

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 3 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
 - Informatics collaboration on various RNA biology projects, 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 custom R app
- **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

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- 🔗 linkedin.com/in/rui-fu-rna
- 🔗 raysinensis.com

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



TEACHING EXPERIENCE

Current
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2020

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

University of Colorado Anschutz

- Teaching with RStudio Cloud 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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2017

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

University of Colorado Anschutz

- Guidance on RNA and computational research questions from students and researchers of CU Anschutz Medical Campus

2020

- **RNA Bioscience Initiative Summer Internship Mentoring**

University of Colorado Anschutz

- Mentoring of undergraduate summer research, systemically exploring published scRNA-seq cell type signatures in the NCBI Gene Expression Omnibus
- Project, archived at github.com/rnabioco/scRNA-seq-Cell-Ref-Matrix, contributed to updates to R Bioconductor packages *clustifyr* and *clustifyrdatahub*

2017

- **Summer Research Mentoring**

Harvard Medical School

- Mentoring of high school student enrolled in the MIT Research Science Institute program in tissue culture, 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 biology 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 in biochemical investigations of RNA-binding protein functions
 - Mentee was awarded Best Poster Presentation Award at 2014 UCSD 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
- **Post-transcriptional regulation dictates steroidogenic gene expression program kinetics**
In Preparation
 - Fu R⁷, Daigneault J⁷, Riemony K, Mukherjee N.
 - **Dynamic RNA regulation in the brain underlies physiological plasticity in a hibernating mammal**
Submitted to Genome Biology
 - Fu R⁷, Gillen A⁷, Grabek K, Riemony 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, 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.
- 2018
- **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.
- Google Scholar:
tinyurl.com/googlescholar-rf
- GitHub Projects:
github.com/rnabioco
- squirrelBox Web App:
tinyurl.com/sqRNABox



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, 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, BAJ, Finlon JM, Gillen A, Kriss MS, Riemondy 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
 - Riemondy 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
 - Riemondy 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 | 2019 ● RNA Bioscience Initiative Grant Review
- Current | 2018 ● **GENETICS Early Career Reviewer (Cellular Genetics section)**
4 manuscripts reviewed for *GENETICS* and *G3*, tinyurl.com/rev-rf
- 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

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

2008
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2006

- XMU University Merit Student

Current
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2019

● SCIENCE OUTREACH

2017
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2016
2016
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2015

- Facilitator at Denver Museum of Nature and Science - Prehistoric Journey section
- Visitor Education Volunteer at the New England Aquarium
- Information Ambassador at the San Diego Zoo

~500 hours of weekend volunteering time logged

Made with [pagedown](#).

Code at github.com/raysinensis/cv.

Last updated on 2020-08-18.