

RUI FU

New York Genome Center

My research interests are in RNA-binding protein-mediated post-transcriptional gene expression regulation, particularly RNA decay, interrogated through biochemical experiments and computational analyses of genomic data.



EDUCATION

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| 2015

2009 | ● Ph.D. Biological Science
University of California San Diego | 📍 La Jolla, CA, USA |
| 2009

2005 | ● B.S. Biological Science
Xiamen University | 📍 Xiamen, Fujian, China |

RESEARCH EXPERIENCE

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| Current

2022 | ● Senior Bioinformatics Scientist
Computational Biology | 📍 New York Genome Center |
| | • Single cell / spatial transcriptomics analyses and tool development | |
| | • CZI Ancestry Networks: Multi-omics Maps of the Human Endometrium Across Diverse Ancestries | |
| 2021

2017 | ● Semi-Independent Postdoctoral Informatics Fellow
Jay Hesselberth's Supervision | 📍 University of Colorado Anschutz |
| | • Development of bioinformatics software for single cell RNA sequencing | |
| | • RNA dynamics modeling of steroidogenesis | |
| | • RNA-seq analysis and transcriptome annotation improvements for hibernating ground squirrel brain and liver | |
| | • Collaboration on various single cell RNA sequencing projects with clinical investigators | |
| | • Analysis of human genetic variation from gnomAD database for insights into nonsense-mediated mRNA decay | |
| 2017

2016 | ● Postdoctoral Research Fellow
Judy Lieberman's Lab | 📍 Harvard Medical School |
| | • Identification of a mitochondrial trigger for apoptotic mRNA decay | |
| | • Purification of cytotoxic granules and cytolytic proteins from NK cells | |
| | • Mouse genetic manipulation by CRISPR-Cas9, and automated genotyping with custom R app | |
| 2015

2009 | ● Graduate Research Assistant
Jens Lykke-Andersen's Lab | 📍 University of California San Diego |
| | • Investigation of co-factors involved in ZFP36-mediated mRNA decay and translational repression during macrophage innate immune response | |
| | • Characterization of the ZFP36 family proteins in cell cycle progression regulation of mouse embryonic fibroblasts | |

CONTACT

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Bioinformatic tools:

clustifyr, automated single cell RNA-seq cell identity assignment Bioconductor package

squirrelBox, RNA-seq data visualization, exploration, and analysis web browser built with R Shiny and JavaScript

someta, automated monitoring of missing cell-level metadata in scRNA-seq GEO deposition, and R Shiny explorer

scraps, Snakemake pipeline for extraction of polyadenylation site and internal priming information from 3' capture scRNA-seq data

SCoreRust, Rust-based reimplementation of single cell transcriptome pathway scoring

Course material:

bioinformatics intro, rnabioco.github.io/practical-data-analysis

scRNA-seq workshop, rnabioco.github.io/cellar

2009
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2007

● **Undergraduate Research Assistant**

Ruichuan Chen's Lab

📍 Xiamen University

- Exploration of cell cycle and apoptosis implications of the transcription elongation regulator HEXIM1
- Mechanistic characterization of p-TEFb activation by HIV-Tat



PUBLICATIONS, AS FIRST OR CORRESP. AUTHOR

2023

- **In situ reconstruction of distinct normal and pathological cell populations within the human adrenal gland using spatial transcriptomics**
In Prep for *Journal of the Endocrine Society*
• **Fu R**, Walters K, Kocs K, Baldwin A, Kiseljak-Vassiliades K, Fishbein L, Mukherjee N.
- **Hudson, a computational pipeline for spatial analysis of single cells in multiplexed fluorescence imaging**
In Prep for *Bioinformatics*, code at github.com/nygctech/hudson
• Singh J[†], Pandit K[†], **Fu R[†]**, Maniatis S, Vickovic S.

2022

- **scraps: alternative poly-adenylation site usage pipeline for 3' capture single cell RNA sequencing**
In Prep for *Genome Biology*, submitted to *bioRxiv*, code at github.com/rnabioco/scraps
• **Fu R**, Riemondy K, Hesselberth J, Jordan C, Gillen A.
- **Spatial transcriptomic analysis delineates epithelial and mesenchymal subpopulations and transition stages in childhood ependymoma**
Neuro-Oncology
• **Fu R**, Norris G, Willard N, Griesinger A, Riemondy K, Amani V, Grimaldo E, Harris F, Gilani A, Hankinson T, Mitra S, Hesselberth J, Ritzmann T, Grundy R, Foreman N, Donson A.

