# 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. Alongside 10 years of bench research experience, I have now worked 3 years in computational roles analyzing genomic and high throughput sequencing data.



#### CONTACT

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

Ø raysinensis.com

# **EDUCATION**

Ph.D. Biological Science

University of California San Diego

🗣 La Jolla, CA, USA

**B.S. Biological Science** 

Xiamen University

🕈 Xiamen, Fujian, China



2015

2009

2009

2005

Current

2017

2017

2016

#### RESEARCH EXPERIENCE

Semi-Independent Informatics Fellow

Jay Hesselberth's Supervision • University of Colorado Anschutz

· Development of bioinformatics software packages

- · RNA post-transcriptional dynamics modeling of steroidogenesis
- RNA-seq analysis and transcriptome annotation improvements for hibernating ground squirrel brain
- · Collaboration on various RNA biology projects

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

2015 | 2009

#### **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
- $\cdot$  Characterization of the ZFP36 family proteins in cell cycle progression regulation of mouse embryonic fibroblasts

2009 | 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

Bioinformatic tool development:

clustifyr, automated single cell RNA-seq cell identity assignment (author)

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

someta, quantification and monitoring of missing cell-level metadata in scRNA-seq GEO deposition (author)

*valr*, tidyverse-style genomic interval analysis (co-developer)

**scraps**, extraction of polyadenylation site info from scRNA-seq data (co-developer)

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## ♣☐ TEACHING EXPERIENCE

#### Current | 2020

#### Online Lecture Instructor (Graduate Level Courses)

University of Colorado Anschutz

- Informatics and Statistics for Molecular Biology (2020) teaching and grading on RStudio Cloud platform
- Foundations in Biomedical Sciences (2020) Zoom lecture, paper discussion, and exam/homework design on RNA biology
- Workshop for scRNA-seq Data Analysis (2020) course development and online lectures

#### Current | 2018

#### Lecture Instructor (Graduate Level Courses)

University of Colorado Anschutz

- · Rigor in Research (2020) lecture on RNA sequencing
- Foundations in Biomedical Sciences (2018, 2019) lectures, paper discussion, and exam/homework design on RNA biology
- Practical Data Analysis with R/RStudio (2018, 2019) course development and lectures
- Workshop for scRNA-seq Data Analysis (2019) course development and lectures

#### Current | 2018

### 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)
- · Paper discussion for Core Topics in Biomedical Sciences (2018)

#### Current | 2017

#### 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 Medical Campus



#### Teaching Assistant (Undergraduate Level Courses)

University of California San Diego

- · Molecular Biology (2012)
- · DNA Recombination Lab (2011, 2012)

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

Developed computational biology course materials:

rnabioco.github.io/practical-data-analysis

rnabioco.github.io/cellar

### **MENTORING EXPERIENCE**

Current 2020

#### **RNA Bioscience Initiative Internship Mentoring**

University of Colorado Anschutz

- · Mentoring of undergraduate computer science student, systemically exploring published scRNA-seq cell type signatures in the NCBI Gene **Expression Omnibus**
- · Mentee's work was integrated into updates to R Bioconductor packages clustifyr and clustifyrdatahub
- · Mentoring is continuing beyond summer intern period, now focusing on manuscript preparation, poster presentation, and further scRNA-seq software development

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-seg informatics analysis, and scientific writing

2015 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
- · Mentee was awarded Best Poster Presentation Award at 2014 UCSD Biological Sciences Annual Student Research Showcase
- · Research project was integrated into the 2016 RNA manuscript, with mentee as second author

### **▶** PUBLICATIONS, AS FIRST AUTHOR

2021

### RNA-binding proteins regulate aldosterone homeostasis in human steroidogenic cells

Submitted to Molecular Systems Biology

• Fu R<sup>1</sup>, Wellman K<sup>1</sup>, Daigneault J, Hammer G, Rainey B, Riemondy K, Mukherjee N.

2021

#### A shifting balance between transcription and RNA stability shapes the dynamic liver transcriptome during hibernation

Submitted to Frontiers in Physiology

· Gillen A<sup>1</sup>, Fu R <sup>1</sup>, Riemondy K, Jager J, Fang B, Lazar M, Martin S.

