Dates: 07/01/2019 - 06/30/2024 (extended to 2025)
Role: PI

Agency: NIH/NCI
Project Title: Quantitative Computational Methods to Accurately Measure Tumor Heterogeneity in Solid Tumors to Inform Development of Evolution-based Treatment Strategies (R01CA230031)
Dates: 06/05/2018 – 05/31/2023
Extended through 5/31/2024
Role: PI
Total award: $2,650,464

Agency: NIH
Title: Data Coordination Center for PDX Net (U24 CA224067-01S1, supplement to support minority PDX Development and Trial Research Centers)
Dates: 08/01/2018-7/31/2023
Role: PI

Agency: NIH
Project Title: Human Cardiac Microtissues with Innate Immune Sensing to Study Adverse Biological Consequences of Genome Editing (U01EB028898)
Dates: 08/01/2019 – 07/31/2023
Role: co-PI (PI Travis Hinson)

Agency: NIH
Title: Data Coordination Center for PDX Net (U24 CA224067)
Dates: 09/25/2017-08/31/2022
No cost extension through 8/2023
Role: PI
Total award: $4,677,705

Agency: NIH
Title: Data Coordination Center for PDX Net (U24 CA224067) – Funded Extension Supplement
Dates: 9/2022-8/2023
Role: PI
Total award: $794,406

Agency: NIH
Project Title: (PQ3) Cellular and Molecular Mechanisms Driving Myeloid Compartment Variation in Human Triple Negative Breast Cancer (R01 CA219880)
Dates: 09/01/2017 – 07/31/2022
Role: co-PI (PI: Palucka)

Agency: NIH / NINDS
Title: Ribosome Dysfunction in Neurological Disorders (R01, NS094637)
Dates: 03/01/2016-05/31/2020 (administratively extended through 5/2021)
Role: co-PI (PI: Ackerman, UCSD)
Total award: $1,590,834

Agency: JAX Director's Innovation Fund
Title: Utilizing PDX Models to Support Clinical Molecular Tumor Board Decision Making
Dates: 09/2018-2/2020
Role: co-PI (co-PIs Carol Bult, Jens Rueter, Susie Airhart)

Agency: NIH
Title: Carboplatin response and resistance at primary metastatic sites (3U54CA224076-01S1, supplemental grant)
Dates: 08/01/2018-07/31/2019
Role: site PI (PIs Alana Welm, U. of Utah; Michael Lewis, Baylor College of Medicine)

Agency: NIH / NHGRI
Title: Big Genomic Data Skills Training for Professors (R25, EB022365)
Dates: 09/30/2015-06/30/2018 (extended to 2019)
Role: PI

Agency: NIH
Title: Identification of Genomic Causes of Morphological Heterogeneity within Tumors (Genomics Data Commons supplement)
Dates: 09/01/2017-08/30/2018 (extended to 2019)
Role: PI

Agency: JAX Director's Innovation Fund
Title: Computational methods for comparing genomic structural ensembles
Dates: 8/1/2016-7/31/2018
Role: PI

Agency: JAX Scientific Services Innovation Fund
Title: Develop an Easy to Use Interface to Launch omics-Seq Analytics Pipelines & Visualize the Results
Dates: 2/1/2017-10/31/2017
Role: co-PI (PIs: Karuturi, Beane)

Agency: NIH/NCI
Title: Dissection of Tumor Evolution Using Patient-Derived Xenografts (R21, CA191848)
Dates: 07/01/15-06/30/17 (extended through 6/30/2018)

Role: PI

Agency: JAX Cancer Center
Title: Computing Phenotypically Important Immune Cell Populations from Tumor RNA-seq Data
Dates: 9/1/2016-8/31/2017
Role: PI (co-PI: Palucka)

Agency: NIH / NHGRI
Title: Big Genomic Data Skills Training for Professors - Supplement (R25, EB022365-02S1)
Dates: 08/01/2016-06/30/2017
Role: PI

Agency: Southwest Oncology Group
Title: Genomic Analysis of Inflammatory Breast Cancer
Dates: 01/01/2016-12/31/2016 (extension requested to 6/30/2017)
Role: Co-PI (Additional Co-PIs: Pusztai and Gerstein, Yale)

Agency: NIH/NCI
(PQB5) Epigenetic Drivers of Hematopoietic Stem Cell Transformation (R21, CA184851)
Dates: 05/05/14-04/30/16 (extended through 4/30/2017)
Role: Co-PI (PI: Trowbridge)

Agency: NIH
Title: Combinatorial RNA Structural Features That Control RNA-Protein Binding (R21, HG007554)
Dates: 01/25/2014 – 12/31/2015 (extended through 12/31/2016).
Role: PI

Agency: NIH/NCI
Title: TCGA-based Validation of a Mutation Filtering Pipeline for Accurate Resolution of Tumor Heterogeneity (R21, CA191848-01A1S1, Supplement to support evaluation of the NCI Cancer Genomics Cloud Pilots).
Dates: 02/03/2016-06/30/2016
Role: PI

Agency: JAX Cancer Center Pilot Project Fund
Title: Targeting Tumor Heterogeneity with Orthogonal Cell State-Specific Drugs
Dates: 11/01/2013-10/31/2014
Role: Collaborator

Agency: JAX-GM Interactive Fund
Title: Differential expression of isodecoder tRNAs in the mammalian brain
Dates: 9/2013-8/2015
Role: co-PI

Agency: JAX-GM Interactive Fund
Title: Epigenetic and Transcriptional Responses to Environmental Stresses
Dates: 9/2013-8/2015

Role: co-PI

Agency: National Science Foundation
Title: Computational and Experimental Approaches to Characterizing Noncoding Selection in Coding Sequences (EF-0850155)
Dates: 8/15/2009-7/31/2012 (extended through 7/2013).
Role: PI

Agency: PhRMA Foundation Informatics Starter Grant
Title: Deciphering Malaria Gene Regulation through Comparative Genomics
Dates: 1/01/08-12/31/09
Role: PI

Agency: National Science Foundation
Title: Computational Comparative Genomic Approaches to Identifying Functional and Neutral DNA (Research Starter Grant DBI-0708206)
Dates: 7/01/07-6/30/08
Role: PI

Agency: National Institutes of Health
Title: Role of Conserved Non-Coding Elements in Vertebrate Brain Development (R21 HD051835)
Dates: 7/01/2006 – 6/30/2008
Role: Consultant (PI : Guo, UCSF)

PUBLICATIONS

92. STRprofiler: efficient comparisons of short tandem repeat profiles for biomedical model authentication. Jared M. Andrews, Michael W. Lloyd, Steven B. Neuhauser, Margaret Bundy, Emily L. Jocoy, Susan D. Airhart, Carol J. Bult, Yvonne A. Evrard, Jeffrey H. Chuang, Suzanne Baker. In press, Bioinformatics.

91. Lessons Learned from 20 Years of Preclinical Testing in Pediatric Cancers
Malcolm A. Smith, Peter J. Houghton, Richard B. Lock, John M. Maris, Richard Gorlick, Raushan T. Kurmasheva, Xiao-Nan Li, Beverly A. Teicher, Jeffrey H. Chuang, Filemon S. Dela Cruz, Michael A. Dyer, Andrew L. Kung, Michael W. Lloyd, Yael P. Mossé, Timothy M. Stearns, Elizabeth A. Stewart, Carol J. Bult, Stephen W. Erickson. Pharmacology & Therapeutics. Volume 264, December 2024, 108742.

90. Spatiotemporal profiling defines persistence and resistance dynamics during targeted treatment of melanoma. Jill C. Rubinstein*, Sergii Domanskyi*, Todd B. Sheridan, Brian Sanderson, SungHee Park, Jessica Kaster, Haiyin Li, Olga Anczukow, Meenhard Herlyn, Jeffrey H. Chuang (in press, Cancer Research).

89. Comprehensive single cell aging atlas of healthy mammary tissues reveals shared epigenomic and transcriptomic signatures of aging and cancer. Brittany Angarola , Siddhartha Sharma , Neerja Katiyar , Hyeon Gu Kang , Djamel Nehar-Belaid , SungHee Park , Rachel Gott , Giray Eryilmaz , Mark LaBarge , Karolina Palucka , Jeffrey Chuang , Ron Korstanje , Duygu Ucar, Olga Anczukow. Nature Aging, in press (2024).

88. Lessons Learned from 20 Years of Preclinical Testing in Pediatric Cancers. Malcolm A. Smith, Peter J. Houghton, Richard B. Lock, John M. Maris, Richard Gorlick, Raushan T. Kurmasheva, Xiao-Nan Li, Beverly A. Teicher, Jeffrey H. Chuang, Filemon S. Dela Cruz, Michael A. Dyer, Andrew L. Kung, Michael W. Lloyd, Yael P. Mossé, Timothy M. Stearns, Elizabeth A. Stewart, Carol J. Bult, Stephen W. Erickson. Pharmacology & Therapeutics. Volume 264, December 2024, 108742.

87. Computational immune synapse analysis reveals T-cell interactions in distinct tumor microenvironments. Victor Wang, Zichao Liu, Jan Martinek, Jie Zhou, Hannah Boruchov, Kelly Ray, Karolina Palucka, Jeffrey Chuang. Communications Biology volume 7, Article number: 1201 (2024).

86. Development and application of genetic ancestry reconstruction methods to study diversity of patient-derived models in the NCI PDXNet Consortium. Paul Lott, Katherine Chiu, Juanita Elizabeth Quino, April Pangia Vang, Michael W Lloyd, Anuj Srivastava, PDXNet Consortium, Jeffrey H Chuang, Luis G Carvajal-Carmona. Cancer Research Communications (2024).

85. Assessment of Patient-Derived Xenograft Growth and Antitumor Activity: The NCI PDXNet Consensus Recommendations. Funda Meric-Bernstam, Michael W. Lloyd, Soner Koc, Yvonne A. Evrard, Lisa M. McShane, Michael T. Lewis, Kurt W. Evans, Dali Li, Lawrence V. Rubinstein, Alana L. Welm, Dennis A. Dean, Anuj Srivastava, Jeffrey W Grover, Min Jin Ha, Huiqin Chen, Xuelin Huang, Kaushik Varadarajan, Jing Wang, Jack A. Roth, Bryan E. Welm, Ramaswamy Govindan, Ding Li, Salma Kaochar, Nicholas Mitsiades, Luis G Carvajal-Carmona, Meenhard Herlyn, Michael A. Davies, Geoffrey I. Shapiro, Ryan C. Fields, Jose Trevino, J.

Chuck Harrell, PDXNet Consortium, Lori Henderson, Tiffany A. Wallace, James H. Doroshow, Jeffrey H. Chuang, and Jeffrey A. Moscow. Mol Cancer Ther (2024) 23 (7): 924–938.