2021

- **Transcriptomic response dynamics of human primary and immortalized adrenocortical cells to steroidogenic stimuli**
Cells
• Wellman K[†], **Fu R[†]**, Baldwin A, Rege J, Rainey W, Mukherjee N.
- **RNA-binding proteins regulate aldosterone homeostasis in human steroidogenic cells**
RNA
• **Fu R[†]**, Wellman K[†], Baldwin A, Rege J, Bartholomay K, Hirsekorn A, Riemondy K, Rainey W, Mukherjee N.
- **Cell-level metadata is indispensable for documenting single cell sequencing datasets**
PLOS Biology
• Puntambekar S, Hesselberth J, Riemondy K^c, **Fu R^c**.
- **Liver transcriptome dynamics during hibernation are shaped by a shifting balance between transcription and RNA stability**
Frontiers in Physiology
• Gillen A[†], **Fu R[†]**, Riemondy K[†], Jager J, Fang B, Lazar M, Martin S.

2020

- **Dynamic RNA regulation in the brain underlies physiological plasticity in a hibernating mammal**
Frontiers in Physiology
• **Fu R[†]**, Gillen A[†], Grabek K, Riemondy K, Epperson E, Bustamant C, Hesselberth J, Martin S.
- **clustifyr: an R package for automated single-cell RNA sequencing cluster classification**
F1000Research
• **Fu R**, Gillen A, Sheridan R, Tian C, Daya M, Hao Y, Hesselberth J, Riemondy K.

2018

- **PNPT1 release from mitochondria during apoptosis triggers decay of poly(A) RNAs**
Cell
• Liu X[†], **Fu R[†]**, Pan Y, Meza-Sosa K, Zhang Z, Lieberman J.

2016

- Recruitment of the 4EHP-GYF2 cap-binding complex to tetraproline motifs of tristetraprolin promotes repression and degradation of mRNAs with AU-rich elements
RNA
 - Fu R, Olsen M, Webb K, Bennett E, Lykke-Andersen J.

PUBLICATIONS, AS CONTRIBUTING AUTHOR

2023

- DUX4 induces the production of truncated RNA binding proteins in human muscle cells. Submitted to *Cell Reports*, *bioRxiv*. Campbell A, Dyle M, Calviello L, Matheny T, Cortazar M, Forman T, Fu R, Gillen A, Floor S, Jagannathan S.
- Adrenal gene expression dynamics support hibernation in 13-lined ground squirrels. *Physiological Genomics*. Gillen A, Epperson L, Orlicky D, Fu R, Martin S.

2021

- Post-transcriptional control of mating-type gene expression during gametogenesis in *Saccharomyces cerevisiae*. *Biomolecules*. Yeager R, Bushkin G, Singer E, Fu R, Cooperman B, McMurray M.
- Srsf3 mediates alternative RNA splicing downstream of PDGFRa signaling in the facial mesenchyme. *Development*. Dennison B, Larson E, Fu R, Mo J, Fantauzzo K.
- Molecular tracking devices quantify antigen distribution and archiving in the lymph node. *eLife*. Walsh S, Sheridan R, Doan T, Lucas E, Ware B, Fu R, Burchill M, Hesselberth J, Tamburini B.
- Single-cell RNA sequencing identifies macrophage transcriptional heterogeneities in granulomatous diseases. *European Respiratory Journal*. Liao S, Shaikh A, Mould K, Konigsberg I, Fu R, Davidson E, Li L, Fontenot A, Maier L, Yang I.

2019

- Monocytic Subclones Confer Resistance to Venetoclax-Based Therapy in Acute Myeloid Leukemia Patients. *Cancer Discovery*. Pei S, Pollyea D, Gustafson A, Stevens B, Minhajuddin M, Fu R, Riemondy K, Gillen A, Sheridan R, Kim J, Costello J, Amaya M, Inguva A, Winters A, Ye H, Krug A, Jones C, Adane B, Khan N, Ponder J, Schowinsky J, Abbott D, Hammes A, Myers J, Ashton J, Nemkov T, D'Alessandro A, Gutman J, Fesik S, Ramsey H, Savona M, Smith C, Jordan C.
- Chronic Liver Disease in Humans Causes Expansion and Differentiation of Liver Lymphatic Endothelial Cells. *Frontiers in Immunology*. Tamburini B, Finlon JM, Gillen A, Kriss M, Riemondy K, Fu R, Schuyler R, Hesselberth J, Rosen H, Burchill M.
- Single cell RNA Sequencing Identifies Transforming Growth Factor β as a Critical Regulator of Alveolar Regeneration. *JCI Insight*. Riemondy K, Jansing N, Jiang P, Redente E, Gillen A, Fu R, Anthony G, Hesselberth J, Zemans R.
- Recovery and analysis of transcriptome subsets from pooled single-cell RNA-seq libraries. *Nucleic Acid Research*. Riemondy K, Ransom M, Alderman C, Gillen A, Fu R, Finlay-Schultz J, Kirkpatrick G, Di Paola J, Kabos P, Sartorius C, Hesselberth J.

