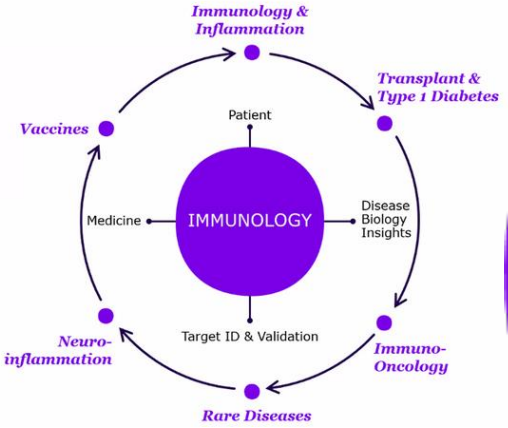

30TH
ANNUAL MEETING
OF THE RNA SOCIETY
May 27th - June 1st, 2025
San Diego, USA
RNA
SOCIETY

mRNA Center of Excellence



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We chase the *miracles* of science to improve people's lives.

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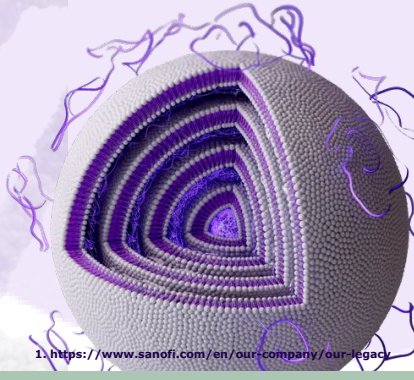
- Unlock the potential of mRNA in Vaccines with Next-Generation platform
- Build an industry leading pipeline to address unmet needs



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1. https://www.sanofi.com/en/our-company/our-legacy

RNA 2025

The 30th Annual Meeting of the RNA Society

May 27th– June 1st, 2025
San Diego, USA

MEETING ORGANIZERS

Katrin Karbstein, Vanderbilt University, USA
Atlanta Cook, University of Edinburgh, Scotland
Anita H. Corbett, Emory University, USA
Jørgen Kjems, Aarhus University, Denmark
Zefeng Wang, Chinese Academy of Sciences, China

Dear RNA colleagues,

Welcome to RNA 2025! This year we return to the United States, where we will enjoy the wonderful facilities and weather of San Diego, California, along with the latest advancements on RNA research. The last time the RNA Society meeting was held in USA was in 2022 in Boulder, Colorado. That was the first 'in-person' meeting after the COVID-19 pandemic, and we were thrilled to reconnect with our friends and discuss science at length without the barrier of a computer screen. This year's meeting also comes at a pivotal moment for science, in the USA and worldwide, and for RNA science in particular. I find it significant that the meeting takes place this year in the USA and look forward to our collective efforts to devise smart ways to address current challenges- scientific, organizational, even political - based on our shared principles of evidence-based decisions and community support. RNA 2025 provides an opportunity to not only talk about RNA science, but also about ways to ensure that science is protected and all of our colleagues supported.

The meeting this year will include the usual scientific sessions, DEI and RNA Junior Scientists panels, Mentoring dinner, Awards Ceremony and celebratory banquet. Significantly, this year we are introducing a special oral presentation session focused on education, which will highlight the importance of training and inspiring the future generation of RNA scientists. This is complemented by a pre-conference workshop designed to address resource gaps in RNA education and ways to share effective strategies.

I encourage you to take full advantage of all that RNA 2025 has to offer—learn, connect, and enjoy the thriving world of RNA science. And don't forget to meet the Editors of the flagship journal of the RNA Society - RNA; they are eager to speak with you about your science!

In closing, I would like to extend heartfelt thanks to our outstanding organizers Katrin Karbstein, Atlanta Cook, Anita Corbett, Jørgen Kjems and Zefeng Wang. Their dedication and effort have made this incredibly attractive meeting program possible.

Thank you for attending RNA 2025, and looking forward to seeing you soon.

Fátima Gebauer
President, RNA Society

The RNA Society

Officers of the RNA Society FY 2025

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Membership Committee
Kristin Koutmou, Univ of Michigan, USA

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Cover image and image above: San Diego at Sunset *was created by RNA Society member Carly Lancaster using acrylic paint on canvas where the paint was thickened with cornstarch to bring texture to the piece. Dr. Lancaster, who now holds an industry research position, completed her PhD in Dr. Anita Corbett's research group at Emory University in Atlanta, Georgia, USA, in 2024.*

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GENERAL MEETING GUIDELINES

All those partaking in RNA 2025 sessions, events and activities must be a registered meeting participant. Meeting badges must be warn by RNA 2025 attendees at all times.

Citation of abstracts presented during RNA 2025 (in bibliographies or other) is strictly prohibited. Material should be treated as personal communication and is to be cited only with the expressed written consent of the author(s).

NO UNAUTHORIZED PHOTOGRAPHY OF ANY MATERIAL PRESENTED DURING THE MEETING

To encourage sharing of unpublished data at the RNA Society Annual Meeting, taking of photographs and/or videos during scientific sessions (oral or poster), or of posters outside of session hours, is strictly prohibited. Violators of this policy may have their equipment confiscated (cameras, cell phones, etc.) and/or be asked to leave the conference and have their registration privileges revoked without reimbursement.

USE OF SOCIAL MEDIA

The official hashtag of the 30th Annual Meeting of the RNA Society is **#RNA25.** Meeting participants are encouraged to share the amazing science they experience at RNA 2025 on social media platforms; however, please respect the following rules when using the #RNA25 hashtag on X/Twitter, or when talking about the meeting on other social media platforms:

1. Be polite and respectful of others and their work in your messaging.
2. Do not transmit photographs of slides or posters - under any circumstance.
3. Do not transmit photographs of conference attendees without their verbal consent.
4. Requests from presenters to refrain from sharing content of their talks and/or posters on social media must be respected and adhered to. Presenters may label their talk slides and/or posters with “DO NOT POST.”

CODE OF CONDUCT

The RNA Society is committed to providing a welcoming and safe environment for scientists to exchange knowledge, research findings, and ideas. With this in mind, we expect all RNA Society event participants to treat each other with the utmost respect and make every effort to ensure a positive experience for everyone. All forms of discrimination and harassment are prohibited at RNA Society sponsored events. It is the shared responsibility of everyone participating in RNA Society events - including members, attendees, presenters, exhibitors, and venue/support supplier staff - to maintain the highest personal standard of professional conduct.

For more information on the Code of Conduct, visit https://www.rnasociety.org/rna-society-code-of-conduct

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Meet **RNA**Connect at RNA 2025!