2020

### Inclusion of processed cell metadata improves single cell sequencing analysis reproducibility and accessibility

Submitted to biorxiv, Under review at PLOS Biology

• Puntambekar S, Hesselberth J, Riemondy  $K^c$ , Fu  $\mathbb{R}^c$ .

Google Scholar: tinyurl.com/googlescholar-rf

GitHub Projects: github.com/rnabioco

squirrelBox Web App: tinyurl.com/sqRNAbox 2020 Dynamic RNA regulation in the brain underlies physiological plasticity in a hibernating mammal

Frontiers in Physiology

- $\cdot$  Fu  $\mathbb{R}^7$ , Gillen  $\mathbb{A}^7$ , Grabek K, Riemondy K, Epperson E, Bustamant C, Hesselberth J, Martin S.
- clustifyr: an R package for automated single-cell RNA sequencing

F1000Research

- Fu R, Gillen A, Sheridan R, Tian C, Daya M, Hao Y, Hesselberth J, Riemondy K.
- PNPT1 release from mitochondria during apoptosis triggers decay of poly(A) RNAs

Cell

- · Liu X<sup>1</sup>, Fu R<sup>1</sup>, 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

2021

· Fu R, Olsen MT, Webb K, Bennett E, Lykke-Andersen J.

### ■ PUBLICATIONS, AS CONTRIBUTING AUTHOR

 BTK signaling regulates real-time microglial dynamics and prevents demyelination in a novel in vivo model of antibody-mediated cortical demyelination

In prep for Nature Medicine

- · Barr H, Given K, McClain C, Gruber R, Ofengeim D, **Fu R**, Macklin W, Bennett J, Owens G, Hughes E
- 2020 Srsf3 mediates alternative RNA splicing downstream of PDGFRa signaling

Submitted to biorxiv and Developmental Cell

- · Dennison B. Larson E. Fu R. Mo J. Fantauzzo K.
- Molecular tracking devices quantify antigen distribution and archiving in the lymph node

Submitted to biorxiv, Revision at eLife

· Walsh S, Sheridan R, Doan T, Lucas E, Ware B, **Fu R**, Burchill M, Hesselberth J, Tamburini B.

# 2020 Single-cell RNA sequencing identifies macrophage transcriptional heterogeneities in granulomatous diseases

Revision at 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.

### Monocytic Subclones Confer Resistance to Venetoclax-Based Therapy in Acute Myeloid Leukemia Patients

Cancer Discovery

2019

2019

2019

2019

2021

2020

2019

• 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.

### POSTERS AND TALKS

 clustifyr2.o: leveraging GEO deposited single cell data for automated cell type classification

Keystone eSymposia on Single Cell Biology (Poster)

 Towards a comprehensive view of dynamic RNA regulation in hibernating 13-lined ground squirrel

EMBL Conference, From Functional Genomics to Systems Biology (Poster)

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	<ul> <li>TTP family proteins regulate the stability of retinoblastoma protein mRNAs during serum-stimulated G<sub>o</sub>-S transition</li> </ul>	
	Cold Spring Harbor Laboratory mRNA Processing Meeting (Poster)	
2012	• The regulation of TTP family mRNA-decay factors during G <sub>o</sub> -S cell cycle progression	
	Keystone Symposia on Protein-RNA Interactions (Poster)	
	PROFESSIONAL SERVICE	
Current	Organizer for CU Anschutz Immuno-Informatics Joint Journal Club	
Current   2020	Organizer for CU Anschutz Immuno-Informatics Joint Journal Club	
	<ul> <li>Organizer for CU Anschutz Immuno-Informatics Joint Journal Club</li> <li>RNA Bioscience Initiative Grant Review</li> </ul>	Cariata manula makin m
2020 Current		Society memberships:
 2020		RNA Society
 2020 Current   2019	<ul> <li>RNA Bioscience Initiative Grant Review</li> <li>GENETICS Early Career Reviewer (Cellular Genetics section)</li> <li>4 manuscripts reviewed for GENETICS and G3, tinyurl.com/rev-rf</li> </ul>	
Current   2019   Current   2018   Curren	<ul> <li>RNA Bioscience Initiative Grant Review</li> <li>GENETICS Early Career Reviewer (Cellular Genetics section)</li> </ul>	RNA Society International Society for
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Made with pagedown.

Code at github.com/raysinensis/cv.

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