84. A pan-cancer PDX histology image repository with genomic and pathological annotations for deep learning analysis. Brian S White, Xingyi Woo, Soner Koc, Todd Sheridan, Steven B Neuhauser, Shidan Wang, Yvonne A Evrard, John David Landua, R Jay Mashl, Sherri R Davies, Bingliang Fang, Maria Gabriela Raso, Kurt W Evans, Matthew H Bailey, Yeqing Chen, Min Xiao, Jill Rubinstein, Ali Foroughi pour, Lacey Elizabeth Dobrolecki, Maihi Fujita, Junya Fujimoto, Guanghua Xiao, Ryan C Fields, Jacqueline L Mudd, Xiaowei Xu, Melinda G Hollingshead, Shahanawaz Jiwani, PDXNet Consortium, Brandi Davis-Dusenbery, Tiffany A Wallace, Jeffrey A Moscow, James H Doroshow, Nicholas Mitsiades, Salma Kaochar, Chong-xian Pan, Moon S Chen Jr., Luis G Carvajal-Carmona, Alana L Welm, Bryan E Welm, Ramaswamy Govindan, Shunqiang Li, Michael A Davies, Jack A Roth, Funda Meric-Bernstam, Yang Xie, Meenhard Herlyn, Li Ding, Michael T Lewis, Carol J Bult, Dennis A Dean II, Jeffrey H Chuang. Cancer Research. 2024;84:2060–72.

83. Nextflow Pipeline for Visium and H&E Data from Patient-Derived Xenograft Samples. Sergii Domanskyi, Anuj Srivastava, Jessica Kaster, Haiyin Li, Meenhard Herlyn, Jill C Rubinstein, Jeffrey H Chuang. Cell Reports Methods (2024). DOI: https://doi.org/10.1016/j.crmeth.2024.100759

82. SAMPLER: unsupervised representations for rapid analysis of whole slide tissue images. Patience Mukashyaka, Todd B. Sheridan, Ali Foroughi pour, Jeffrey H. Chuang. eBioMedicine (2024). 99:104908

81. High-throughput deconvolution of 3D organoid dynamics at cellular resolution for cancer pharmacology with Cellos. Patience Mukashyaka, Pooja Kumar, David J. Mellert, Shadae Nicholas, Javad Noorbakhsh, Mattia Brugiolo, Olga Anczukow, Edison T. Liu, Jeffrey H. Chuang. Nature Communications 14, 8406 (2023).

80. Combining the Tyrosine Kinase Inhibitor Cabozantinib and the mTORC1/2 Inhibitor Sapanisertib Blocks ERK Pathway Activity and Suppresses Tumor Growth in Renal Cell Carcinoma. Wu Y, Chen S, Yang X, Sato K, Lal P, Wang Y, Shinkle AT, Wendl MC, Primeau TM, Zhao Y, Gould A, Sun H, Mudd JL, Hoog J, Mashl RJ, Wyczalkowski MA, Mo CK, Liu R, Herndon JM, Davies SR, Liu D, Ding X, Evrard YA, Welm BE, Lum D, Koh MY, Welm AL, Chuang JH, Moscow JA, Meric-Bernstam F, Govindan R, Li S, Hsieh J, Fields RC, Lim KH, Ma CX, Zhang H, Ding L, Chen F. Cancer Res. 2023 Dec 15;83(24):4161-4178. doi: 10.1158/0008-5472.CAN-23-0604. PMID: 38098449; PMCID: PMC10722140.

79. Papillary Thyroid Cancer Immune Phenotypes via Tumor–Infiltrating Lymphocyte Spatial Analysis. Myungwoo Nam, Woojung Yang, Hye Sung Kim, Jewel Park, Gahee Park, Sukjun Kim, Sanghoon Song, Chan-Young Ock, Victor G Wang, Jeffrey H Chuang, and Young Kwang Chae. Endocrine-Related Cancer, 2023. 30:9 e230110

78. In Vivo Activity of the Dual SYK/FLT3 Inhibitor TAK-659 Against Pediatric Acute Lymphoblastic Leukemia Xenografts. Keira Hughes, Kathryn Evans, Eric J. Earley, Christopher M. Smith, Stephen W. Erickson, Tim Stearns, Vivek M. Philip, Steven B. Neuhauser, Jeffrey H. Chuang, Emily L. Jocoy, Carol J. Bult, Beverly A. Teicher, Malcolm A. Smith, Richard B. Lock. Pediatric Blood and Cancer, 2023, 70:9, e30503

77. Spatial mapping of cellular senescence: emerging challenges and opportunities NIH SenNet Consortium. Nature Aging. Volume 3, pages 776–790 (2023).

77. Integrative deep learning analysis improves colon adenocarcinoma patient stratification at risk for mortality. Jie Zhou, Ali Foroughi pour, Hany Deirawan, Fayez Daaboul, Thazin Aung, Rafic Beydoun, Fahad Shabbir Ahmed, Jeffrey H. Chuang. eBioMedicine. (2023). Vol. 94, 104726.

76. Challenges and opportunities for modeling aging and cancer. Anczuków O, Airhart S, Chuang JH, Coussens LM, Kuchel GA, Korstanje R, Li S, Lucido AL, McAllister SS, Politi K, Polyak K, Ratliff T, Ren G, Trowbridge JJ, Ucar D, Palucka K. Challenges and opportunities for modeling aging and cancer. Cancer Cell. 2023 Mar 22:S1535-6108(23)00079-X. doi: 10.1016/j.ccell.2023.03.006. Epub ahead of print. PMID: 37001528.

75. NIH SenNet Consortium: Mapping the landscape of senescent cells throughout the human lifespan to understand physiological health. NIH SenNet Consortium, Nature Aging (2022).

74. A path to translation: How 3D patient tumor avatars enable next generation precision oncology. Shree Bose, Margarida Barroso, Milan G. Chheda, Hans Clevers, Elena Elez, Salma Kaochar, Scott E. Kopetz, Xiao-Nan Li, Funda Meric-Bernstam, Clifford A. Meyer, Haiwei Mou, Kristen M. Naegle, Martin F. Pera, Zinaida Perova, Katerina A. Politi, Benjamin J.Raphael, Paul Robson, Rosalie C. Sears, Josep Tabernero, David A. Tuveson, Alana L. Welm, Bryan E.Welm, Christopher D. Willey, Konstantin Salnikow, Jeffrey H.Chuang, Xiling Shen. Cancer Cell. Volume 40, Issue 12, 12 December 2022, Pages 1448-1453.

73. Deep Learning Image Analysis Quantifies Tumor Heterogeneity and Identifies Microsatellite Instability in Colon Cancer. Jill C. Rubinstein, Ali Foroughi pour, Jie Zhou, Todd Sheridan, Brian S White, and Jeffrey H. Chuang. 17 October 2022 Journal of Surgical Oncology.

72. Genetically Diverse Mouse Platform to Xenograft Cancer Cells. Jennifer K Sargent, Mark A Warner, Benjamin E Low, Willian H Schott, Todd Hoffert, David Coleman, Xing Yi Woo, Todd Sheridan, Sonia Erattupuzha, Philipp P Henrich, Vivek M Philip, Jeffrey H. Chuang, Michael V. Wiles, and Muneer G Hasham. Disease Models and Mechanisms (2022) 15 (9): dmm049457.

71. Regulated dicing of pre-mir-144 via reshaping of its terminal loop. Renfu Shang, Dmitry A. Kretov, Scott I. Adamson, Thomas Treiber, Nora Treiber, Jeffrey Vedanayagam, Jeffrey H. Chuang, Gunter Meister, Daniel Cifuentes and Eric C. Lai. In press, Nucleic Acids Research.

70. Deep Learning Features Encode Interpretable Morphologies within Histological Images Ali Foroughi Pour, Brian S. White, Jonghanne Park, Todd B. Sheridan, Jeffrey H. Chuang. Scientific Reports volume 12, Article number: 9428 (2022)

69. Cancer stem cells, not bulk tumor cells, determine mechanisms of resistance to SMO inhibitors. Joshy George, Yaohui Chen, Nourhan Abdelfattah, Keiko Yamamoto, Thomas D. Gallup, Scott I. Adamson, Brad Rybinski, Anuj Srivastava, Parveen Kumar, Min Gyu Lee, David S. Baskin, Wen Jiang, Jong Min Choi, William Flavahan, Jeffrey H. Chuang, Betty Y.S. Kim, Jiaqiong Xu, Sung Yun Jung, Kyuson Yun; *Cancer Research Communications* 2022; crcres.0124.2022.

68. PDXNet Portal: Patient-Derived Xenograft model, data, workflow, and tool discovery. Soner Koc, Michael W Lloyd, Jeffrey Grover, Sara Seepo, Sai Lakshmi Subramanian, Manisha Ray, Christian Frech, John DiGiovanna, Phillip Webster, Steven Neuhauser, Anuj Srivastava, Xing Yi Woo, Brian J. Sanderson, Brian White, Paul Lott, PDXNet Consortium, Yvonne A. Evard, Tiffany A. Wallace, Jeffrey A. Moscow, James H. Doroshow, Nicholas Mitsuades, Salma Kaochar, Chong-xian Pan, Moon S. Chen Jr., Luis Carvajal-Carmona, Alana L. Welm, Bryan E. Welm, Michael T. Lewis, Govindan Ramaswarmy, Li Ding, Shunquang Li, Meenherd Herlyn, Mike Davies, Jack Roth, Funda Meric-Bernstam, Peter N. Robinson, Carol J. Bult, Brandi Davis-Dusenbery, Dennis A. Dean II, Jeffrey H. Chuang. NAR Cancer, Volume 4, Issue 2, June 2022, zcac014

67. Transcriptional profiling of macrophages in situ in metastatic melanoma reveals localization-dependent phenotypes and function. Jan Martinek, Jianan Lin, Kyung In Kim, Victor G.Wang, Te-ChiaWu, Michael Chiorazzi, Hannah Boruchov, Ananya Gulati, Shamreethaa Seeniraj, LiliSun, Florentina Marches, Paul Robson, Anthony Rongvaux, Richard A. Flavell, Joshy George, Jeffrey H. Chuang, Jacques Banchereau, Karolina Palucka. Cell Reports Medicine. Volume 3, Issue 5, 17 May 2022, 100621.

66. A breast cancer patient-derived xenograft and organoid platform for drug discovery and precision oncology. Katrin P Guillen; Maihi Fujita; Andrew J Butterfield; Sandra D Scherer; Matthew H Bailey; Zhengtao Chu; Yoko S DeRose; Ling Zhao; Emilio Cortes-Sanchez; Chieh-Hsiang Yang; Jennifer Toner; Guoying Wang; Yi Qiao; Xiaomeng Huang; Jeffery A Greenland; Jeffery M Vahrenkamp; David H Lum; Rachel E Factor; Edward W Nelson; Cindy B Matsen; Jane M Porretta; Regina Rosenthal; Anna C Beck; Saundra S Buys; Christos Vaklavas; John H Ward; Randy L Jensen; Kevin B Jones; Zheqi Li; Steffi Oesterreich; Lacey E Dobrolecki; Satya S Pathi; Xing Yi Woo; Kristofer C Berrett; Mark E Wadsworth; Jeffrey H Chuang; Michael T Lewis; Gabor T Marth; Jason Gertz; Katherine E Varley; Bryan E Welm; Alana Welm. Nature Cancer vol. 3, pages 232–250 (2022).