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JOIN OUR ORAL PRESENTATION

Transcriptome-wide profiling of intron retention events using a powerful intron-encoded reverse transcriptase in RNA-seq

Presenter: George Maio, PhD, Sr. Research Scientist, RNAConnect

ENJOY BREAKFAST DURING OUR SPONSORED SESSION

Enhancing Transcriptomic Resolution: Covering the End-to-End cDNA Synthesis Gap

Presenters:
Jason Underwood, PhD, VP of Technology Development, RNAConnect

Anthony Mustoe, PhD, Assistant Professor of Biochemistry & Molecular Pharmacology, Baylor College of Medicine

Friday, May 30th, 7:45-8:45 AM
Town and Country Ballroom

REGISTER HERE

RNAConnect

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PROGRAM SUMMARY

TUESDAY, MAY 27

Registration
13:00 – 20:30, Town and County Foyer

RNA 2025 Pre-Meeting RNA Education Workshop
14:00 – 16:00, Town and Country Ballroom B
Bridging the Gap in RNA Education: Building Networks to Support, Educate and Train the Next Generation of RNA Scientists

RNA Society President's Welcome & Opening Keynotes
16:15 – 18:45, Town and Country Ballroom C & D

Keynote 1: Erin Schuman, Max Planck Institute for Brain Research, Germany
Chair: Anita Corbett
Keynote 2: Tracy Johnson, University of California–Los Angeles, USA
Chair: Atlanta Cook

Welcome Reception
18:45 – 20:30, Flamingo Lawn and Lapper Lawn

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WEDNESDAY, MAY 28

Sponsored Seminar: Lexogen
7:45 – 8:45, Town and Country Ballroom B

LEXOGEN
The RNA Experts

Registration
7:45 – 18:30, Town and Country Foyer

Plenary 1: RNA Modification and Editing
9:00 – 11:10, Town and Country Ballroom C & D
Chair: Nicole Martinez, Stanford University, USA

Refreshment Break
11:10 – 11:40, Golden State Ballroom
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Plenary Session
11:40 – 12:55, Town and Country Ballroom C & D

Meet the *RNA* Journal Editors

2024 RNA Society Lifetime Achievement in Science Award
Winner: Jennifer Doudna
Chair: Sandra Wolin, NCI - NIH, USA

Lunch
12:55 – 14:25, Golden State Ballroom

RNA Society Meetings Committee Meeting
12:55 – 14:25, California 2

Sponsored Seminar:
Oxford Nanopore Technologies
13:10 – 14:10, Town and Country Ballroom B

Concurrent 1: Translation Regulation
14:25 – 16:00, Town and Country Ballroom C & D
Chair: Chris LaPointe, Fred Hutch Cancer Center, USA

Concurrent 2: Transcription, Chromatin, and Epigenetics
14:25 – 16:00, Town and Country Ballroom B
Chair: Sihem Cheloufi, UC Riverside, USA

Concurrent 3: New Technologies
14:25 – 16:00, Town and Country Ballroom A
Chair: Ebbe Anderson, Aarhus University, Denmark

Refreshment Break
Sponsored by Pfizer
16:00 – 16:30, Golden State Ballroom

Concurrent 4: Viral RNAs and Innate Immunity
16:30 – 18:40, Town and Country Ballroom A
Chair: Lena Steckelberg, Columbia University, USA

Concurrent 5: Bioinformatics
16:30 – 18:40, Town and Country Ballroom C & D
Chair: Xiao Wang, Massachusetts Institute of Technology, USA

Concurrent 6: RNA Structure, Folding and Modeling
16:30 – 18:40, Town and Country Ballroom B
Sponsored by Sanofi
Chair: Katie Eichhorn, University of Nebraska-Lincoln, USA

RNA Society Mentoring Dinner
18:40 – 20:30, Golden State Ballroom
Organizer: Nancy Greenbaum

Dinner (for all non-Mentoring Dinner attendees)
18:40 – 20:30, Golden State Ballroom

Poster Session 1
20:30 – 22:30, Golden State Ballroom

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THURSDAY, MAY 29

Sponsored Seminar: Sanofi
7:45 – 8:45, Town and Country Ballroom B

Registration
8:00 – 17:00, Town and Country Foyer

Plenary 2: RNA and Disease
9:00 – 10:40, Town and Country Ballroom C & D
Chair: Paul Donlin-Asp, University of Edinburgh, Scotland

Refreshment Break (marked Affinity Zones)
Sponsored by Pfizer
10:40 – 11:10, Golden State Ballroom

Keynote 3: Matt Disney, The Herbert Wertheim UF Scripps Institute for Biomedical Innovation & Technology, USA
11:10 – 12:10, Town and Country Ballroom C & D
Chair: Zefeng Wang

Lunch
12:10 – 13:30, Golden State Ballroom

Sponsored Seminar: Eclipsebio
12:25 – 13:25, Town and Country Ballroom B
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Plenary 3: RNA Therapeutics I
Sponsored by Sanofi
13:30 – 14:40, Town and Country Ballroom C & D
Chair: Kristopher Brannan, Houston Methodist Research Institute, USA

Break (transition to concurrent sessions)
14:40 – 14:55

Concurrent 7: The Current and Future State of RNA Medicines
14:55 – 16:30, Town and Country Ballroom A
Panel hosted by the RNA Society Junior Scientists Group

Concurrent 8: RNA Therapeutics II
14:55 – 16:30, Town and Country Ballroom C & D
Chair: Alicia Bicknell, Moderna, USA

Concurrent 9: Training Future Scientists Through RNA
14:55 – 16:30, Town and Country Ballroom B
Chair: Suzanne Lee, Western Washington University, USA

RNA Society Jr. Scientist Group hosted "Meet & Greet"
16:30 – 17:30, Town and Country Foyer
Sponsored by Sanford Laboratories for Innovative Medicines and the University of California, San Diego Center for RNA Therapeutics and Technologies

Free Evening
16:30

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FRIDAY, MAY 30

Sponsored Seminar: RNA Connect
7:45 – 8:45, Town and Country Ballroom B

Registration
8:00 – 18:30, Town and Country Foyer

Plenary 4: Translations Mechanisms
Sponsored by Sanofi
9:00 – 10:40, Town and Country Ballroom C & D
Chair: Sezen Meydan, Vanderbilt University, USA
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Refreshment Break
10:40 – 11:10, Golden State Ballroom

Keynote 4: Ling-Ling Chen, Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences 3, China
11:10 – 12:10, Town and Country Ballroom C & D
Chair: Jørgen Kjems

RNA for All
12:10 – 12:55, Town and Country Ballroom C & D
Panel hosted by the RNA Society Committee on Diversity, Equity and Inclusion

Lunch
12:55 – 14:25, Golden State Ballroom

Concurrent 10: RNA Processing Events
14:25 – 15:30, Town and Country Ballroom A
Chair: Jeff Chao, FMI, Switzerland

Concurrent 11: Splicing Mechanisms and Regulation
14:25 – 15:30, Town and Country Ballroom C & D
Chair: Ruixue Wan, Westlake University, China

