

RUI FU

RNA Bioscience Initiative, University of Colorado Anschutz Medical Campus

My research interests are in the various aspects of post-transcriptional gene expression regulation, particularly RNA degradation. In lieu of 10 years of bench research experience, I have now worked several years in computational roles analyzing high throughput sequencing data.

EDUCATION

2015
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2009

- **Ph.D. Biological Science**
University of California San Diego 📍 La Jolla, CA, USA
- **B.S. Biological Science**
Xiamen University 📍 Xiamen, Fujian, China

RESEARCH EXPERIENCE

Current
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2017

- **Semi-Independent Informatics Fellow**
Jay Hesselberth's Supervision 📍 University of Colorado Anschutz
 - Development of bioinformatics software packages
 - RNA-seq analysis and transcriptome annotation improvements for hibernating ground squirrel brain regions
 - Informatics support on various RNA biology collaborations, analyzing genomic and sequencing data
- **Postdoctoral Research Fellow**
Judy Lieberman's Lab 📍 Harvard Medical School
 - Identification of the mitochondrial trigger of apoptotic mRNA decay
 - Purification of cytotoxic granules and key cytolytic proteins
 - Mouse genetic manipulation by CRISPR-Cas9, and automated genotyping with R
- **Graduate Research Assistant**
Jens Lykke-Andersen's Lab 📍 University of California San Diego
 - Investigation of co-factors involved in ZFP36 (TTP)-mediated mRNA decay and translational repression during the immune response of macrophages
 - Characterization of the roles of ZFP36 family proteins in cell cycle progression regulation of mouse embryonic fibroblasts
- **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

CONTACT

- ✉ Rui.Fu@CUanschutz.edu
📞 +1 858-344-2507
🔗 github.com/raysinensis
🔗 linkedin.com/in/rui-fu-rna
🔗 raysinensis.com

Bioinformatic tool development:
1) *clustifyr*, single cell RNA-seq cell identity assignment (author);
2) *valr*, tidyverse-style genomic interval analysis (co-developer);
3) *scraps*, extraction of polyadenylation site info from scRNA-seq data (co-developer);
4) *squirrelBox*, RNA-seq data visualization and analysis browser using R Shiny and JavaScript (author)



TEACHING EXPERIENCE

Current
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2020

- **Online Lecture Instructor (Graduate Level Courses)**

University of Colorado Anschutz

- RStudio Cloud lecture for *Informatics and Statistics for Molecular Biology*
- Zoom lectures, paper discussion, and exam/homework design for RNA section of *Foundations in Biomedical Sciences*

Current
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2018

- **Lecture Instructor (Graduate Level Courses)**

University of Colorado Anschutz

- Lecture for RNA sequencing section of *Rigor in Research* (2020)
- Lectures, paper discussion, and exam/homework design for RNA section of *Foundations in Biomedical Sciences* (2018, 2019)
- Course Development and Lectures for *Practical Data Analysis with R/RStudio* (2018, 2019)
- Workshop for *scRNA-seq Data Analysis* (2019)

Current
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2018

- **Teaching Assistant (Graduate Level Courses)**

University of Colorado Anschutz

- *Practical Computational Biology for Biologists: R*
- *Practical Computational Biology for Biologists: Python*
- Paper discussion for *Core Topics in Biomedical Sciences*

Current
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2018

- **RNA Bioscience Initiative Informatics Office Hour (weekly)**

University of Colorado Anschutz

- Guidance on RNA and computational research questions from students and researchers

2020

- **RNA Bioscience Initiative Summer Internship Mentoring**

University of Colorado Anschutz

- Mentoring of undergraduate summer research, systemically exploring published scRNA-seq cell type signatures

2017

- **Summer Research Mentoring**

Harvard Medical School

- Mentoring of high school student enrolled in the MIT Research Science Institute program in tissue culture and RNA-related bench experiments, RNA-seq informatics analysis, and scientific writing

Additional pedagogy training through the Harvard Medical School Scientists Teaching Science Course

Developed computational course materials: 1) rnabioco.github.io/practical-data-analysis; 2) rnabioco.github.io/cellar

2015
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2013

- **BS/MS Student Research Mentoring**
University of California San Diego
 - Mentoring of student research spanning undergraduate honor thesis and master thesis
 - Mentee was awarded Best Poster Presentation Award at 2014 Biological Sciences Annual Student Research Showcase
- **Teaching Assistant (Undergraduate Level Courses)**
University of California San Diego
 - *Molecular Biology, DNA Recombination Lab x2*

2012
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2011

≡ PUBLICATIONS, AS FIRST AUTHOR

- 2020
- **Dynamic Gene Expression in Three Brain Regions during Mammalian Hibernation: Cause or Consequence of Physiology?**
Submitted to *bioRxiv* and *Genome Biology*
 - Fu R⁷, Gillen A⁷, Grabek K, Riemony K, Epperson E, 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, Riemony K.
 - **PNPT1 release from mitochondria during apoptosis triggers decay of poly(A) RNAs**
Cell
 - Liu X⁷, Fu R⁷, Pan Y, Meza-Sosa K, Zhang Z, Lieberman J.
 - **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 MT, Webb K, Bennett EJ, Lykke-Andersen J.
- 2020
- 2018
- 2016
- Google Scholar:
tinyurl.com/googlescholar-rf
- GitHub Projects:
github.com/rnabioco