65. Deep learning trained on H&E tumor ROIs predicts HER2 status and Trastuzumab treatment response in HER2+ breast cancer. Saman Farahmand, Aileen Fernandez, Fahad Shabbir Ahmed, David Rimm, Jeffrey H Chuang, Emily Reisenbichler, Kourosh Zarringhalam. Modern Pathology 35, 44–51 (2022).

64. The Clp1 R140H mutation alters tRNA metabolism and mRNA 3’ processing in mouse models of pontocerebellar hypoplasia. Caitlin E. Monaghan, Scott I. Adamson, Mridu Kapur, Jeffrey H. Chuang, and Susan L. Ackerman. PNAS (2021) 118 (39) e2110730118.

63. Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidates for targeted treatment. Hua Sun, Song Cao, R. Jay Mashl, Chia-Kuei Mo, Simone Zaccaria, Michael C. Wendl, Sherri R. Davies, Matthew H. Bailey, Tina M. Primeau, Jeremy Hoog, Jacqueline L. Mudd, Dennis A. Dean, II, Rajesh Patidar, Lily Chen, Matthew A. Wyczalkowski, Reyka G. Jayasinghe, Fernanda Martins Rodrigues, Nadezhda V. Terekhanova, Yize Li, Kian-Huat Lim, Andrea Wang-Gillam, Brian A. Van Tine, Cynthia X. Ma, Rebecca Aft, Katherine C. Fuh, John F. Dipersio, The NCI PDXNet Consortium, Brandi Davis-Dusenbery, Michael T. Lewis, Michael Davies, Meenhard Herlyn, Bingliang Fang, Jack A. Roth, Alana L. Welm, Bryan E. Welm, Funda Meric-Bernstam, Feng Chen, Ryan C. Fields, Shunqiang Li,

Ramaswamy Govindan, James H. Doroshow, Jeffrey A. Moscow, Yvonne A. Evrard, Jeffrey H. Chuang, Benjamin J. Raphael, Li Ding. Nature Communications. (2021) 12:5086

62. Defects in translation-dependent quality control pathways lead to convergent molecular and neurodevelopmental pathology. Markus Terrey, Scott Adamson, Jeffrey Chuang, and Susan Ackerman. eLife 2021;10:e66904

61. Human KIT+ myeloid cells facilitate visceral metastasis by melanoma. Chun Yu, Jan Martinek, Te-Chia Wu, Kyung In Kim, Joshy George, Elaheh Ahmadzadeh, Rick Maser, Florentina Marches, Patrick Metang, Pierre Authie, Vanessa Oliveira, Victor Wang, Jeffrey Chuang, Paul Robson, Jacques Banchereau, and Karolina Palucka. J Exp Med (2021) 218 (6): e20182163.

60. The effect of blurring on lung cancer subtype classification accuracy of convolutional neural networks. Tejal Nair, Ali Foroughi pour, **Jeffrey H. Chuang**. 2020 IEEE International Conference on Bioinformatics and Biomedicine, conference abstract.

59. GTPBP1 resolves paused ribosomes to maintain neuronal homeostasis. Markus Terrey, Scott I. Adamson, Alana Gibson, Tianda Deng, Ryuta Ishimura, **Jeffrey H. Chuang**, and Susan L. Ackerman. eLife 2020;9:e62731 doi: 10.7554/eLife.62731.

58. Conservation of copy number profiles during engraftment and passaging of patient-derived cancer xenografts. Xing Yi Woo, Jessica Giordano, Anuj Srivastava, Zi-Ming Zhao, Michael W. Lloyd, Roebi de Bruijn, Yun-Suhk Suh, Rajesh Patidar, Li Chen, Sandra Scherer, Matthew Bailey, Chieh-Hsiang Yang, Emilio Cortes-Sanchez, Yuanxin Xi, Jing Wang, Jayamanna Wickramasinghe, Andrew V. Kossenkov, Vito Rebecca, Hua Sun, R. Jay Mashl, Sherri Davies, Ryan Jeon, Christian Frech, Jelena Randjelovic, Jacqueline Rosains, Francesco Galimi, Andrea Bertotti, Adam Lafferty, Alice C. O'Farrell, Elodie Modave, Diether Lambrechts, Petra ter Brugge, Violeta Serra, Elisabetta Marangoni, Rania El Botty, Hyunsoo Kim, Jong-Il Kim, Han-Kwang Yang, Charles Lee, Dennis A. Dean II, Brandi Davis-Dusenbery, Yvonne A. Evrard, James H. Doroshow, Alana L. Welm, Bryan E. Welm, Michael T. Lewis, Bingliang Fang, Jack A. Roth, Funda Meric-Bernstam, Meenhard Herlyn, Michael Davies, Li Ding, Shunqiang Li, Ramaswamy Govindan, Claudio Isella, Jeffrey A. Moscow, Livio Trusolino, Annette T. Byrne, Jos Jonkers, Carol J. Bult, Enzo Medico, **Jeffrey H. Chuang**, PDXNET consortium, EurOPDX consortium. Nature Genetics 53:86–99 (2021).

57. Deep learning-based cross-classifications reveal conserved spatial behaviors within tumor histological images. Javad Noorbakhsh , Saman Farahmand, Ali Foroughi pour, Sandeep Namburi, Dennis Caruana, David Rimm, Mohammad Soltanieh-ha, Kourosh Zarringhalam, and **Jeffrey H Chuang**. Nature Communications (2020) 11:6367.

56. Integrative Deep Learning for PanCancer Molecular Subtype Classification Using Histopathological Images and RNAseq Data. Fatima Zare, Javad Noorbakhsh, Tianyu Wang, **Jeffrey H. Chuang**, and Sheida Nabavi. ACM-BCB Conference 2020 proceedings, accepted. https://dl.acm.org/doi/10.1145/3388440.3412414

55. Expression of the neuronal tRNA n-Tr20 regulates synaptic transmission and seizure susceptibility. Mridu Kapur, Archan Ganguly, Gabor Nagy, Scott I. Adamson, **Jeffrey H. Chuang**, Wayne N. Frankel, Susan L. Ackerman. Neuron 108(1):193-208.e9 (2020).

54. pyBedGraph: a Python package for fast operations on 1-dimensional genomic signal tracks Henry B. Zhang, Minji Kim, **Jeffrey H. Chuang**, Yijun Ruan. Bioinformatics (2020), 36;10:3234–3235.

53. Systematic Establishment of Robustness and Standards in Patient-Derived Xenograft Experiments and Analysis. Yvonne A. Evrard, Anuj Srivastava, Jelena Randjelovic, Sasi Arunachalam, Carol J. Bult, Huiqin Chen, Lily Chen, Michael Davies, Sherri Davies, Brandi Davis-Dusenbery, Jack DiGiovanna, Li Ding, James H. Doroshow, Bingliang Fang, Christian Frech, Ramaswamy Govindan, Min Jin Ha, Meenhard Herlyn, Ryan Jeon, Andrew Kossenkov, Michael T. Lewis, Shunqiang Li, Michael Lloyd, Funda Meric-Bernstam, Nevena Miletic, Jeffrey A. Moscow, Steven Neuhauser, David Nix, Rajesh Patidar, Vito Rebecca, Peter N. Robinson, Jacqueline Rosains, Jack Roth, Isheeta Seth, Tamara Stankovic, Adam Stanojevic, Brian A. Van Tine, Alana L. Welm, Bryan E. Welm, Jayamanna Wickramasinghe, XingYi Woo, Min Xiao, Zi-ming Zhao, Dennis A. Dean II, Jeffrey S. Morris, **Jeffrey H. Chuang**. Cancer Res 80:2286–97 (2020).

52. MIA-Sig: multiplex chromatin interaction analysis by signal processing and statistical algorithms. Minji Kim, Meizhen Zheng, Simon Zhongyuan Tian, Byoungkoo Lee, **Jeffrey H. Chuang**, Yijun Ruan. Genome Biology 20:251 (2019).

51. Longitudinal molecular trajectories of diffuse glioma patients. Barthel FP, Johnson KC, Varn FS, Moskalik AD, Tanner G, Kocakavuk E, Anderson KJ, Abiola O, Aldape K, Alfaro KD, Alpar D, Amin SB, Ashley DM, Bandopadhayay P, Barnholtz-Sloan JS, Beroukhim R, Bock C, Brastianos PK, Brat DJ, Brodbelt AR, Bruns AF, Bulsara KR, Chakrabarty A, Chakravarti A, **Chuang JH**, Claus EB, Cochran EJ, Connelly J, Costello JF, Finocchiaro G, Fletcher MN, French PJ, Gan HG, Gilbert MR, Gould PV, Grimmer MR, Iavarone A, Ismail A, Jenkinson MD, Khasraw M, Kim H, Kouwenhoven MCW, LaViolette PS, Li M, Lichter P, Ligon KL, Lowman AK, Malta TM, Mazor T, McDonald KL, Molinaro AM, Nam DH, Nayyar N, Ng HK, Ngan CY, Niclou SP, Niers JN, Noushmehr H, Noorbakhsh J, Ormond DR, Park CK, Poisson LM, Rabadan R, Radlwimmer B, Rao G, Reifenberger G, Sa JS, Schuster M, Shaw BL, Short SC, Sillevis Smitt PA, Sloan AE, Smits M, Suzuki H, Tabatabai G, Van Meir EG, Watts C, Weller M, Wesseling P, Westerman BA, Widhalm G, Woehrer A, Yung WKA, Zadeh G, Huse JT, de Groot JF, Stead LF, Verhaak RGW, the GLASS Consortium. Nature 576:112–120 (2019).

50. BMP signaling mediates glioma stem cell quiescence and confers treatment resistance in glioblastoma. Sachdeva R, Wu M, Johnson K, Kim H, Celebre A, Shahzad U, Graham MS, Kessler JA, **Jeffrey H. Chuang**, Karamchandani J, Bredel M, Verhaak R, Das S. Scientific Reports 9(1):14569 (2019).

49. Clinical and immunological implications of frameshift mutations in lung cancer. Young Kwang Chae, Pedro Viveiros, Gilberto Lopes, Bhoomika Sukhadia, Muhammad Mubbashir Sheikh, Diana Saravia, Vaia Florou, Ethan S. Sokol, Garrett M. Frampton, Zachary R. Chalmers, Siraj M. Ali, Jeffrey S. Ross, Sangmin Chang, Si Wang, Lauren Chiec, Ashkon Rahbari1, Nisha Mohindra, Victoria Villaflor, Sang Ha Shin, Michael Oh, Jonathan Anker, Lee Chun Park, Victor Wang, **Jeffrey Chuang**, Wungki Park. J Thorac Oncol. S1556-0864(19)30496-4 (2019).

48. Fostering bioinformatics education through skill development of professors: Big Genomic Data Skills Training for Professors. Yingqian Ada Zhan, Charles Gregory Wray, Spencer T.

Glantz, Reinhard Laubenbacher, **Jeffrey H. Chuang**. PLoS Computational Biology 15(6): e1007026 (2019).