Refreshment Break (marked Affinity Zones)
Sponsored by Pfizer
15:30 – 16:00, Golden State Ballroom

Plenary 5: Alternative Splicing
16:00 – 17:20, Town and Country Ballroom C & D
Chair: Yongbo Wang, Fudan University, China

Plenary 6: RNA and Neuroscience
17:20 – 18:30, Town and Country Ballroom C & D
Chair: Ezgi Hacisuleyman, UF Scripps Institute, USA

Dinner
18:30 – 20:00, Golden State Ballroom

RNA Society Board of Directors Meeting
18:30 –20:00, California 2

Poster Session 2
20:00 – 22:00, Golden State Ballroom

SATURDAY, MAY 31

Registration
8:30 – 18:00, Town and Country Foyer

Plenary 7: RNA Surveillance and Degradation
9:00 – 10:40, Town and Country Ballroom C & D
Chair: Derrick Morton, University of Southern California, USA

Refreshment Break
10:40 – 11:00, Town and Country Foyer

Plenary 8: RNA Protein Interactions
11:00 – 12:40, Town and Country Ballroom C & D
Chair: Daniel Dominguez, University of North Carolina, USA

Lunch
12:40 – 1:40, Town and Country Foyer (boxed lunch pick up)

Concurrent 12: RNA Condensates
13:40 – 15:10, Town and Country Ballroom C & D
Chair: Maria Hondele, BioZentrum Basel, Switzerland

Concurrent 14: RNA Transport and Localization
13:40 – 15:10, Town and Country Ballroom B
Chair: Dorothy Lerit, Emory University, USA

Refreshment Break
Sponsored by Pfizer
15:10 – 15:30, Golden State Ballroom

Concurrent 15: lncRNAs and circRNAs
15:30 – 16:40, Town and Country Ballroom C & D
Chair: Antony Mustoe, Baylor University, USA

Concurrent 16: miRNA and siRNA
15:30 – 16:40, Town and Country Ballroom A
Chair: Sebastian Falk, University of Vienna, Austria

Concurrent 17: Diverse RNA Processes
15:30 – 16:40, Town and Country Ballroom B
Chair: Colin Wu, NCI/CCR, USA

Break (transition to Awards Ceremony)
16:40 – 17:00

Awards Ceremony and 2025 Lifetime Achievement Award Winner: David Tollervey
17:00 – 18:30, Town and Country Ballroom A
Chairs: Ambro van Hoof and Fátima Gebauer

RNA 2026 Announcement, Closing Remarks and Ackowledgements
18:30 – 18:45, Town and Country Ballroom A

Closing Reception, Dinner and Dance
18:45 – 19:30, Reception at the Flamingo and Lapper Lawns

19:30 – Midnight, Dinner and Dancing, Town and Country Ballrooms B, C, D

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Thank you, RNA Connect, for your support!

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INVITATION TO MEMBERSHIP

The RNA Society gathers worldwide experts in all things RNA. Since 1993, the RNA Society has promoted RNA education and research all over the world, and encouraged interdisciplinary and inclusive collaborations. Join this community to network with the greatest RNA scientists, and advance your research and career!

The RNA Society welcomes new members from all disciplines, careers and professional stages, and appreciate the unique perspectives all of our members contribute to the organization. We are an inclusive and diverse community that focuses on scientific excellence and collaboration.

Members work in numerous areas of RNA science including, but not limited to:

Bioinformatics/ Computational Biology
Heterochromatin Silencing
Integration of Nuclear Gene Expression Processes
Methods/Protocol Development
Noncoding RNA (e.g. tRNA, lncRNA, piRNA)
Ribonucleases
Ribosomes & Translational Regulation
RNA & Disease
RNA Binding Proteins
RNA Catalysis
RNA Dynamics
RNA Editing
RNA High-throughput Analysis
RNA Maturation
RNA-Protein Interactions
RNA Stability/Degradation
RNA Structure & Folding
RNA Therapeutics
RNA Transport & Localization
RNA Quality Control/ Surveillance
RNA Viruses & Viral RNA Mechanisms
RNAi & miRNA
RNP Biosynthesis, Structure and Function
Splicing & Alternative Splicing Mechanisms
Telomerase

Benefits of RNA Society membership include:

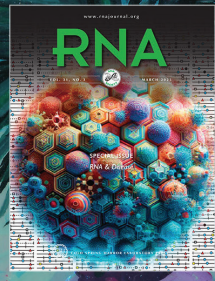
- Complementary personal subscription to the RNA Society journal, ***RNA***
- Reduced Author Page Charges for publishing in ***RNA***
  - Discounted manuscript publication fees - $1,000 ($1,500 for non-members)
  - Reduced Open Access fees - $2,000 ($3,750 for non-members)
  - Unlimited FREE color figures
- Reduced registration fees to attend the RNA Society Annual Meeting – a savings of $300–$400
- Professional Development opportunities for junior scientists, including our successful Mentoring Program
- Free job posting on the RNA Society website
- As a member of the RNA Society you are eligible to apply for:
  - RNA Society-sponsored annual Awards & Prizes
  - RNA Society sponsorship of an RNA-related conference you organize
  - Research presentation fellowships (waiving registration fees to attend the RNA Society Annual Meeting)
  - Childcare, Dependent Care and Disability Allowances to attend the RNA Society Annual Meeting
  - RNA Salon Program sponsorship of recurring RNA events in your area
- And, best of all, being part of an active and supportive international community of RNA researchers!

RNA Society membership fees are highly competitive with reduced rates for student and post-doctoral researchers. Multi-year and lifetime memberships are also available at further discounted rates.

Visit the RNA Society website at www.rnasociety.org for more information and to apply today.

RNA

Visit the ***RNA*** journal booth
to view the March 2025
Special Issue on
RNA & Disease



Find out more about
publishing in ***RNA*** at the

Meet the Editors

presentation

Wednesday, May 28th

at 11:40 am

RNA SOCIETY

Visit ***RNA***
journal here

RNA SOCIETY AWARDS

Applications due September 30th

All along your career path, the **RNA Society** has an award for you!

The RNA Society Awards Program celebrates the achievements of **trainees, faculty** and **research scientists** with 12 awards in 9 categories. Help us recognize **scientific excellence, diversity** in RNA science, **mentoring** and **leadership** by applying (or nominating) an RNA Society member today at **RNASociety.org/Awards.**

2025 RNA SOCIETY AWARD WINNERS

THE RNA SOCIETY LIFETIME ACHIEVEMENT IN SCIENCE AWARD

David Tollervey

The RNA Society Lifetime Achievement in Science Award acknowledges the outstanding contributions of an RNA researcher on the general scientific community. Each year, the RNA Society Board of Directors seeks nominations to identify a recipient based on their long-time research achievements.The award is presented at the Annual RNA Meeting, where the recipient gives a special address to the RNA Society.

