

RUI FU

RNA Bioscience Initiative, University of Colorado Anschutz Medical Campus

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

- 2015
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2009 • **Ph.D. Biological Science**
University of California San Diego La Jolla, CA, USA
- 2009
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2005 • **B.S. Biological Science**
Xiamen University Xiamen, Fujian, China

RESEARCH EXPERIENCE

- Current
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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
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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
- 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

CONTACT

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Bioinformatic tool development:

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, quantification and automated monitoring of missing cell-level metadata in scRNA-seq GEO deposition

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

Developed course material:

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

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



PUBLICATIONS, AS FIRST OR CORRESP. AUTHOR

- 2021 • **scraps: alternative poly-adenylation site usage pipeline for 3' capture single cell RNA sequencing**
In Prep for *Genome Biology*, GitHub repository <https://github.com/rnabioco/scraps>
• Fu R, Riemondy K, Hesselberth J, Jordan C, Gillen A.
- 2021 • **Single cell profiling of airway associated CD4+ T cells in chronic beryllium disease**
Submitted to *European Respiratory Journal*
• Shaikh A¹, Fu R¹, Falta M, Martin A, Yang I, Maier L, Fontenot A.
- 2021 • **Transcriptomic response dynamics of human primary and immortalized adrenocortical cells to ACTH and Angiotensin II**
Revisions at *Cells*
• Wellman K¹, Fu R¹, Baldwin A, Rege J, Rainey W, Mukherjee N.
- 2021 • **RNA-binding proteins regulate aldosterone homeostasis in human steroidogenic cells**
RNA (IF: 4.942)
• Fu R¹, Wellman K¹, Baldwin A, Rege J, Bartholomay K, Hirsekorn A, Riemondy K, Rainey W, Mukherjee N.
- 2021 • **Cell-level metadata is indispensable for documenting single cell sequencing datasets**
PLOS Biology (IF: 8.029)
• Puntambekar S, Hesselberth J, Riemondy K^c, Fu R^c.
- 2021 • **Liver transcriptome dynamics during hibernation are shaped by a shifting balance between transcription and RNA stability**
Frontiers in Physiology (IF: 4.566)
• Gillen A¹, Fu R¹, Riemondy K¹, 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 (IF: 4.566)
• Fu R¹, Gillen A¹, Grabek K, Riemondy K, Epperson E, Bustamant C, Hesselberth J, Martin S.
- 2020 • **clustifyr: an R package for automated single-cell RNA sequencing cluster classification**
F1000Research (CiteScore: 4.4)
• 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 (IF: 41.582)
• Liu X¹, Fu R¹, 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 (IF: 4.942)
• Fu R, Olsen MT, Webb K, Bennett E, Lykke-Andersen J.



PUBLICATIONS, AS CONTRIBUTING AUTHOR

- 2021 • Microglia engulf myelin during antibody-mediated cortical demyelination. Submitted to *Nature Medicine*. Barr H, Given K, McClain C, Fu R, Stockton M, Hickman J, Lee L, Gruber R, Ofengeim D, Macklin W, Bennett J, Owens G, Hughes E.
- 2021 • DUX4 induces the production of truncated RNA binding proteins in human muscle cells. *bioRxiv*, submitted to *eLife*. Campbell A, Dyle M, Calviello L, Matheny T, Cortazar M, Forman T, Fu R, Gillen A, Floor S, Jagannathan 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.

- 2021 • Srsf3 mediates alternative RNA splicing downstream of PDGFRa signaling in the facial mesenchyme. *Development*. Dennison B, Larson E, **Fu R**, Mo J, Fantauzzo K.
- 2021 • 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.
- 2021 • 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.
- 2019 • 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.
- 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

- 2021 • Practical guide to spatial transcriptomics. (Pulmonary Division Excellence in Respiratory and Critical Care Seminar Series - Invited Presentation)
- 2021 • 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 • Towards a comprehensive view of dynamic RNA regulation in hibernating 13-lined ground squirrel. (EMBL Conference, From Functional Genomics to Systems Biology - Poster)
- 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 Research Showcase - Poster)
- 2015 • TTP-mediated mRNA repression involves recruitment of the 4EHP-GYF2 complex. (Cold Spring Harbor Laboratory mRNA Processing Meeting - Selected 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)



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 | 2020 • **RNA Bioscience Initiative Internship Mentoring**
University of Colorado Anschutz
• Mentee: 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.
- 2017 • **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
- 2015 | 2013 • **BS/MS Student Research Mentoring**
University of California San Diego
• Mentee: 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.

SERVICE AND TRAINING

- Current | 2019 • **RNA Bioscience Initiative Grant Review**
- Current | 2018 • ***GENETICS* Early Career Reviewer (Cellular Genetics section)**
12 reviews in *GENETICS*, *G3*, *Frontiers in Immunology*, *Frontiers in Genetics*, *ncRNA*, *Genes*, *CSBJ*, *BB Reports*.
- 2020 • **Organizer for CU Anschutz Immuno-Informatics Joint Journal Club**
- 2017 • **Data Incubator Data Science Fellowship**
- 2016 • **Grant writing workshop, Dr. Lieberman**
- 2016 • **Harvard Medical School Scientists Teaching Science Course**

DIVERSITY, EQUITY, AND INCLUSION

- 2021 | 2019 • **Admissions and Evaluation Committees for CU Graduate Experiences for Multicultural Students Program**

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



RECOGNITION AND FUNDING

- 2021 • **CU Anschutz Medical Campus Spatial Transcriptomics Pilot Grant**
 - Award Amount: \$15,000
 - 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
- 2021 • **Substantial NIH U01 Grant Writing**
 - Submitted to National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK)
 - Spatial proteomics and transcriptomics of acute kidney injury and chronic kidney disease
 - Drafted all content (~25% of entire proposal) on spatial RNA profiling; In collaboration with Dr. Joshua Thurman, Dr. Elena Hsieh, and Dr. Kimberly Jordan
- 2021 • **Colorado RNA Newsletter Spotlight**
- 2011 | 2009 • **Dr. Huang Memorial Scholarship, UC San Diego**
 - Award Amount: \$108,000
- 2008 | 2006 • **First-Class Scholarship, XMU University Merit Student**



SCIENCE OUTREACH

- 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)



REFERENCES

- **Dr. Jens Lykke-Andersen, Professor**
Division of Biological Sciences, University of California, San Diego
• jlykkeandersen@ucsd.edu
• 858-822-3659
- **Dr. Judy Lieberman, Professor and Chair**
Cellular and Molecular Medicine, Boston Children's Hospital of Harvard Medical School
• judy.lieberman@childrens.harvard.edu
• 617-713-8600
- **Dr. Jay Hesselberth, Associate Professor**
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• 303-724-5384

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Code at github.com/raysinensis/cv.

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