47. Genomic data analysis workflows for tumors from patient-derived xenografts (PDXs): challenges and guidelines. Xing Yi Woo, Anuj Srivastava, Joel H. Graber, Vinod Yadav, Vishal Kumar Sarsani, Al Simons, Glen Beane, Stephen Grubb, Guruprasad Ananda, Rangjiao Liu, Grace Stafford, **Jeffrey H. Chuang**, Susan D. Airhart, R. Krishna Murthy Karuturi, Joshy George, Carol J. Bult. BMC Medical Genomics 12:92 (2019).

46. Unstable Genome and Transcriptome Dynamics during Tumor Metastasis Contribute to Therapeutic Heterogeneity in Colorectal Cancers. Cho SY, Chae J, Na D, Kang W, Lee A, Min S, Kang J, Choi B, Lee J, Sung CO, **Jeffrey H. Chuang**, Lee C, Lee WS, Park H, Kim JI. Clinical Cancer Research. 25:2821-2834 (2019).

45. CCNE1 Amplification Is Associated with Poor Prognosis in Patients with Triple Negative Breast Cancer. Zi-Ming Zhao, Susan E. Yost, Katherine E. Hutchinson, Sierra Min Li, Yate-Ching Yuan, Javad Noorbakhsh, Zheng Liu, Charles Warden, Xiwei Wu, **Jeffrey Chuang**, Yuan Yuan. BMC Cancer 19:96 (2019).

44. Mutations in DNA repair genes are associated with increased neoantigen burden and a distinct immunophenotype in lung squamous cell carcinoma. Young Kwang Chae, Jonathan Anker, Michael Oh, Preeti Bais, Sandeep Namburi, Sarita Agte, Francis Giles, **Jeffrey Chuang**. Scientific Reports 9:3235 (2019).

43. Whole-exome sequencing capture kit biases yield false negative mutation calls in TCGA cohorts. Victor G. Wang, Hyunsoo Kim, **Jeffrey H. Chuang**. PLoS ONE 13(10): e0204912. (2018).

42. High-resolution deconstruction of evolution induced by chemotherapy treatments in breast cancer xenografts. Hyunsoo Kim, Pooja Kumar, Francesca Menghi, Javad Noorbakhsh, Eliza Cerveira, Mallory Ryan, Qihui Zhu, Guruprasad Ananda, Joshy George, Henry Chen, Susan Mockus, Chengsheng Zhang, Yan Yang, James Keck, R. Krishna Murthy Karuturi, Carol J Bult, Charles Lee, Edison T Liu, **Jeffrey H Chuang**. Scientific Reports 8: 17937 (2018).

41. Distribution-based measures of tumor heterogeneity are sensitive to mutation calling and lack strong clinical predictive power. Javad Noorbakhsh, Hyunsoo Kim, Sandeep Namburi, **Jeffrey Chuang**. Scientific Reports 8:11445 (2018).

40. SARNAclust: Semi-Automatic Detection of RNA Protein Binding Motifs From Immunoprecipitation Data. Ivan Dotu, Scott Adamson, Benjamin Coleman, Cyril Fournier, Emma Ricart-Altimiras, Eduardo Eyras, and **Jeffrey H Chuang**. PLoS Comput Biol 14 (3): e1006078. (2018)

39. Alterations in the Rho pathway contribute to Epstein-Barr virus-induced lymphomagenesis in immunosuppressed environments. Sung-Yup Cho, Chang Ohk Sung, Jeesoo Chae, Jieun Lee, Deukchae Na, Wonyoung Kang, Jinjoo Kang, Seoyeon Min, Ahra Lee, Eunhye Kwak, Jooyoung Kim, Boram Choi, Hyunsoo Kim, **Jeffrey H. Chuang**, Hyo-Kyung Pak, Chan-Sik Park, Sanghui Park, Young Hyeh Ko, Dakeun Lee, Jin Roh, Min-Sun Cho, Seongyeol Park, Young Seok Ju, Yun-Suhk Suh, Seong-Ho Kong, Hyuk-Joon Lee, James Keck, Jacques Banchereau, Edison T.

Liu, Woo-Ho Kim, Hansoo Park, Han-Kwang Yang, Jong-Il Kim and Charles Lee. Blood 131:1931-1941 (2018).

38. Mutations in DNA repair genes are associated with increased neo-antigen load and activated T cell infiltration in lung adenocarcinoma. Young Kwang Chae, Jonathan F. Anker, Preeti Bais, Sandeep Namburi, Francis J. Giles and **Jeffrey H. Chuang**. Oncotarget. 9:7949-7960 (2017).

37. Uncertainties in tumor allele frequencies limit power to infer evolutionary pressures. Javad Noorbakhsh and **Jeffrey H. Chuang.** Nature Genetics 49, 1288–1289 doi:10.1038/ng.3876 (2017).

36. CloudNeo: A cloud pipeline for identifying patient-specific tumor neoantigens. Preeti Bais, Sandeep Namburi, Daniel M. Gatti, Xinyu Zhang, **Jeffrey H. Chuang**. Bioinformatics, doi: 10.1093/bioinformatics/btx375 (2017).

35. Activation of GCN2 by Ribosome Stalling Links Translation Elongation with Translation Initiation. Ryuta Ishimura, Gabor Nagy, Ivan Dotu, **Jeffrey H. Chuang**, and Susan Ackerman. eLife 5:e14295 doi:10.7554/eLife.14295. (2016)

34. The Tandem Duplicator Phenotype as a distinct genomic configuration associated with therapeutic response in cancer. Francesca Menghi, Koichiro Inaki, XingYi Woo, Pooja A. Kumar, Krzysztof R. Grzeda, Ankit Malhotra, Hyunsoo Kim, Eladio J. Marquez, Duygu Ucar, Phung T. Shreckengast, Joel P. Wagner, R. Krishna Murthy Karuturi, James Keck, **Jeffrey H. Chuang**, and Edison T. Liu. PNAS 113:17 E2373-E2382 (2016).

33. Genetic Architectures of Quantitative Variation in RNA Editing Pathways. Tongjun Gu, Daniel M. Gatti, Anuj Srivastava, Elizabeth M. Snyder, Narayanan Raghupathy, Petr Simecek, Karen L. Svenson, Ivan Dotu, **Jeffrey H. Chuang**, Mark P. Keller, Alan D. Attie, Robert E. Braun, and Gary A. Churchill. Genetics 202:787-798 (2016).

32. Identification of Tumor Subtypes of Endometrial Carcinoma by Integration of Heterogeneous Datasets. Kim H, Bredel M, Park H, **Chuang JH** (2015) J Med Diagn Meth 4:189 (2015). doi: 10.4172/2168-9784.1000189

31. Loss of Tumor Suppressive MicroRNA-31 Enhances TRADD/NF-κB Signaling in Glioblastoma. Rajani Rajbhandari, Braden McFarland, Ashish Patel, G Gray, Samuel Fehling, Markus Bredel, Nicolas Berbari, Hyunsoo Kim, Margaret Marks, Gordon Meares, Tanvi Sinha, **Jeffrey H Chuang**, Etty Benveniste, and Susan Nozell. Oncotarget 6:17085 (2015).

30. Functional chromatin features are associated with structural mutations in cancer. Krzysztof R Grzeda, Beryl Royer-Bertrand, Koichiro Inaki, Hyunsoo Kim, Axel M Hillmer, Edison T Liu, **Jeffrey H Chuang**. BMC Genomics 15: 1013 (2014).

29. Ribosome stalling induced by mutation of a CNS-specific tRNA causes neurodegeneration. Ryuta Ishimura, Gabor Nagy, Ivan Dotu, Huihao Zhou, Xiang-Lei Yang, Paul Schimmel, Satoru Senju, Yasuharu Nishimura, **Jeffrey H. Chuang**, and Susan L. Ackerman. Science 345: 455–459 (2014).

28. Dynamics of the ethanolamine glycerophospholipid remodeling network. Lu Zhang, Kourosh Zarringhalam, Norberto Diaz-Diaz, and **Jeffrey H. Chuang**. PLoS ONE 7(12): e50858 (2012).

27. Integrating chemical footprinting data into RNA secondary structure prediction. Kourosh Zarringhalam, Michelle Meyer, Ivan Dotu, **Jeffrey H. Chuang**, and Peter Clote. PLoS ONE 7(10): e45160. (2012).

26. Statistical analysis of the processes controlling choline and ethanolamine glycerophospholipid molecular species composition. Kourosh Zarringhalam, Lu Zhang, Michael A Kiebish, Kui Yang, Xianlin Han, Richard W Gross, and **Jeffrey H. Chuang**. PLoS ONE 7(5): e37293 (2012).

25. Transcriptional Enhancers in Protein-Coding Exons of Vertebrate Developmental Genes Deborah I Ritter, Zhiqiang dong, Su Guo, and **Jeffrey H. Chuang**, PLoS ONE 7(5): e35202 (2012).

24. CodingMotif: Determination of Overrepresented Nucleotide Motifs in Coding Sequences. Yang Ding, William Lorenz, and **Jeffrey H. Chuang**. BMC Bioinformatics 13:32 (2012). *"Highly Accessed Article."*

23. Expression Divergence Measured by Transcriptome Sequencing of Four Yeast Species. M.A. Busby, J. Gray, A.M. Costa, D. Stewart, M. Stromberg, D. Barnett, **Jeffrey H. Chuang**, M. Springer, G.T. Marth. 2011. BMC Genomics 12:635 (2011). *"Highly Accessed Article."*

22. A mathematical model for the determination of steady-state cardiolipin remodeling mechanisms using lipidomic data. L. Zhang, R.J.A. Bell, M. A. Kiebish, T. N. Seyfried, X. Han, R. Gross, and **Jeffrey H. Chuang.** PLoS ONE 6:e21170 (2011).

21. The Importance of Being Cis: Evolution of Orthologous Fish and Mammalian Enhancer Activity. D. I. Ritter, Q. Li, D. Kostka, K. S. Pollard, S. Guo and **Jeffrey H. Chuang**. Molecular Biology and Evolution 27:2322 (2010). *Highlighted on the Nature Molecular Systems Biology Blog.*

20. A molecular-imprint nanosensor for ultrasensitive detection of proteins. D. Cai, L. Ren, H. Zhao, Chenjia Xu, L. Zhang, Y. Yu, H. Wang, Y. Lan, M. F. Roberts, **Jeffrey H. Chuang**, M. J. Naughton, Z. Ren and T. C. Chiles. Nature Nanotechnology 5:597 (2010). *Highlighted on Nature Chemistry and Nature Methods.*

19. Dynamic simulation of cardiolipin remodeling: Greasing the wheels for an interpretative approach to lipidomics. M. A. Kiebish, R. Bell, K. Yang, T. Phan, Z. Zhao, W. Ames, T. N. Seyfried, R. W. Gross, **Jeffrey H. Chuang**, and X. Han. J. Lipid Res. 51:2153 (2010).

18. A systematic approach to identify functional motifs within vertebrate developmental enhancers. Q. Li, D. Ritter, N. Yang, Z. Dong, H. Li, **Jeffrey H. Chuang**, S. Guo. Developmental Biology 337:484 (2010).

17. COMIT: Identification of Noncoding Motifs under Selection in Coding Sequences. D. Kural, Y. Ding, J. Wu, A. M Korpi, **Jeffrey H. Chuang**. Genome Biology 10:R133 (2009).