Previous winners include Joan Steitz (2003), Harry Noller (2004), John Abelson (2005), Christine Guthrie (2006), Walter Keller (2007), Norm Pace (2008), Thomas Cech (2009), Fritz Eckstein (2010), Witold Filipowic (2011), Olke Uhlenbeck (2012), Phillip Sharp (2013), Reinhard Lührmann (2014), Anita Hopper (2015), Eric Westhof (2016), Lynne Maquat (2017), Jean Beggs (2018), Adrian Krainer (2019), Matthia Hentze (2020), Melissa Moore (2021), Gideon Dreyfus (2022), Marlene Belfort (2023), and Jennifer Doudna (2024).

Congratulations to ***David Tollervey,*** *Wellcome Principal Research Fellow and Professor of RNA Biology at the Centre for Cell Biology, University of Edinburgh, and recognized for his pioneering work in the fields of ribosome biogenesis and RNA surveillance. He contributed to establishing the role of snoRNAs in ribosomal RNA processing, described the function of fibrillarin- a conserved protein now known to be involved in autoimmune disorders and cancer- in this process, and identified dozens of trans-acting factors involved in rRNA cleavage, modification or remodeling. On the way to characterize 5.8S rRNA 3' end maturation, the Tollervey lab discovered the RNA exosome, a prominent cell nanomachine responsible for the surveillance of most classes of RNA. More recently, he has described methods for the high-throughput mapping of RNA-RNA and RNA-protein interactions (CRAC, CLASH, TRAPP) that are widely used by the community, and has characterized the role of imprinted snoRNAs in Prader-Willi Syndrome. Tollervey's seminal contributions are now textbook material. In addition to his scientific discoveries, Tollervey has been a generous member of the RNA Society, serving as President (2007–2008), Director (2003–2004) and annual meeting organizer (1999, 2002, 2024). For his outstanding contributions to RNA science and the RNA Society, we celebrate David Tollervey with the 2025 RNA Society Lifetime Achievement in Science Award.*

THE RNA SOCIETY LIFETIME ACHIEVEMENT IN SERVICE AWARD

Nancy Greenbaum

The RNA Society Lifetime Service Award is given in appreciation of outstanding dedication and service to the RNA Society and greater RNA community. Each year, the RNA Society Board of Directors seeks nominations and selects the recipient of this award based on exemplary contributions and commitment to fulfilling the mission of the RNA Society and promoting RNA research and education world-wide.

Previous winners include Tim Nilsen (2003), Chris Greer (2004), Jean Beggs (2005), Olke Uhlenbeck (2006), Marvin Wickens (2007), Eric Westhof (2008), Anita Hopper (2009), Lynne Maquat (2010), Evelyn Jabri (2011), Brenda Peculis (2012), Ann Marie Micenmacher (2014), David Lilley (2015), Andrea Barta (2016), Andrew Feig (2017), Elizabeth Tran (2018), Jim McSwiggen (2019), Sarah Woodson (2020), Juan Valcárcel (2021), Anna Marie Pyle (2022), Benoît Chabot (2023), and Ute Kothe (2024).

Congratulations to ***Nancy Greenbaum,*** *Professor at Hunter College, City University of New York (CUNY), is recognized for her outstanding contributions to mentoring junior scientist members of the RNA Society and within the greater RNA research community. Nancy has led efforts to provide mentorship to junior members by organizing the Career Mentoring event of the RNA Society Annual Meeting for the last 11 years. Since 2017, Greenbaum has also coordinated the RNA Society Individual Mentoring Initiative, a program initially launched by Juan Valcárcel providing one-on-one mentoring to over 40 young RNA researchers per year. These programs and Nancy's leadership have been instrumental for the professional development and success of junior members of our RNA community. More broadly, in addition to numerous PhD students and postdocs, Greenbaum has trained over 100 undergraduate students in her research lab, many of whom have gone on to pursue PhD or MD-PhD degrees. Nancy also serves as the Coordinator of the CUNY Intensive Research Experience (CIRE) Program at Hunter College, aimed at preparing undergraduate students from less favored communities for careers in STEM (Science, Technology, Engineering and Medicine) research. For her unreserved dedication to mentoring RNA Society junior scientists, we celebrate Nancy Greenbaum with the 2025 RNA Society Lifetime in Service Award.*

THE ELISA IZAURRALDE AWARD FOR INNOVATION IN RESEARCH, TEACHING AND SERVICE

Kristin Koutmou

The Elisa Izaurralde Award for Innovation in Research, Teaching and Service was established in 2019 to celebrate the life and achievements of Dr. Elisa Izaurralde, former Director of the Department of Biochemistry at the Max Planck Institute for Developmental Biology in Tubingen, Germany, and a generous friend and colleague to the RNA community. The award is presented to an early career researcher who embodies Elisa's dedication to science and employs innovative approaches to their research, teaching and service. This award is open to early career scientists (5–15 years post-PhD) who hold an independent research position at an academic institution.

Previous winners include Lori Passmore (2020), Gene Yeo (2021), Luisa Cochella (2022), Amanda Hargrove (2023), and Stefanie Jonas (2024).

*Congratulations to **Kristin Koutmou,** an associate professor in the Department of Chemistry at the University of Michigan, USA, where she has made impactful discoveries into the chemical biology of RNA and its modifications. Koutmou is a dedicated teacher and mentor, and teaches university courses in biochemistry and chemical biology. She also developed activities to get students in grades 6 to 12 excited about science, publishes science education materials, and has won national-level awards for her education efforts. Within the RNA Society, Koutmou serves as Chair of the Membership Committee, where she administers the Small Meetings Sponsorship Program as well as membership recruitment and renewal.*

THE RNA SOCIETY MID-CAREER AWARD

Yanli Wang

The RNA Society Mid-Career Award is given in recognition of scientists who have made significant contributions to their field in the first 15 years of their career as an independent investigator.

Previous winners include Karla Neugebauer (2017), Nils Walter (2017), Erik Sontheimer (2018), Ailong Ke (2019), Jernej Ule (2020), Ling-Ling Chen (2021), Julius Brennecke (2022), Nicholas Ingolia (2023) and Chase Beisel (2024).

*Congratulations to **Yanli Wang,** a principal investigator and HHMI International Scholar at the Institute of Biophysics of the Chinese Academy of Sciences. Throughout her career,*

Wang has made seminal contributions to our mechanistic understanding of how small RNAs guide their partner enzymes to DNA and RNA targets. This theme emerged during her training period when she studied Argonaute proteins and miRNA regulation. As an independent scientist, Wang has focused on diverse CRISPR systems, making key inroads into our fundamental understanding of RNA-mediated immune systems that facilitate development of precision genome-editing technologies. Her research has provided key insights into the acquisition of new immune specificities by bacteria, the processing of their guide RNAs, and the execution of immune defense.

THE RNA SOCIETY EARLY CAREER AWARD

The RNA Society Early Career Award is given in recognition of scientists who have made significant contributions to their field in the first seven years of their career as an independent investigator.