RECOGNITION AND FUNDING

2023

- **New York Science Forward: Towards Inclusive Excellence in Academia Fellow**
Award Amount: Travel costs ~\$1,000

2022

- **Substantial grant writing, National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) Kidney Precision Medicine Project U01**
Award Amount: \$500,000 per year
 - Spatial Mapping of Proteomic and Transcriptional Signatures in Kidney Disease
 - Drafted all content and preliminary data on spatial RNA profiling (~25% of entire proposal)
 - In collaboration with Dr. Joshua Thurman, Dr. Elena Hsieh, and Dr. Julia Wrobel

2021	<ul style="list-style-type: none"> ● CU Anschutz Medical Campus Spatial Transcriptomics Pilot Grant Award Amount: \$15,000 <ul style="list-style-type: none"> • Spatiotemporal Analysis of Microglial Contribution to Immune-Mediated Demyelinating Lesion Formation • Formulated plans and drafted proposal, now carrying out experiments and analysis • Joint submission with Dr. Wendy Macklin
2011 2009	<ul style="list-style-type: none"> ● Colorado RNA Newsletter Spotlight ● Dr. Huang Memorial Scholarship, UC San Diego Award Amount: \$108,000
2008 2006	<ul style="list-style-type: none"> ● First-Class Scholarship, XMU University Merit Student

↳ POSTERS AND PRESENTATIONS

2023	<ul style="list-style-type: none"> ● scraps: an end-to-end pipeline for measuring alternative polyadenylation at high resolution using single-cell RNA-seq. (Science Forward Symposium - Invited Poster) ● Multiplexing samples for simultaneous measurement of RNA and ATAC in single-nuclei: a bioinformatic perspective. (Advances in Genome Biology and Technology General Meeting - Poster)
2022	<ul style="list-style-type: none"> ● MIBI meets Visium. (Human Immunology and Immunotherapy Initiative Translational Immunology Seminar Series - Invited Presentation)
2021	<ul style="list-style-type: none"> ● Practical guide to spatial transcriptomics. (Pulmonary Division Excellence in Respiratory and Critical Care Seminar Series - Invited Presentation) ● Interactive scRNA-seq cell-type classification identifies widespread omission of cell-level annotations in public data repositories. (Keystone eSymposia on Single Cell Biology - Poster with mentee)
2020	<ul style="list-style-type: none"> ● Towards a comprehensive view of dynamic RNA regulation in hibernating 13-lined ground squirrel. (EMBL Conference, From Functional Genomics to Systems Biology - Poster)
2019	<ul style="list-style-type: none"> ● ClustifyR: automated single-cell RNA sequencing cluster classification. (Keystone Symposia on Single Cell Biology - Poster)
2017	<ul style="list-style-type: none"> ● PNPT1 release from the mitochondrial intermembrane space triggers rapid decay of mRNA and poly(A)-tailed ncRNA during apoptosis. (Boston Children's Hospital Research Showcase - Poster)
2015	<ul style="list-style-type: none"> ● TTP-mediated mRNA repression involves recruitment of the 4EHP-GYF2 complex. (Cold Spring Harbor Laboratory mRNA Processing Meeting - Selected Presentation)
2013	<ul style="list-style-type: none"> ● TTP family proteins regulate the stability of retinoblastoma protein mRNAs during serum-stimulated G₀-S transition. (Cold Spring Harbor Laboratory mRNA Processing Meeting - Poster)
2012	<ul style="list-style-type: none"> ● The regulation of TTP family mRNA-decay factors during G₀-S cell cycle progression. (Keystone Symposia on Protein-RNA Interactions - Poster)