16. The effect of Plasmodium falciparum Sir2a histone deacetylase on clonal and longitudinal variation in expression of the var family of virulence genes. C. J. Merrick, R. Dzikowski, H. Imamura, **Jeffrey Chuang**, K. Deitsch, M. T. Duraisingh. Int J Parasitol. 40:35 (2009).

15. Weak preservation of local neutral mutation rates across mammalian genomes. H. Imamura, J. E. Karro and **Jeffrey H. Chuang**. BMC Evolutionary Biology 9:89 (2009).

14. Cardiolipin and electron transport chain abnormalities in mouse brain tumor mitochondria: Lipidomic evidence supporting the Warburg theory of cancer. M. A. Kiebish, X. Han, H. Cheng, **Jeffrey H. Chuang** and T. N. Seyfried. Journal of Lipid Research, 49:2545 (2008). *Cover article.*

13. cneViewer: A Database of Conserved Noncoding Elements for Studies of Tissue-Specific Gene Regulation. J. Persampieri, D. I. Ritter, D. Lees, J. Lehoczky, Q. Li, S. Guo, and **Jeffrey H. Chuang**. Bioinformatics, 24:2418 (2008).

12. Brain Mitochondrial Lipid Abnormalities in Mice Susceptible to Spontaneous Gliomas. M.A. Kiebish, X. Han, H. Cheng, **Jeffrey H. Chuang**, and T.N. Seyfried. Lipids 43:951 (2008).

11. Measuring the Prevalence of Regional Mutation Rates: An Analysis of Silent Substitutions in Mammals, Fungi, and Insects. A.K. Fox, B.B. Tuch, and **Jeffrey H. Chuang**. BMC: Evolutionary Biology 8:186 (2008). *"Highly accessed article."*

10. Lipidomic Analysis and Electron Transport Chain Activities in C57BL/6J Mouse Brain Mitochondria. M.A. Kiebish, X. Han, H. Cheng, A. Lunford, C.F. Clarke, H. Moon, **Jeffrey H. Chuang**, and T.N. Seyfried. Journal of Neurochemistry 106:299 (2008).

9. Sequences Conserved by Selection across Mouse and Human Malaria Species. H. Imamura, J. Persampieri, and **Jeffrey H. Chuang**. BMC: Genomics 8:372 (2007).

8. Similarity of Synonymous Substitutions Rates Across Mammalian Genomes. **Jeffrey H. Chuang** and H. Li. Journal of Molecular Evolution 65:236 (2007).

7. Genome-wide Regulatory Complexity in Yeast Promoters: Separation of Functional and Neutral Sequence. C.S. Chin, **Jeffrey H. Chuang**, and H. Li. Genome Research, 15:205 (2005).

6. Functional Bias and Spatial Organization of Genes in Mutational Hot and Cold Regions in the Human Genome. **Jeffrey H. Chuang** and H. Li. PLoS Biology, 2(2):e29 (2004). *Faculty of 1000 highlighted article.*

5. Anomalous Dynamics of Translocation. **Jeffrey Chuang**, Y. Kantor, and M. Kardar. Physical Review E 65:011802 (2001).

4. Effect of Reversible Cross-linker, N,N'-Bis(acryloyl)-cystamine, on Calcium Ion Adsorption by Imprinted Gels. H. Hiratani, C. Alvarez-Lorenzo, **Jeffrey Chuang**, O. Guney, A. Yu.Grosberg, and T. Tanaka. Langmuir 17:4431 (2001).

3. Free Energy Self-Averaging in Protein-Sized Heteropolymers. **Jeffrey Chuang**, A. Yu. Grosberg, and M. Kardar. Physical Review Letters 87:078104 (2001).

2. Frustrations in Polymer Gels and Their Minimization through Molecular Imprinting. T. Enoki, K. Tanaka, T. Watanabe, T. Oya, T. Sakiyama, Y. Takeoka, K. Ito, G. Wang, M. Annaka, K. Hara, R. Du, **Jeffrey Chuang**, K. Wasserman, A. Yu. Grosberg, S. Masamune, and T. Tanaka. Physical Review Letters 85:5000 (2000).

1. Topological Repulsion between Polymer Globules. **Jeffrey Chuang**, A. Yu. Grosberg, and T. Tanaka. Journal of Chemical Physics 112:6434 (2000).

Reviews

4. Molecular biology and evolution of cancer: from discovery to action. Jason A Somarelli, Heather Gardner, Vincent L Cannataro, Ella F Gunady, Amy M Boddy, Norman A Johnson, J Nicholas Fisk, Stephen G Gaffney, **Jeffrey H Chuang**, Sheng Li, Francesca D Ciccarelli, Anna R Panchenko, Kate Megquier, Sudhir Kumar, Alex Dornburg, James DeGregori, Jeffrey P Townsend. Molecular Biology and Evolution 37:320-326 (2020).

3. Treating Cancer as an Invasive Species. Javad Noorbakhsh, Zi-ming Zhao, James Russell, **Jeffrey H. Chuang.** Molecular Cancer Research 18:20-26 (2020).

2. Multiple Contact Adsorption of Target Molecules by Heteropolymer Gels. K. Ito, **Jeffrey Chuang**, C. Alvarez-Lorenzo, T. Watanabe, N. Ando, and A. Yu. Grosberg. Macromolecular Symposia 207:1 (2004).

1. Multiple point adsorption in a Heteropolymer Gel and the Tanaka Approach To Imprinting: Experiment and Theory. K. Ito, **Jeffrey Chuang**, C. Alvarez-Lorenzo, T. Watanabe, N. Ando, and A. Yu. Grosberg. Progress in Polymer Science, 28:1489 (2003).

Book chapters

1. Smart Polymers: Applications in Biotechnology and Biomedicine, Second Edition. Chapter title: Imprinting Using Smart Polymers. C. Alvarez-Lorenzo, A. Concheiro, **Jeffrey Chuang** and A. Yu. Grosberg. CRC Press: Boca Raton (2007).

INTELLECTUAL PROPERTY

1. Provisional patent: U.S. Application No.: 62/876,563
   Title: CONVOLUTIONAL NEURAL NETWORKS FOR CLASSIFICATION OF CANCER HISTOLOGICAL IMAGES
   Provisional filing Date: July 19, 2019
   Official Filing: July 19, 2020
   Inventor(s): Jeffrey Chuang

SOFTWARE AND ONLINE RESOURCES DEVELOPED (selected)

19. SAMPLER: unsupervised representations for rapid analysis of whole slide tissue images.
https://github.com/TheJacksonLaboratory/SAMPLER

18. STQ: Nextflow Pipeline for Visium and H&E Data from Patient-Derived Xenograft Samples.
https://github.com/TheJacksonLaboratory/STQ

17. CISA: Computational Immune Synapse Analysis. Communications Biology volume 7, Article number: 1201 (2024).
https://github.com/SamLiu1218/CISA

16. Cellos: High-throughput deconvolution of 3D organoid dynamics at cellular resolution for cancer pharmacology.
https://github.com/TheJacksonLaboratory/Cellos

15. nf-score Spatial Transcriptomics: a bioinformatics best-practice analysis pipeline for Spatial Transcriptomics. 11832 downloads, as of 4/3/2023
https://nf-co.re/spatialtranscriptomics?q=spatialtranscriptomics

14. PDXNet Portal: The PDX Network portal centralizes access to the National Cancer Institute-funded PDXNet consortium resources, to facilitate collaboration among researchers and to make these data easily available for research.
http://portal.pdxnetwork.org

13. MIA-Sig: multiplex chromatin interaction analysis by signal processing and statistical algorithms. https://github.com/TheJacksonLaboratory/mia-sig

12. HistCNN – cloud software tools for deep convolutional neural network classification analysis of cancer images. https://github.com/javadnoorb/HistCNN

11. PDXNet Data Commons and Coordination Center.
My lab works closely with Seven Bridges Genomics to develop the definitive data and computational workflow resource for PDXs, via our leadership of the Coordinating Center for the NCI PDXNet.
https://www.pdxnetwork.org

10. SARNAclust: Semi-Automatic Detection Of RNA Protein Binding Motifs From Immunoprecipitation Data (Dotu et al 2018).
https://github.com/idotu/SARNAclust

9. CloudNeo – A cloud pipeline for identifying patient-sepcific tumor neoantigens. (Bais et al 2017).
https://github.com/TheJacksonLaboratory/CloudNeo

8. DLipid – Software to identify lipid remodeling pathways from lipidomic data (developed for Zhang et al 2012).
http://nbidiaz.github.com/DLipid/

7. CodingMotif – Software to identify overrepresented motifs important for post-transcriptional regulation of genes (developed for Ding et al 2011).
http://bioinformatics.bc.edu/chuanglab/codingmotif.tar

6. Cardiolipin Remodeling Simulator – Software to simulate the process by which the population of acyl chains evolves in lipids. This software allows one to test mechanistic hypotheses using lipidomic data (developed for Kiebish et al 2010).
http://bioinformatics.bc.edu/~jchuang/dynamic.html

5. COMIT – Software for the identification of noncoding motifs under selection in coding sequences (developed for Kural et al 2009).
http://bioinformatics.bc.edu/chuanglab/COMIT/COMIT-v.0.02012010.tar.gz

4. cneViewer – A database of conserved noncoding elements for studies of tissue-specific gene expression (developed for Persampieri et al 2008).
http://bioinformatics.bc.edu/chuanglab/cneViewer/

3. cneBrowser – A database of experimentally validated conserved noncoding elements in the zebrafish genome (developed for Ritter et al 2010 and Li et al 2009).
http://bioinformatics.bc.edu/chuanglab/cneBrowser/

2. Malaria Conserved Noncoding Sequences – A database of sequences under purifying selection across rodent and human malaria species (developed for Imamura et al 2007).
http://bioinformatics.bc.edu/chuanglab/malaria/malaria.html

1. Yeast Conserved Noncoding Sequences – A database of sequences under purifying selection across the *sensu stricto* yeasts (developed for Chin et al 2005).
http://genome.ucsf.edu/YeastReg/

PRESENTATIONS

Invited Talks and Seminars (selected)

126. Predicting cancer outcome from spatial tissue analysis. University of Arizona, Biomedical Engineering. Tucson, AZ. November 2024 (invited).

125. Spatial omic profiling to understand PDXs and their microenvironment. EuroPDX Conference. Barcelona, Spain. October 2024 (invited).

124. Patient Derived Xenografts Models and Analysis Workshop. JAX Cancer Course. Bar Harbor, ME. August 2024 (invited).

123. Elucidating cancer evolution and treatment susceptibilities through image analysis. JAX Cancer Course. Bar Harbor, ME. August 2024 (invited).

122. PDXNet Goals and Progress. PDXNet Annual Meeting. San Diego, CA. April 2024.

121. Genomic Data Harmonization – PDXNet and PIVOT Perspectives. Childhood Cancer Data Initiative Meeting, National Cancer Institute. Rockville, MD. February 2024. (invited)

120. AI approaches for interpreting cancer topography. Precision Medicine World Conference. Silicon Valley, CA. January 2024.