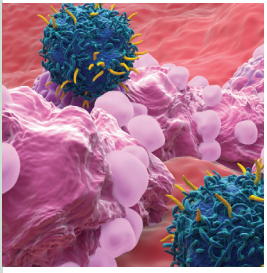
Previous winners include Wendy Gilbert (2017), Gene Yeo (2017), Andrei Korostelev (2018), Maria Barna (2019), Igor Ulitsky (2020), Schraga Schwartz (2021) and Nicholas Guydosh (2022), Jinwei Zhang (2023), and Chun Kit Kwok (2024).

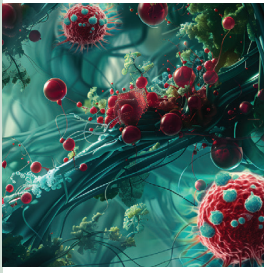
Samuel Sternberg

Congratulations to ***Samuel Sternberg,*** *an HHMI investigator and associate professor in the Department of Biochemistry and Molecular Biophysics at Columbia University in New York, NY, USA. Sternberg received his PhD from the University of California, Berkeley researching CRISPR-Cas biology and, as a trainee, co-authored a popular science book with Jennifer Doudna on the discovery and development of CRISPR-based gene editing technology. After a stint in industry and brief postdoctoral training, Sternberg opened his lab on RNA-guided biology in 2018, where he has deciphered how CRISPR and transposon-associated protein complexes promote RNA-guided transposition and RNA-guided transposon proliferation.*

THE RNA SOCIETY AWARD FOR EXCELLENCE IN INCLUSIVE LEADERSHIP

The Inclusive Leadership award was established in 2021 to recognize outstanding leadership that promotes the training and/or professional development of underrepresented scientists and greater inclusion of RNA researchers within our scientific community. This award is open to all current members of the RNA Society having a demonstrated record of promoting diversity and inclusion in RNA science. Activities can include, but are not limited to, achievements in research mentorship of underrepresented scientists, development of





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September 19-21 | Denver, CO

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September 28-October 1 | Boston, MA

AACR-NCI-EORTC INTERNATIONAL CONFERENCE ON MOLECULAR TARGETS AND CANCER THERAPEUTICS
October 22-26 | Boston, MA

AACR-KCA JOINT CONFERENCE ON PRECISION MEDICINE IN CANCER
November 13-14, 2025 | Busan, Korea

CANCER EVOLUTION
December 4-6 | Albuquerque, NM

SAN ANTONIO BREAST CANCER SYMPOSIUM
December 9-12 | San Antonio, TX

THE RISE IN EARLY ONSET CANCERS – KNOWLEDGE GAPS AND RESEARCH OPPORTUNITIES
December 10-13 | Montreal, QC, Canada

FUSION-POSITIVE CANCERS
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2501044C

Michelle Scott

programs or initiatives that promote inclusion in the RNA scientific community, and/or long-standing advocacy and/or commitment to scientific inclusion and opportunities for all.

Previous winners were Anita Corbett (2022), Wendy Gilbert (2023), and Shobha Vasudevan (2024).

Congratulations to ***Michelle Scott,*** *a professor of Biochemistry and Functional Genomics at the Université de Sherbrooke, in Sherbrooke, Quebec, Canada, and who serves as Director of the university's RNA Excellence Pole. Her research focuses on noncoding RNA function, including the expression and function of snoRNAs and miRNAs. Scott is a founding member of RNA Canada, a recently established society fostering RNA research and collaboration across Canada, and chairs the Equity, Diversity and Inclusion committee. Additionally, Scott has spearheaded workshops in Quebec to encourage high school girls to consider careers in STEM.*

THE RNA SOCIETY OUTSTANDING CAREER RESEARCHER AWARD

The RNA Society Outstanding Career Researcher Award was established in 2021 to recognize the exceptional contributions of career research scientists in advancing the field of RNA. The award is open to all career researchers who performs his/her/their scientific role in the framework of a larger research group. Examples of career RNA researchers eligible for this award include Research Assistants, Research Associates, Technicians, Lab Managers, Staff Scientists, or those in equivalent positions.

Previous winners were Arthur Zaug (2022), Sara Olson (2023), and Jason Stagno (2024).

Maxime Wery

Congratulations to ***Maxime Wery,*** *a senior scientist in the laboratory of Antonin Morillon at the Curie Institute in Paris, France. Wery has worked alongside Morillon for 15 years and has over 20 peer-reviewed publications investigating RNA decay mechanisms and long noncoding RNA metabolism. Wery's contributions span form wet-lab work to computational analysis and mentoring trainees. Beyond the Morillon laboratory, he has served as a member of the scientific committee organizing the annual "Noncoding Genome" international course at the Curie Institute and is an active member of the RNA Spotlight writing team for the RNA Society.*

THE RNA SOCIETY/COLD SPRING HARBOR LABORATORY PRESS AWARD FOR RESEARCH EXCELLENCE BY AN UNDERREPRESENTED SCIENTIST

The RNA Society/Cold Spring Harbor Laboratory Press Award for Research Excellence by an Underrepresented Scientist is sponsored by Cold Spring Harbor Laboratory Press (CSHLP), a long-time partner of the RNA Society and publisher of RNA, the official journal of the Society. This award was established in 2021 to recognize exceptional contributions to RNA research by a scientific trainee who is underrepresented in biomedical research. This award is open to all qualifying graduate students and post-doctoral fellow trainees (or equivalent).

Previous winners were Jillian Ramos (2022), Sezen Meydan (2023), and Mariela Cortés López (2024).

Luciana Castellano

*Congratulations to **Luciana Castellano** who is originally from Argentina and who is currently a graduate student in the laboratory of Ariel Bazzini at the Stowers Institute for Medical Research in Kansas City, USA. Castellano studies the role of codon optimality during RNA virus infection. Her work has revealed how viruses adapt to host codon preferences - uncovering a novel mechanism in host-pathogen evolution and opening avenues for therapeutic innovation. Her leadership extends to the mentoring of others, fostering collaborations, and organizing professional development events for local trainees. As a Latina woman in STEM, Castellano's dedication and accomplishments serve to inspire others while advancing RNA science.*

THE RNA SOCIETY/COLD SPRING HARBOR LABORATORY PRESS DISTINGUISHED RESEARCH MENTOR AWARD

The RNA Society/Cold Spring Harbor Laboratory Press Distinguished Research Mentor Award is supported by Cold Spring Harbor Laboratory Press (CSHLP), a long-time partner of the RNA Society and publisher of RNA, the official journal of the Society. This award was established in 2021 to recognize outstanding mentorship by our members and to highlight the importance of fostering the academic and professional development of trainees in RNA research. This award is open to all current and Full Members of the RNASociety with a track record of active and impactful mentoring; mentoring can be broadly considered to include any activity that contributes to the sustained vibrancy and growth of the RNA scientific community.