↳ TEACHING EXPERIENCE

- **Lecture Instructor (Graduate-Level Courses)**
University of Colorado Anschutz
 - Foundations in Biomedical Sciences (2018, 2019, 2020 online) - lectures, paper discussion, and homework/exam design on RNA biology
 - Workshop for scRNA-seq Data Analysis (2019, 2020 online, 2021) - course development and lectures
 - Practical Data Analysis with R/RStudio (2018, 2019) - course development and lectures
 - Informatics and Statistics for Molecular Biology (2020 online) - teaching and grading on RStudio Cloud
 - Rigor in Research (2020) - lecture on RNA sequencing

- **Weekly RNA Bioscience Initiative Informatics Office Hour**
University of Colorado Anschutz
 - Guidance on RNA and computational research questions from students and researchers of CU Anschutz
- **Teaching Assistant (Graduate-Level Courses)**
University of Colorado Anschutz
 - Practical Computational Biology for Biologists: R (2018, 2019)
 - Practical Computational Biology for Biologists: Python (2018, 2019)
 - Core Topics in Biomedical Sciences (2018)
- **Teaching Assistant (Undergraduate-Level Courses)**
University of California San Diego
 - Molecular Biology (2012)
 - DNA Recombination Lab (2011, 2012)

MENTORING EXPERIENCE

Current
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2022

- **NYGC Summer Internship Mentoring**
New York Genome Center
 - Mentee: African American female undergraduate summer intern
 - Project: single cell analysis of influenza-infected mouse lung
- **Analyst Supervision**
New York Genome Center
 - Mentee: female senior bioinformatics analyst
 - Projects: various single cell and bulk transcriptomics analyses, with a focus on moving analysis pipelines to Google Cloud
- **RNA Bioscience Initiative Internship Mentoring**
University of Colorado Anschutz
 - Mentee: AAPI undergraduate computer science student for 2020 summer internship and beyond
 - Project: systemic exploration of published scRNA-seq cell type signatures in the Gene Expression Omnibus
 - Mentee's work was integrated into first-author data-driven essay, updates to R Bioconductor packages *clustifyr* and *clustifyrdatahub*, GitHub repo *someta*, and poster presentation.
- **Summer Research Mentoring**
Harvard Medical School
 - Mentee: high school student enrolled in the MIT Research Science Institute program
 - Topics: tissue culture, RNA-related bench experiments, RNA-seq informatics analysis, and scientific writing
 - Facilitated research opportunity for mentee at Tsinghua University a year later.
- **BS/MS Student Research Mentoring**
University of California San Diego
 - Mentee: female undergraduate/master student
 - Project: biochemical investigation of RNA-binding protein functions
 - Mentee's work was integrated into second-author 2016 RNA publication. Mentee was awarded Best Poster Presentation Award at 2014 UCSD Biological Sciences Annual Student Research Showcase.

DIVERSITY, EQUITY, AND INCLUSION

Current
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2022

- **NYGC Diversity, Equity, & Inclusion Advisory Group and Faculty/Mentorship Subcommittee member**
- **Autism in the Workplace Training**
- **Admission and Evaluation Committees for CU Graduate Experiences for Multicultural Students Program**

- 2021
- RNA Society Volunteer – Writer for Scientist Spotlight
 - CU Anschutz Medical Campus Equity Certificate Program training and LGBTQ+ Hub Diversity training
- 2019
- Inclusive STEM Teaching Course training
 - Mentor for CU Anschutz and Denver Campus ISCORE undergraduate mentorship program

📢 SERVICE AND TRAINING

- Current | 2018
- ***GENETICS* Early Career Reviewer (Cellular Genetics section)**
20 reviews for *Genetics*, *Scientific Reports*, *Frontiers in Immunology*, *BMC Bioinformatics*, etc; bit.ly/publons-rui-fu
- 2023
- Organizing committee member for 2023 Bioconductor conference
- 2021 | 2019
- Annual RNA Bioscience Initiative Grant Review
- 2020
- Organizer for CU Anschutz Immuno-Informatics Joint Journal Club
- 2017
- Data Incubator Data Science Fellowship
- 2016
- Harvard Medical School Scientists Teaching Science Course

🐠 SCIENCE OUTREACH

- Educational Explainer at American Museum of Natural History - Butterfly Conservatory (2023 -)
- Facilitator at Denver Museum of Nature and Science - Prehistoric Journey section (2019 - 2020)
- Visitor Education Volunteer at the New England Aquarium (2016 - 2017)
- Information Ambassador at the San Diego Zoo (2015 - 2016)
- Organizer for UCSD Ethics Center's Silent Spring 50th Anniversary Project (2012)