119. PDXNet and PDX-omics Studies to Develop Clinical Trials. EuroPDX 10th Anniversary Symposium. Paris, France. November 2023 (invited).

118. Spatial Dynamics of Acquired Resistance in BRAF-mutant Melanoma. Northeast Bioimage Analysis Meeting. Farmington, CT. October 2023 (invited).

117. Spatial Dynamics of Acquired Resistance in BRAF-mutant Melanoma, International Conference on Systems Biology, Hartford, CT. October 2023 (invited).

116. Multomic Analysis of Patient-Derived Xenografts, 9th Asian Federation of Laboratory Animal Science Congress, Jeju Island, Korea. September 2023 (invited).

115. How to be in the Right Place at the Right Time: Tumor Tissue Analysis. JAX-GM Scientific Director's Forum. Farmington, CT. August 2023

114. Elucidating cancer evolution and treatment susceptibilities through image analysis. JAX Cancer Course. Bar Harbor, ME. August 2023 (invited).

113. Spatial Dynamics of Acquired Resistance in BRAF-mutant Melanoma. 2nd International Spatial Biology Congress, Rotterdam, Netherlands. July 2023 (invited).

112. Deciphering tumor physiology from spatial data, Candiolo Cancer Institute, Torino, Italy. July 2023 (invited).

111. Computational analysis of breast cancer images for outcome prediction. Updates on Advanced Breast Cancer Meeting, Houston, TX. May 2023 (invited)

110. Developing Approaches for Single Cell and Spatial Expression Analysis in Tumors. American Association for Cancer Research Annual Meeting. Orlando, FL. April 2023 (invited).

109. Imaging Analysis to Guide Precision Medicine. Maine Cancer Genomics Initiative Forum. Rockport, ME. April 2023 (invited).

108. Deep Learning Approaches for Cancer Image Analysis. Hartford Hospital, Department of Pathology. Hartford, CT. November 2022 (invited).

107. Classifying cancers from images and sequence data. JAX Cancer Course. Farmington, CT. August 2022 (invited).

106. Treatment Response Data for Patient-Derived Xenografts. Joint Statistical Meeting. Washington, DC. August 2022 (invited).

105. Quantification of Organoids at Cellular Resolution. NCI 3D Models of Cancer Workshop. Farmington, CT. July 2022.

104. Cancer Discovery and Preclinical Validation Using Patient-Derived Xenografts. NCI Moonshot Seminar Series, online. June 2022 (invited).

103. Robustness of deep learning methods across cohorts in cancer image analysis. New York, Ny. 8th Digital Pathology & AI Congress: USA. June 2022 (invited).

102. Deciphering cancer from images and sequences. JAX Cancer Course. Bar Harbor, ME. August 2021 (invited).

101. Image Analysis in the Patient-Derived Xenografts Network. NCI Cancer Systems Biology Consortium – Image Analysis Group. July 2021 (invited).

100. Artificial Intelligence Approaches for Biomedical Image Analysis. 8th International Conference on Smart Computing and Communications, Muthoot Institute of Technology and Science. Kochi, India. July 2021 (invited).

99. Deciphering cancer from images and sequences. MD Anderson Translational Molecular Pathology, Distinguished Speaker Seminar Series. Houston, TX. March 2021 (invited).

98. Deciphering cancer from images and sequences. JAX-GM Scientific Director's Forum. Farmington, CT. January 2021.

97. Patient-derived xenograft models and analysis. JAX Cancer Course. Bar Harbor, ME. August 2020 (invited).

96. Quantitative approaches for interpreting cancer image and sequence data. NCI Immuno-Oncology Models Workshop. Online. July 2020. (invited)

95. Harnessing Digital Pathology for Cancer Trials. Southwest Oncology Group Spring Group Meeting, Early Therapeutics and Rare Cancer Committee. Online. June 2020. (invited)

94. Integrating Patience Derived Xenografts and Data for Cancer Research. NCI Patient Derived Models Consortium seminar. Online. January 2020. (invited)

93. Combining Cancer Genomics and Image Analysis Using Artificial Intelligence. Korea Advanced Institute of Science and Technology. Daejeon, Republic of Korea. December 2019. (invited)

92. Integrating Patient Derived Xenografts and Data for Cancer Research. NCI Cancer Moonshot Meeting. Rockville, MD. November 2019.

91. Combining Cancer Genomics and Image Analysis Using Artificial Intelligence. University of Rochester Medical Center Department of Pathology. Rochester, NY. November 2019. (invited)

90. Leveraging patient-derived xenografts for pre-clinical cancer studies. American Society for Human Genetics JAX Lunch and Learn. Houston, TX. October 2019.

89. Patient-Derived Xenograft Model and Data Sharing. Foundation for the National Institutes of Health Preclinical Pediatric Oncology Public-Private Partnership Design Meeting. Bethesda, MD. September 2019 (invited).

88. Patient-derived xenograft models and analysis. JAX Cancer Course. Bar Harbor, ME. August 2019 (invited).

87. Large-scale DNA-based tracking of the evolution of copy number alterations during xenograft engraftment and passaging. Society for Molecular Biology and Evolution 2019. Manchester, United Kingdom. July 2019.

86. Big Data Genomics for Professors. Morgan State University. Baltimore, MD. May 2019.

85. Quantifying Tumor Evolution in Response to Treatment. Xian Jiaotong University and 1st Affiliated Hospital of Xian Jiaotong University Inaugural International Precision Medicine Symposium. Xian, China. April 2019. (invited)

84. Quantifying Tumor Evolution in Response to Treatment. SMBE Satellite Meeting on Molecular Evolution of Cancer. Yale University. New Haven, CT. April 2019. (invited)

83. Quantifying Tumor Evolution in Response to Treatment. UCONN Health Dean's Informatics Seminar. Farmington, CT. April 2019 (invited).

82. Overview of the PDXNet Data Commons and Coordinating Center. PDXNet / Drug Resistance and Sensitivity Network joint meeting. Atlanta, GA. March 2019.

81. PDX Data Commons and Coordinating Center Update. PDXNet Annual Meeting. Atlanta, GA. March 2019.

80. Quantifying Tumor Evolution in Response to Treatment. Weill Cornell Institute for Computational Biomedicine. New York, NY. Sept 2018 (invited).

79. Patient-derived xenograft computational biology workshop. JAX Cancer Course. Bar Harbor, ME. August 2018 (invited).

78. Evolutionary Dynamics of Response to Chemotherapies in Breast Cancer Xenografts. SMBE 2018. Yokohama, Japan. July 2018.

77. Population Evolution in Tumors. 60th Birthday Symposium for Prof. Mehran Kardar (MIT Physics). Cambridge, MA. June 2018.

76. Genomic Analysis for Immunotherapy-Treated Rare Cancers. Southwest Oncology Group Spring Group Meeting. San Francisco, CA. April 2018.

75. Evolutionary Dynamics of Response to Chemotherapies in Breast Cancer Xenografts. International Society for Evolution, Ecology and Cancer Conference. Tempe, AZ. December 2017.

74. Sequencing the genome to fight cancer. Public outreach for Connecticut high school students. Farmington, CT. Oct 2017 (invited).

73. Patient-derived xenograft computational biology workshop. JAX Cancer Course. Bar Harbor, ME. August 2017 (invited).

72. Intratumoral evolution of breast cancer. JAX Scientific Symposium. Bar Harbor, ME. May 2017 (invited).

71. Interpreting tumor heterogeneity using the Cancer Genomics Cloud. American Medical Informatics Association Joint Summits on Translational Science. San Francisco, CA. March 2017 (invited).

70. Intratumoral evolution of breast cancer in response to therapy. Columbia University Medical School. New York, NY. January 2017 (invited).

69. Intratumoral evolution of breast cancer in response to therapy. Pompeu Fabra University. Barcelona, Spain. December 2016 (invited).

68. Intratumoral evolution of breast cancer in response to therapy. University of Connecticut Health – Center for Molecular Medicine. Farmington, CT. October 2016 (invited).

67. Resolving Tumor Heterogeneity Using the Cancer Genomics Cloud. American Association for Cancer Research Conference. New Orleans, LA. April 2016 (invited).

66. Training Undergraduates in Big Data Genomics. University of Illinois. Urbana-Champaign, IL. April 2016 (invited).

65. Comparing sequence data from related tumors and xenografts. JAX Cancer Interest Group. The Jackson Laboratory for Genomic Medicine. Farmington, CT. January 2016.

64. Subclonal Selection in Patient-Derived Xenografts. JAX faculty retreat. Northport, ME. October 2015.

63. Computational Approaches to Tumor Heterogeneity. JAX Cancer Center External Advisory Board Meeting. Farmington, CT. August 2015.

62. Computational Approaches to Tumor Heterogeneity. JAX group visit to Bristol Myers Squibb. Princeton, NJ. June 2015.

61. Measures and Models of Tumor Evolution. JAX Scientific Director's Series. Farmington, CT. May 2015.

60. Evolution in Cancer Genomes. University of Connecticut Health Center, Department of Genetics and Genome Sciences. Farmington, CT. April 2015.

59. Patient-Derived Xenograft Genomics. Center for Quantitative Medicine / Jackson Laboratory for Genomic Medicine. Farmington, CT. January 2015.

58. Genomic Approaches to Tumor Heterogeneity Using Patient-Derived Xenografts. University of Connecticut Health Center – Center for Vascular Biology. Farmington, CT. December 2014 (invited).

57. Mechanism of a Translational Regulatory Defect Leading to Neurodegeneration. Rutgers University – Camden. Camden, NJ. December 2014 (invited).

56. Developing Individualized Cancer Therapies Using Patient Derived Xenografts. Leo & Anne Albert Institute for Bladder Cancer Care and Research 1st Annual Symposium. Hartford, CT. September 2014 (invited).

55. Genomic Approaches to Treating Breast Cancer. Connecticut Breast Health Initiative Seminar. New Britain, CT. August 2014 (invited).

54. Computational Challenges in Cancer Genomics. 23rd Annual Short Course on Experimental Models of Human Cancer. Bar Harbor, ME. August 2014 (invited).

53. Computational Studies in Cancer Genomics and Gene Regulation. University of Connecticut Institute for Systems Genomics Networking Workshop. Storrs, CT. May 2014 (invited).

52. Inferring Post-Transcriptional Regulatory Mechanisms from Genomics Data. Academia Sinica. Taipei, Taiwan. April 2014 (invited).

51. The PDX Model for Cancer Research. 6th Seoul Breast Cancer Symposium. Seoul, Korea. April 2014 (invited).

50. Solving Tumor Heterogeneity Using Patient-Derived Xenografts. Seoul National University Hospital. Seoul, Korea. April 2014 (invited).

49. Genomics of Evolving Xenografts. The Jackson Laboratory for Genomic Medicine - faculty seminar series. Farmington, CT. April 2014.

48. Mechanism of a Translational Regulatory Defect Leading to Neurodegeneration. University of Connecticut Department of Molecular and Cell Biology. Storrs, CT. April 2014 (invited).