Previous winners were Susan Gerbi (2022), Doug Turner (2023), and Phillip Zamore (2024).

Roy Parker

Congratulations to ***Roy Parker,*** *an HHMI investigator and a distinguished professor in the Department of Biochemistry at the University of Colorado in Boulder, USA. As a mentor he focuses on clarity of thought and effective communication. For over three decades, Roy has cultivated a lab culture focused on the development of curiosity, rigor, and scientific integrity for his trainees. He advocates for the development of a broad skill set by graduate students during their training (2012 Mol Cell 46:377) while recognizing that every mentee is an individual who needs their own personalized approach. Parker is well known for his guidance and sponsorship - always willing to provide input into the scientific direction one should take, while also stimulating individuals to take their own path.*

THE RNA SOCIETY/SCARINGE YOUNG SCIENTIST AWARD

The RNA Society/Scaringe Young Scientist Awards were established to recognize the achievements of young scientists engaged in RNA research and to encourage them to continue to pursue a career in RNA science. In 2004 and 2005, the RNA Society/Scaringe Award was given to the student author(s) of the best paper published during the previous year in *RNA* the official journal of the RNA Society, as selected by the Editors. The winners of the 2004 and 2005 awards were Stefano Marzi and Ramesh Pillai, respectively. In 2006, eligibility for this award was opened up to all junior scientists (Graduate Students and Post-doctoral Fellows) who have made significant research contributions to the area of RNA. The award includes full support to attend the RNA Society Annual Meeting and a small cash prize.

Previous Graduate Student winners include Jeff Barrick (2006), Malte Beringer (2007), Qi Zhang (2008), Jeremey Wilusz (2009), John Calarco (2010), Jasmine Perez (2011), Chenguang Gong (2012), Tatjana Trcek Puliic (2012), Wenwen Fang (2013), David Weinberg (2014), Samuel Sternberg (2015), Katherine Warner (2015), Ryan Flynn (2016), Nian Liu (2016), Malik Chaker-Margot (2017), Madeline Sherlock (2018), Boxuan Zhao (2018), Michael Chen (2019), Max Wilkinson (2019), Robert Battaglia (2020), Junuka Athukoralage (2021), Jonathan Bohlen (2021), Sanna Klompe (2022), Jonas Tholen (2023, and Jennifer Porat (2024).

Previous Post-doctoral Fellow winners include Megan Talkington (2006), Zefeng Wang (2007), Alexei Aravin (2008), Shobha Vasudevan (2009), Luciano Marraffinin (2010), Hani Zaher (2011), Kotaro Nakanishi (2012), Dipali Sashital (2012), Je-Hyun Yoon (2013), Jinwei Zhang (2014), Olga Anczukow-Camarda (2015), Schraga Schwartz (2015), Basil Greber (2016), Thi Hoang Duong Nguyen (2016), Zhipeng Lu (2017), Fuguo Jiang (2018), Xuebing

Wu (2019), Furqan Fazal (2020), Sebastian Fica (2020), Anna Loveland (2021), Kathrin Leppek (2021), Margaret Rodgers (2022), Charles Bou-Nader (2023), and Arnaud Vanden Broeck (2024).

Jimmy Ly

Chance Meers

Congratulations to the winners of the 2025 RNA Society/ Scaringe Young Scientist Awards:
Graduate student ***Jimmy Ly,*** *a doctoral trainee in the laboratory of Iain Cheeseman at The Whitehead Institute and Department of Biology, Massachusetts Institute of Technology in Boston, USA. Ly's pioneering work focuses on unraveling the molecular mechanisms regulating protein synthesis and expression of alternative protein variants during the mammalian cell cycle. His research has revealed how start codon selection plays a role in ensuring mitotic cell viability. In a separate line of research investigation, Ly has identified a crucial alternative splicing event in the transcript encoding a cell division protein, providing valuable insights into the distinct chromosome segregation behaviors observed in mitosis and meiosis.*

Postdoctoral fellow ***Chance Meers,*** *in the Sternberg laboratory at Columbia University in New York, USA. Meers studies the evolutionary origins of fundamental RNA-guided pathways, including elucidating the mechanisms behind RNA-guided DNA cleavage by transposon-encoded nucleases that are the precursor to CRISPR systems and discovering the evolutionary roots of RNA-guided RNA 2'-O-methylation. Beyond his scientific accomplishments, Meers has been instrumental in mentoring junior scientists and fostering a vibrant intellectual community at Columbia.*

THE ECLIPSE AWARD FOR INNOVATION IN HIGH-THROUGHPUT BIOLOGY

ECLIPSEBIO
THE RNA GENOMICS COMPANY

The Eclipse Award for Innovation in High Throughput Biology was established in 2021 to recognize research achievements by junior researchers in the growing areas of high throughput experimentation and analysis. This award, sponsored by Eclipse BioInnovations Inc., is open to all Graduate Students and Post-doctoral Fellows and is awarded based on research accomplishments in the broad area of high throughput RNA biology. The award includes full support to attend the RNA Society Annual Meeting, a small cash prize and the opportunity to interview with Eclipse BioInnovations Inc. leadership and perform an internship at their worksite in San Diego, California.

Previous winners were Oguzhan Begik (Graduate Student, 2022), Aldema Sas-Chen (Post-doctoral Fellow, 2022), Han Altae-Tran, (Graduate Student, 2023) and Shira Weingarten-Gabbay (Post-doctoral Fellow, 2023), Morghan Lucas (Graduate Student, 2024) and Giulia Biancon (2024).

Dawn Chen

Nandan Gokhale

Congratulations to the winners of the 2024 Eclipse Award for Innovation in High-Throughput Biology:
Graduate student ***Dawn Chen,*** *a researcher in the laboratory of Fei Chen at The Broad Institute and Harvard University in Boston, USA. Chen has developed innovative methods for characterizing, perturbing, and engineering novel RNA regulatory mechanisms throughout the mRNA lifecycle. Her work includes creating a tool that controls gene expression by sensing specific RNA transcripts in mammalian cells and developing a system that enables long-range mutagenesis of DNA which facilitates continuous evolution across multiple cell generations. Using the latter approach, she has identified mutations in the splicing factor SF3B1 that are important for driving alternative 3' splice site usage.*

Postdoctoral fellow ***Nandan Gokhale,*** *in the laboratory of Ram Savan at the University of Washington, in Seattle, USA. Gokhale is employing high throughput methods to study the role of RNA in innate immune signaling complexes. Beyond his lab activities, Gokhale has made important contributions to teaching and mentoring, and serves as an independent peer reviewer for a number of scientific journals.*

THE RNA SOCIETY MODERNA AWARD FOR BIOMEDICAL INNOVATION IN RNA

moderna

The RNA Society Moderna Award for Biomedical Innovation in RNA recognizes innovative contributions in the use or function of RNA in biomedicine, disease processes, and treatments by independent researchers within the first ten years of their independence.