≡ PUBLICATIONS, AS CONTRIBUTING AUTHOR

- 2020
- **Single-cell RNA sequencing identifies macrophage transcriptional heterogeneities in granulomatous diseases**
Submitted to *American Journal of Respiratory and Critical Care Medicine*
 - Liao S, Shaikh A, Konigsberg I, Fu R, Davidson E, Li L, Mould K, Fontenot A, Maier L, Yang I.

- 2019 ● **Monocytic Subclones Confer Resistance to Venetoclax-Based Therapy in Acute Myeloid Leukemia Patients**
Cancer Discovery
• Pei S, Polleyea D, Gustafson A, Stevens B, Minhajuddin M, **Fu R**, Riemony 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.
- 2019 ● **Chronic Liver Disease in Humans Causes Expansion and Differentiation of Liver Lymphatic Endothelial Cells**
Frontiers in Immunology
• Tamburini, BAJ, Finlon JM, Gillen A, Kriss MS, Riemony K, **Fu R**, Schuyler R, Hesselberth J, Rosen HR, Burchill MA.
- 2019 ● **Single cell RNA Sequencing Identifies Transforming Growth Factor β as a Critical Regulator of Alveolar Regeneration**
JCI Insight
• Riemony K, Jansing N, Jiang P, Redente E, Gillen A, **Fu R**, Anthony G, Hesselberth J, Zemans R.
- 2019 ● **Recovery and analysis of transcriptome subsets from pooled single-cell RNA-seq libraries.**
Nucleic Acid Research
• Riemony K, Ransom M, Alderman C, Gillen A, **Fu R**, Finlay-Schultz J, Kirkpatrick G, Di Paola J, Kabos P, Sartorius C, Hesselberth J.

► POSTERS AND TALKS

- 2019 ● **ClustifyR: automated single-cell RNA sequencing cluster classification**
Keystone Symposia on Single Cell Biology (Poster)
- 2017 ● **PNPT1 release from the mitochondrial intermembrane space triggers rapid decay of mRNA and poly(A)-tailed ncRNA during apoptosis**
Boston Children's Hospital PCMM Research Poster Session (Poster)
- 2016 ● **PNPT1 release from the mitochondrial intermembrane space triggers rapid decay of mRNA during apoptosis**
Boston Children's Hospital PCMM Research Poster Session (Poster)
- 2015 ● **TTP-mediated mRNA repression involves recruitment of the 4EHP-GYF2 complex**
Cold Spring Harbor Laboratory mRNA Processing Meeting (Presentation)
- 2014 ● **TTP represses translation of target mRNAs through the 4EHP-GYF2 complex**
UCSD Mechanisms of Gene Expression Seminar (Presentation)

- 2013
- 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
- The regulation of TTP family mRNA-decay factors during G₀-S cell cycle progression
Keystone Symposia on Protein-RNA Interactions (Poster)

❸ SERVICE, TRAINING, RECOGNITION

- Current | 2020
- RNA Bioscience Initiative Grant Review
- Current | 2018
- *GENETICS* Early Career Reviewer (Cellular Genetics section)
4 manuscripts reviewed for *GENETICS* and *G3*
- Current | 2011
- Peer review of manuscripts under Dr Lykke-Andersen, Dr Lieberman, Dr Hesselberth
- 2019
- Admissions Committee Member for CU Graduate Experiences for Multicultural Students
- 2019
- Mentor for CU Anschutz and Denver Campus ISCORE undergraduate mentorship program
- 2018
- BioFrontiers Hackathon
- 2017
- Data Incubator Data Science Fellowship
- 2016
- Grant Writing Training under Dr Lieberman
- 2016
- Harvard Medical School Scientists Teaching Science Course
- 2012
- Organizer for UCSD Ethics Center's Silent Spring (50th Anniversary) Project
- 2011 | 2009
- Dr Huang Memorial Scholarship, UC San Diego
- 2009 | 2007
- National College Students Creativity Experiment Project
- 2008 | 2006
- First-Class Scholarship
- 2008 | 2006
- XMU University Merit Student

Society memberships: 1) RNA Society; 2) International Society for Computational Biology; 3) Genetics Society of America

❹ SCIENCE OUTREACH

- Current | 2019
- Facilitator at Denver Museum of Nature and Science - Prehistoric Journey section

~500 hours of weekend volunteering time logged

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- Visitor Education Volunteer at the New England Aquarium
 - Information Ambassador at the San Diego Zoo

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Code at github.com/raysinensis/cv.

Last updated on 2020-07-01.