47. New Approaches in Genomics and Bioinformatics at JAX-GM. Connecticut Children's Medical Center. Hartford, CT. March 2014 (invited).

46. Computational Approaches to Cancer Genomics. Connecticut College Workshop on Bridging the Gap Between Computer Science and the Life Sciences. New London, CT. January 2014 (invited).

45. Gene Regulation and Cancer Genomics. JAX/UCONN Workshop on Computational Biology. Storrs, CT. September 2013.

44. Integrating Chemical Footprinting Data into RNA Secondary Structure Prediction. Rutgers University Biological Physics Seminar Series. Piscataway, NJ. May 2013. (invited)

43. Gene Regulation and Cancer Genomics at JAX-GM. University of Connecticut Center for Cell Analysis and Modeling. Farmington, CT. February 2013. (invited)

42. The Prevalence of Hidden Functional Elements in Coding Regions. University of Connecticut Department of Cell and Genome Sciences. Farmington, CT. May 2012. (invited)

41. Statistical Approaches to Identifying Functional Elements in Coding Sequences. Harvard School of Public Health – Program in Quantitative Genomics. Boston, MA. April 2012. (invited)

40. Statistical Approaches to Identifying Functional Elements in Coding Sequences. Shanghai Jiao Tong University Bio-X Institute. Shanghai, China. April 2012. (invited)

39. The Functions of Enhancer Elements. Children's Hospital of Fudan University. Shanghai, China. April 2012. (invited)

38. Detecting Hidden Functional Elements in Coding Sequences. Genome Institute of Singapore. Singapore. March 2012. (invited)

37. Next Generation Sequencing and Its Applications to RNA Biology. Conference on Next Generation Sequencing Applications Asia. Singapore. March 2012. (invited)

36. The Prevalence of Hidden Functional Elements in Coding Regions. The Jackson Laboratory. Bar Harbor, ME. March 2012. (invited)

35. Computational Approaches to Identifying Functional Elements in Coding Sequences. Virginia Bioinformatics Institute at Virginia Tech. Blacksburg, VA. March 2012. (invited)

34. Computational Approaches to Identifying Functional Elements in Coding Sequences. Worcester Polytechnic Institute. Worcester, MA. February 2012. (invited)

33. Detecting Hidden Functional Elements in Coding Sequences. Michigan State University. East Lansing, MI. February 2012. (invited)

32. CodingMotif: Exact Determination of Overrepresented Motifs in Coding Sequences. Intelligent Systems for Molecular Biology Rocky Mountain Conference. Aspen, CO. December 2011.

31. Algorithms for Identifying Functional Elements in Coding Sequences. Miami University of Ohio. Miami, OH. December 2011. (invited)

30. The Prevalence of Hidden Functions in Coding Regions. National Institute of Environmental Health Sciences (NIH). Research Triangle Park, NC. November 2011. (invited)

29. Detecting Hidden Regulatory Functions in Coding Sequences. Virginia Commonwealth University. Richmond, VA. October 2011. (invited)

28. The Evolution of Enhancers in Vertebrate Coding Sequences. Presented at Stonehill College Biology Department. Easton, MA. September 2011. (invited)

27. Functional Elements in Vertebrate Coding Sequences. Presented at the Michigan State Summer Symposium on Transcriptional Dynamics, Evolution, and Systems Biology. East Lansing, MI. July 2011. (invited)

26. Whose Code Is It Anyway? Transcriptional Enhancers Are Embedded in Protein-Coding Exons of Vertebrate Developmental Genes. Presented at the Biology of Genomes Conference. Cold Spring Harbor Laboratory (talk given by lab student D. Ritter). May 2011.

Writing about Scientific Topics (also judged Science Fair) Pioneer Charter School of Science. Everett, MA. April 2011.

25. Highly Conserved Coding Sequences Act as Enhancers. Presented at the RECOMB Satellite Meeting on Regulatory Genomics at Columbia University. New York, NY. November 2010.

24. Regulation, Evolution, and Networks: Some Insights from Computational Biology. Presented at the Boston College Biology Colloquium. Chestnut Hill, MA. October 2010.

23. Evolution of Orthologous Fish and Mammalian Enhancer Activity. Presented at the Society for Molecular Biology and Evolution Meeting. Lyon, France. July 2010.

22. Noncoding Selection on Motifs in Coding Regions. Presented at Dana Farber Cancer Institute, Boston, MA. June 2009. (invited)

21. Noncoding Selection on Motifs in Coding Regions. Presented at the Society for Molecular Biology and Evolution Meeting, Iowa City, Iowa. June 2009.

20. Comparative Analysis of Enhancers and Regulatory Motifs for Gene Expression in the Vertebrate Brain. Presented at the RECOMB Satellite Conference on Regulatory Genomics, Broad Institute of MIT and Harvard, Cambridge, MA. November 2008.

19. Sequences Conserved by Selection Across Mouse and Human Malaria Species. Presented at the Comparative Genomics of Malaria Parasites Meeting, American Museum of Natural History, New York, NY. September 2007. (invited)

18. Sequences Conserved by Selection Across Mouse and Human Malaria Species. Presented at the Society for Molecular Biology and Evolution Meeting, Halifax, Canada. June 2007.

17. Computational Identification of Malaria Gene Regulation. Presented at the New England Association of Parasitologists Meeting, Brown University, Providence, RI. November 2006.

16. Plasmodium Comparative Genomics and Gene Regulation. Presented at the Boston Pathogen and Vector Encounter, Boston College, Chestnut Hill, MA. July 2006. (invited, talk given by lab postdoc H. Imamura)

15. Selection in Synonymous Sites of Mammalian Genes. Presented at the Society for Molecular Biology and Evolution Meeting (Genomes, Evolution, and Bioinformatics), Tempe, AZ. May 2006.

14. Functional and Neutral Sequence in Genome Comparisons. Presented at Condensed Matter Theory Biophysics Seminar, Massachusetts Institute of Technology, Cambridge, MA. October 2005. (invited)

13. Insights from Comparative Genomics: From Genome Organization to Regulatory Complexity. Presented at CSAIL Computational Biology Seminar, Massachusetts Institute of Technology, Cambridge, MA. October 2005. (invited)

12. Computational Approaches to Comparative Genomics. Presented at Department of Physics Colloquium – Boston College, Chestnut Hill, MA. September 2005. (invited)

11. Insights from Comparative Genomics: From Genome Organization to Regulatory

Complexity. Presented at New York University, Department of Biology, New York, NY. February 2005. (invited)

10. Insights from Comparative Genomics: From Genome Organization to Regulatory Complexity. Presented at Boston College, Department of Biology. Chestnut Hill, MA. February 2005. (invited)

9. Insights from Comparative Genomics: From Genome Organization to Regulatory Complexity. Presented at the Bauer Center for Genomics Research – Harvard University, Cambridge, MA. March 2005. (invited)

8. Insights from Comparative Genomics: From Genome Organization to Regulatory Complexity. Presented at Rice University, Department of Bioengineering, Houston, TX. March 2005. (invited)

7. Functional Significance of Spatial Variations in Mutation Rates: Mammals and Yeast. Presented at the Intelligent Systems for Molecular Biology Workshop on Biopathways, Glasgow, Scotland. July 2004. (invited)

6. Functional Bias and Spatial Organization of Genes in Mutational Hot and Cold Regions in the Human Genome. Presented at the UCSF Research in Progress Seminar Series, San Francisco, CA. October 2003.

5. Multiple Point Adsorption in a Heteropolymer Gel and the Tanaka Approach to Imprinting. Presented at the Europolymer Conference, Gargnano, Italy. June 2002.

4. Entropic Slowdowns in Aggregation and Translocation of Biopolymers. Presented at the National Institute of Standards and Technology, Gaithersburg, Maryland. March 2001. (invited)

3. Free Energy Self-Averaging in Protein-Sized Random Heteropolymers. Presented at American Physical Society March Meeting, Seattle, WA. March 2001.

2. Free Energy Self-Averaging in Protein-Sized Random Heteropolymers. Presented at the 84th Statistical Mechanics Conference - Rutgers University, New Brunswick, NJ. December 2000.

1. Free Energy Self-Averaging in Protein-Sized Random Heteropolymers. Presented at the American Physical Society March Meeting, Minneapolis, Minnesota. March 2000.

Laboratory Personnel

Name	Dates	Role	Subsequent Position
Dr. Hyeongu Kang	6/23-	Postdoc (joint with O. Anczukow)	
Jie Zhou	5/20-	PhD student	
Zichao Sam Liu	5/21-	PhD student	
Adam Thiesen	8/22-	MD/PhD student	
Dr. Jill Rubinstein	10/20-	Research scientist	
Dr. Todd Sheridan	7/21-	Research scientist	
Dr. Javad Noorbakhsh	8/24-	Consultant (research scientist)	

Research scientists in JAX Computational Sciences. Partial effort.

Dr. Mike Lloyd	9/17-
Dr. Brian White	9/20-
Dr. Sergii Domanskyi	7/21-
Dr. Ardian Ferraj	1/24-

Dr. Ali Foroughi pour	6/19-6/24	Research scientist	Senior Staff Scientist, St. Jude's
Patience Mukashyaka	5/19-5/24	PhD student	Senior Scientist, Abbvie
Dr. Anuj Srivastava	9/17-2/24	Computational scientist	Moderna
Jingyan Zhang	6/24-8/24	Summer intern	Undergrad, Johns Hopkins
Ben Mulligan	7/24-8/24	Summer intern	Undergrad, RIT

Dr. Brian Sanderson	10/20-8/23	Computational scientist	U. Kansas, Bioinformatics Core Leader
Dr. Minji Kim	6/17-12/22	Postdoc (joint with Y. Ruan)	Asst Prof., U. Michigan
Shauna Schiffman	6/22-8/22	Summer intern	Undergrad, UCSD
Amaris Huang	6/22-8/22	Summer intern	Undergrad, Duke University
Dr. Xingyi Woo	9/17-2/22	Research scientist	Head of Research Data Integration and Senior Principal Investigator, Bioinformatics Institute, A*STAR
Victor Wang	7/17-4/21	MD/PhD student	Residency, Johns Hopkins
Scott Adamson	8/15-4/21	PhD student	Postdoc, UConn.
Dr. Dimitrios Drekolias	5/20-7/20	Visiting MD scientist	
Tejal Nair	1/20-8/20	High school intern	
Fatima Zare	6/19-8/20	PhD student intern (UConn).	Postdoc, Harvard School of Public Health
Jon Park	2/20-6/20	Visiting MD scientist.	Rutgers medical residency
Dr. Chad Smith	12/19-4/20	25% effort, research scientist in JAX Computational Sciences.	Industry
Dr. Jeremy Teitelbaum	4/18-8/19	Visiting professor	Professor, UConn
Lisa Frieden	6/19-8/19	Student intern	Undergrad, Tufts University
Sherry Zhang	5/16-8/16, 6/17-8/17	Student intern	Undergrad, U. Connecticut
Smrithi Raman	10/16-5/17	Student intern	Undergrad, MIT
Lucas Melo	6/17-8/17	Summer intern	High school student
Aiszlyn Zupkus	7/17-8/17	Summer intern	High school student
Alex Iyabor	6/16-8/16	Summer intern	Undergrad, Stanford
Kathryn Rankin	6/16-8/16	Summer intern	
Victor Wang	6/16-8/16	Rotation student (joining as grad student 7/17)	
Benjamin Coleman	6/15-8/15, 6/16-8/16	Summer intern	High school student