Previous winner was Raman Bahal (2024).

Jordan Meier

Congratulations to ***Jordan Meier,*** *a senior investigator at the National Institutes of Health in Frederick, Maryland, USA, where his research seeks to understand the complex landscape of chemical modifications that regulate RNA function. Meier's work has illuminated fundamental principles of RNA biology by focusing on N4-acetylcytidine (ac4C). This modification offers a compelling example of RNA regulation: it is found in almost every living organism, chemically mirrors acetyl modifications that control transcription, and is installed by an essential enzyme associated with human disease. By developing innovative chemical methods, Meier has revealed how Nature deploys ac4C to stabilize RNA structure, regulate protein synthesis, and enable cellular adaptation to stress. His work has revealed diverse roles for RNA acetylation, from enabling microbial survival at near-boiling temperatures to regulating human development and preventing cancer spread. Furthermore, studies of ac4C in synthetic mRNA are informing the development of future RNA therapeutics.*

ORAL ABSTRACT LISTINGS

TUESDAY, MAY 27

Keynote 1: Erin Schuman

Town and Country Ballroom C & D
Introduced by Anita Corbett

Keynote 2: Tracy Johnson

Town and Country Ballroom C & D
Introduced by Atlanta Cook

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WEDNESDAY, MAY 28

Plenary Session 1: RNA Modification & Editing

Town and Country Ballroom C & D
Session Chair: Nicole Martinez

T-1 GlycoRNA biology on the cell surface
Ryan Flynn, Harvard University, Boston, MA, USA

T-2 Guide RNA translocation during mitochondrial mRNA editing in trypanosomes
Ruslan Afasizhev[1], Shiheng Liu[2], Takuma Suematsu[1], Clinton Yu[3], Lan Huang[3], Liye Zhang[4], Inna Afasizheva[1], Z. Hong Zhou[2]
[1]UCLA, Los Angeles, CA, USA. [2]UCLA, Los Angeles, CA, USA. [3]UC Irvine, Irvine, CA, USA. [4]ShanghaiTech, Shanghai, China

T-3 Molecular basis of substrate recognition and catalysis by the intrinsic 16S ribosomal methyltransferase RsmI
Mohamed Barmada, Natalia Zelinskaya, Graeme Conn, Emory University, Atlanta, Georgia, USA

T-4 Investigating the sequence, structure, and cell-type specificity of PUS7-mediated pseudouridylation with Nanopore sequencing
Rebecca Rodell[1], Ronit Jain[1], Hossein Shenasa[1], Matias Montes[1], Nicole Martinez[1,2,3]
[1]Chemical and Systems Biology, Stanford University, Stanford, CA, USA.
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[2]Developmental Biology, Stanford University, Stanford, CA, USA. [3]Sarafan ChEM-H Institute, Stanford, CA, USA

T-5 PUS7 cytoplasmic localization directs a pseudouridine-mediated cellular stress response
Minli Ruan[1], Sean Engels[2], Matthew Burroughs[2], Dylan Bloch[3], Oleksandra Fanari[3], Stuart Akeson[3], Daniel Eyler[1], Xiaoyan Li[1], Chase Weidmann[1], Sara Rouhanifard[3], Miten Jain[3], Lydia Contreras[2], Kristin Koutmou[1]
[1]University of Michigan, Ann Arbor, MI, USA. [2]University of Texas, Austin, Texas, USA. [3]Northeastern University, Boston, Massachusetts, USA

T-6 NAT10 and N4-Acetylcytidine restrain R-loop levels and related inflammatory responses
Turja Debnath[1], Nathan Abell[1], Yi-Ru Li[1,2], Sravan Devanathan[1], Enrique Navedo[1], Blerta Xhemalçe[1,2]
[1]University of Texas at Austin, Austin, TX, USA. [2]Emory University School of Medicine, Atlanta, GA, USA

T-7 Balancing stem cell fates by snoRNA-guided methionine tRNA modifications and one-carbon metabolism
Zhipeng Lu, USC, Los Angeles, CA, USA

T-8 Context-dependent essentiality of RNA modifications in human cells
Sascha Wani[1], Selay Kaya[1], Jiyeong Ryu[1], Geraldine Rodschinka[1], Danny Nedialkova[1,2]
[1]Max Planck Institute of Biochemistry, Martinsried, Germany. [2]Department of Bioscience, TUM School of Natural Sciences, Technical University of Munich, Garching, Germany

2024 RNA Society Lifetime Achievement in Science Award Winner: Jennifer Doudna

Town and Country Ballroom C & D
Introduced by Sandra Wolin

Concurrent 1: Translation Regulation

Town and Country Ballroom C & D
Session Chair: Chris Lapointe

T-9 The nuclear RNA binding protein CELF2 regulates mRNA-specific translation through controlling PUS7 expression

Timothy Cater, Kristen Lynch, University of Pennsylvania, Philadelphia, PA, USA

T-10 Regulation of human translation initiation by pseudouridine
Ryan Stanton, Wendy Gilbert, Yale University, New Haven, CT, USA

T-11 FMRP drives mRNP targets into translationally silenced complexes
Tatsuaki Kurosaki[1,2], Hana Cho[1], Elizabeth Abshire[1], Christoph Pröschel[3], Shuhei Mitsutomi[1,4], Hanae Sato[1,5], Eric Simko[6], Christopher Fraser[7], Hitomi Sakano[8,9], Lynne Maquat[10]
[1]Department of Biochemistry and Biophysics, School of Medicine and Dentistry, University of Rochester, Rochester, NY, USA. [2]Department of Biotechnical and Clinical Laboratory Sciences, Jacobs School of Medicine & Biomedical Sciences, State University of New York at Buffalo, Buffalo, NY, USA. [3]Department of Biomedical Genetics, School of Medicine and Dentistry, University of Rochester, Rochester, NY, USA. [4]Research Institute, National Cancer Center, Tokyo, Japan. [5]WPI Nano Life Science Institute, Kanazawa, NY, Japan. [6]National Cancer Institute, National Institutes of Health, Frederick, MD, USA. [7]Department of Molecular and Cellular Biology, College of Biological Sciences, University of California, Davis, Davis, CA, USA. [8]Department of Otolaryngology, School of Medicine and Dentistry, University of Rochester, Rochester, NY, USA. [9]Departments of Otolaryngology and Neuroscience, Peter O'Donnell Junior Brain Institute, University of Texas Southwestern, Dalals, TX, USA. [10]Department of Biochemistry and Biophysics, School of Medicine and Dentistry, University of Rochester, Rochester, Rochester, NY, USA

T-12 Systematic identification of downstream ORFs and the sequences that drive dORF translation
Cameron Berry, Eugenia Cortina, Ariel Bazzini, Stowers Institute for Medical Research, Kansas City, MO, USA