Dr. Ziming Zhao	2/17-1/20	Research sci.	Senior Sci, in Translational Oncology, Eisai
Dr. Javad Noorbakhsh	1/15-12/19	Postdoc; research scientist	Scientist, Broad Institute
Dr. Ada Zhan	11/16-3/19	Postdoc (joint with Y. Ruan)	Research scientist, MSKCC
Dr. Hyunsoo Kim	1/13-5/18	Research scientist	Research scientist, St. Jude's.
Dr. Ivan Dotu	9/12-6/17	Visiting scientist	Startup company founder.
Dr. Houman Younessi	8/14-12/15	Visiting prof.	
Dr. Dong-Guk Shin	12/14-12/15	Visiting prof.	Professor, U. Conn.
Emma Ricart Altimiras	3/15-8/15	Research assistant.	Graduate student, ETH.
Cyril Fournier	2/14-8/14	Visiting masters student	Industry
Meredith Shea	6/14-8/14	Summer intern	Undergraduate, Case Western
Jared Graveley	6-8/13, 5/14-8/14	Summer intern	Undergraduate, U. Conn.
Beryl Royer-Bertrand	2/13-7/13	Visit. masters stud.	PhD student, Universite de Lausanne
Dr. Krzysztof Grzeda	11/12-6/15	Research scientist	Bioinformatics consultant
Dr. Kourosh Zarringhalam	6/10-8/12	Postdoctoral	Asst Prof, UMass-Boston
Ningtao Shi	2/11-6/12	Masters student	Software consultant
David Gostine	1/11-8/11	Undergrad	

Lu Zhang	2/08-6/12	Ph.D. student	Scientist, Seven Bridges Genomics
Deborah Ritter	4/07-9/11	Ph.D. student	Postdoc, Wheeler Lab, Baylor College of Medicine
Norberto Diaz-Diaz	7/11-10/11	Visiting sci.	Asst. Prof., Universidad de Pablo de Olavide
Dr. Hideo Imamura	3/06-12/08	Postdoctoral	Inst. of Tropical Med.- Antwerp and Wellcome Trust Sanger Institute research scientist
Dr. Zehua Chen	12/06-12/07	Postdoctoral	Broad Institute of Harvard and MIT research scientist.
Dr. Jessica Lehoczky	6/07-12/07	Visit. Sci.	Harvard Medical School postdoc
Jason Persampieri	12/06-6/08	Programmer	Software engineer, Affinity Circles

Aleah Fox	1/06-5/08	Undergrad	UCSF Ph.D. student
Robert Bell	9/06-7/09	Undergrad	UCSF Ph.D. student (Winner, BC best senior biology thesis 2009)
Hwi Moon	1/06-5/08	Undergrad	Severance Hospital, Seoul, S. Korea
Alicia Korpi	9/08-5/10	Undergrad	U. S. Peace Corps
Toan Phan	6/08-5/10	Undergrad	Tufts U. pre-medical training
Daniel Lees	6/06-8/06	Undergrad	Technology consultant Exeter Group
Jeffrey Wang	6/10-7/10	Summer res.	Auburn H. S., Rockford, IL

Ruoyu Yang	Summer 2022	Rotation Student
Alex Mitchell	Summer 2021	Rotation Student
Adam Thiesen	Summer 2021	Rotation Student
Sam Liu	Spring 2021	Rotation Student
Jie Zhou	Summer 2020	Rotation Student
Patience Mukashyaka	Fall 2018	Rotation Student
Yuliana Tan	Fall 2017	Rotation Student
Victor Wang	Summer 2016	Rotation Student
Laura Urbanski	Summer 2015	Rotation Student
Scott Adamson	Summer 2015	Rotation Student

Bandita Adhikari	Fall 2015	Rotation Student

Rohit Reja	Spring 2011	Rotation Student
Shermin Pei	Fall 2010	Rotation Student
Rashmi Dubey	Fall 2010	Rotation Student
Ningtao Shi	Fall 2010	Rotation Student
Mengyao Zhao	Fall 2009	Rotation Student
Andrew Farrell	Fall 2009	Rotation Student
Yi Qiao	Fall 2009	Rotation Student
Deniz Kural	Fall 2008	Rotation Student
Jiantao Wu	Fall 2008	Rotation Student
Lu Zhang	Fall 2007	Rotation Student
Yang Ding	Fall 2007	Rotation Student
Genevieve Toutain	Summer 2007	Rotation Student
Deborah Ritter	Spring 2007	Rotation Student
Derek Barnett	Fall 2006	Rotation Student
Michele Busby	Fall 2006	Rotation Student
Aliz Axmann	Fall 2006	Rotation Student
Michael Stromberg	Fall 2005	Rotation Student
Didem Demirbas	Fall 2005	Rotation Student

Membership on Graduate Comprehensive Exam Committees
2006. Aaron Quinlan
2007. Michael Stromberg
2007. Didem Demirbas
2008. Derek Barnett
2008. Michele Busby
2008. Brooke Anderson-White
2009. Yang Ding
2010. Deniz Kural
2010. Amit Indap
2010. Jiantao Wu
2011. Mengyao Zhao
2011. Zeynep Akgoc
2014. Gopinath Rajadinakaran
2015. Jufen Zhu
2016. Scott Adamson
2017. Victor Wang
2019. Fatima Zare

Graduate research thesis committees

2006-2008	Aaron Quinlan (Ph.D.)
2007	Jayme Flynn (M.S.)
2007-2010	Michael Stromberg (Ph.D.)
2008	Michael Kiebish (Ph.D.)
2008	Manal Alamery (Ph.D.)
2008-2010	Yang Ding (M.S.)
2007-2011	Deborah Ritter (Ph.D.)
2008-2012	Lu Zhang (Ph.D.)

2010-2012	Ningtao Shi (M.S.)
2008-2012	Michele Busby (Ph.D.)
2008-2012	Derek Barnett (Ph.D.)
2010-2013	Amit Indap (Ph.D.)
2010-2014	Deniz Kural (Ph.D.)
2010-2012	Jiantao Wu (Ph.D.)
2010-2012	Chenjia Xu (Ph.D.)
2010-2012	Linh Ta (Ph. D.)
2014-2018	Gopinath Rajadinakaran (Ph.D.)
2015-2019	Jufen Zhu (Ph.D.)
2017-2019	Russell Posner (M.D./Ph.D.)
2019-2020	Fatima Zare (Ph.D., UConn CSE)
2016-2021	Scott Adamson (Ph.D.)
2017-2021	Victor Wang (M.D./Ph.D.)
2017-2021	Laura Urbanski (M.D./Ph.D.)
2020-2021	Saman Farahmand (PhD., UMass-Boston Math)
2019-2024	Patience Mukashyaka (Ph.D.)
2020-2024	Ziwei Pan (Ph.D.)
2020-2025	Ruoyun Xiong (Ph. D.)
2020-	Jie Zhou (Ph.D.)
2021-	Zichao (Sam) Liu (Ph.D.)
2022-	Adam Thiesen (M.D./Ph.D.)
2022-	Ruoyu Yang (Ph.D.)

Teaching

Undergraduate

Harvard

Math 22a. Fall 1993. Linear Algebra and Multivariable Calculus for Physics Majors. Teaching Fellow.

MIT

Physics 8.08. Spring 2000. Statistical Physics. Teaching Assistant.

Boston College

BI420. Fall 2006. Introduction to Bioinformatics. Guest lecture on Computational Identification of Functional Sequences.

BI420. Fall 2007. Introduction to Bioinformatics. 15 students. 2.5 hours per week. Course co-taught with Prof. G. Marth, who taught a second section. 4 problem sets, 2 midterms, and a final presentation. Teacher rating 3.86 (Bio avg = 3.43)

BI420. Fall 2009. Introduction to Bioinformatics. 25 students. 2.5 hours per week. Course co-taught with Prof. G. Marth, who taught a second section. 3 problem sets, 2 midterms, and a final presentation. Teacher rating 4.00 (Bio avg =3.49)

BI420. Spring 2011. Introduction to Bioinformatics. 39 students. 2.5 hours per week. 3 problem sets, 2 midterms, and a final presentation.

BI462. Spring 2006. Undergraduate Research. 2 students.

BI461. Fall 2006. Undergraduate Research. 3 students.

BI462. Spring 2007. Undergraduate Research. 3 students. Aleah Fox's research was honored by the Society of Molecular Biology and Evolution with a travel fellowship and

poster presentation at SMBE 2007 in Halifax, Canada. It was also published in the BC undergraduate journal Elements.
BI461. Fall 2007. Undergraduate Research. 3 students.
BI462. Spring 2008. Undergraduate Research. 3 students. Aleah Fox wrote a senior thesis.
BI461. Fall 2008. Undergraduate Research. 3 students.
BI462. Spring 2009. Undergraduate Research. 3 students. Robert Bell wrote a senior thesis honored as the best in the BC Biology Department.
BI461. Fall 2009. Undergraduate Research. 2 students.
BI462. Spring 2010. Undergraduate Research. 2 students.
BI462. Spring 2011. Undergraduate Research. 1 student.
BI305. Spring 2006. Genetics. Guest lecture on Molecular Evolution.
BI529. Spring 2012. Molecular Driving Forces. 6 guest lectures on statistical mechanics of biomolecules.

Graduate

Boston College
BI83201 Spring 2006. Literature of Computational Genomics Graduate Seminar. 6 students. 1.5 hours per week. Weekly paper presentations and discussions.
BI561. Spring 2007. Molecular Evolution. 10 students. 2.5 hours per week. 4 problem sets, one midterm, a final exam, and a final presentation. Note: BI561 is also open to advanced undergraduates Rating 4.50 (Bio avg = 3.47)
BI561. Spring 2008. Molecular Evolution. 13 students. 2.5 hours per week. 4 problem sets, a midterm, a final exam, and a final presentation. Rating 4.00 (Bio avg = 3.49)
BI561. Spring 2009. Molecular Evolution. 5 students. 2.5 hours per week. 4 problem sets, a midterm, a final exam, and a final presentation. Rating 5.00 (Bio avg = 3.74)
BI561. Spring 2010. Molecular Evolution. 8 students. 2.5 hours per week. 4 problem sets, a midterm, a final exam, and a final presentation. Rating 4.71 (Bio avg =3.63)
BI561. Fall 2011. Molecular Evolution. 13 students. 2.5 hours per week.

UCONN Health
MEDS 369. Spring 2017. Guest lecture on “Computationally Analyzing Tumor Heterogeneity.”
MEDS 6498. Fall 2017. Guest lecture on “Patient Derived Xenograft Computational Biology.”
MEDS 369. Spring 2019. Guest lecture on “Identifying Selection in Cancer Cells.”
MEDS 369. Spring 2020. Guest lecture on “Identifying Selection in Cancer Cells.”