T-13 Mitoribosome profiling reveals the off-target mechanisms of antibiotics
James Marks[1], Emma Young[2], Markus Hafner[2], Sezen Meydan[1]
[1]Vanderbilt University, Nashville, TN, USA. [2]NIH, Bethesda, MD, USA

T-14 Genome-wide CRISPR screens reveal an allele-specific enhancer of pathogenic C9ORF72 repeat RNAs in ALS/FTD
Lianhuan Wei[1], Suzhou Yang[1], Udit Sheth[2], Tania Gendron[2], Junjie Guo[1]
[1]Yale, New Haven, Connecticut, USA. [2]Mayo Clinic, Jacksonville, Florida, USA

T-15 Deep Learning-guided analyses for full-length mRNA translation links genetic variation and diseases
Siqi Wang[1,2], Chuyun Chen[2], Xinshu Xiao[1], Zefeng Wang[3,2]
[1]Department of Integrative Biology and Physiology, University of California, Los Angeles, Los Angeles, California, USA. [2]CAS Key Laboratory of Computational Biology, Shanghai Institute of Nutrition and Health, Chinese Academy of Sciences, Shanghai, Shanghai, China. [3]School of Life Science, Southern University of Science and Technology, Shenzhen, Guangdong, China

Concurrent 2: Transcription, Chromatin, and Epigenetics

Town and Country Ballroom B
Session Chair: Sihem Cheloufi

T-16 RNA Pol I activity maintains chromatin condensation and the H3K4me3 gradient essential for oogenesis, independent of ribosome production
Raquel Mejia-Trujillo, Qiuxia Zhao, Elif Sarinay Cenik
The University of Texas at Austin, Austin, TX, USA

T-17 RNA:RNA duplexes in expression regulation of INO80E and HIRIP3 head-to-head overlapping protein-coding genes
Natalia Ryczek, Aneta Łyś, Elżbieta Wanowska, Joanna Kozłowska-Masłoń, Izabela Makałowska
Institute of Human Biology and Evolution, Adam Mickiewicz University, Poznań, Wielkopolska, Poland

T-18 A time-resolved framework for the recruitment of mRNP processing and assembly factors to a site of transcription in *S. cerevisiae*
Theresa Wechsler, Ryuta Asada, Andrew Dominguez, Rachel Montpetit, Ben Montpetit
University of California Davis, Davis, CA, USA

T-19 Runaway transcription necessitates purine bias in bacterial coding sequences
K Julia Dierksheide[1], James Taggart[2], Grace Johnson[3], Gene-Wei Li[1]
[1]Massachusetts Institute of Technology, Cambridge, MA, USA. [2]Harvard University, Cambridge, MA, USA. [3]Princeton University, Princeton, NJ, USA

T-20 Direct RNA-seq reveals diverse effects of substitutions in Hrp1/CF1B on the 3' ends of mRNAs and non-coding RNAs
Emma Goguen, Kylie Zawisza, Moyao Wang, David Brow
Dept. of Biomolecular Chemistry, University of Wisconsin School of Medicine and Public Health, Madison, WI, USA

T-21 Nuclear accumulation of select RNA binding proteins induces Pol II transcriptional repression
Sam Rider[1], Britt Glaunsinger[2,1,3]
[1]Dept. of Molecular and Cell Biology, University of California Berkeley, Berkeley, CA, USA. [2]Dept. of Plant and Microbial Biology, University of California Berkeley, Berkeley, CA, USA. [3]Howard Hughes Medical Institute, University of California Berkeley, Berkeley, CA, USA

T-22 A biophysical basis for the spreading behavior and limited diffusion of Xist

Mingrui Ding[1], Danni Wang[2,3], Hui Chen[4], Barry Kesner[2,3], Niklas-Benedikt Grimm[2,3,5], Uri Weissbein[2,3], Anna Lappala[6,3], Jiying Jiang[1], Carlos Rivera[2,3], Jizhong Lou[4], Pilong Li[1], Jeannie T LEE[2,7]

[1]State Key Laboratory of Membrane Biology, Beijing Frontier Research Center for Biological Structure, School of Life Sciences, Tsinghua University, Tsinghua-Peking Center for Life Sciences, Beijing, China. [2]Department of Molecular Biology, Massachusetts General Hospital, Boston, MA, USA. [3]Department of Genetics, Harvard Medical School, Boston, MA, USA. [4]Key Laboratory of RNA Biology, CAS Center for Excellence in Biomacromolecules, Institute of Biophysics, Chinese Academy of Sciences, Beijing, China. [5]Centre for Genomic Regulation (CRG), The Barcelona Institute of Science and Technology, Universitat Pompeu Fabra (UPF), Barcelona, Spain. [6]Department of Molecular Biology, Boston, MA, USA. [7]Department of Genetics, Boston, MA, USA

Concurrent 3: New Technologies

Town and Country Ballroom A

Session Chair: Ebbe Andersen

T-23 Identifying global protein biomarkers in biofluids by profiling highly complex chemically modified RNA aptamer libraries

Jørgen Kjems, Asger Jørgensen, Daniel Dupont, Claus Bus
Aarhus University, Aarhus, Denmark

T-24 Quantum-dot lateral flow assay to detect ribonuclease in liquids and surfaces

Joseph Krebs, Lance Ford, Bradon Oddo
Attogene, Austin, TX, USA

T-25 RNA-linked CRISPR screening decodes gene regulatory networks for RNA metabolism in human cells

Patrick Nugent, Heungwon Park, Arvind Rasi Subramaniam
Fred Hutchinson Cancer Center, Seattle, WA, USA

T-26 Break-and-repair editing of RNA with CRISPR-guided ribonucleases

Artem Nemudry[1], Anna Nemudraia[1], Blake Wiedenheft[2]
[1]University of Florida, Gainesville, FL, USA. [2]Montana State University, Bozeman, MT, USA

T-27 Connectome-seq: Using RNA barcodes to map brain connections and discover molecular signatures of neural circuits

Danping Chen[1], Alina Isakova[2], Zhou Wan[1], Mark Wagner[3], Yunming Wu[2], Boxuan Zhao[1]

[1]University of Illinois Urbana-Champaign, Urbana, IL, USA. [2]Stanford University, Stanford, CA, USA. [3]NIH, Bethesda, MD, USA

T-28 Spatially-resolved translatome sequencing at molecular resolution in early embryogenesis

Rena Ren[1,2,3], Haowen Zhou[2,4], Seth Furniss[2,3], Chengjie Zhou[1], Yota Hagihara[1], Yi Zhang[1,5], Xiao Wang[2,3]
[1]Boston Children's Hospital, Boston, MA, USA. [2]Broad Institute of MIT and Harvard, Cambridge, MA, USA. [3]Massachusetts Institute of Technology, Cambridge, MA, USA. [4]University of California San Diego, La Jolla, CA, USA. 5Harvard Medical School, Boston, MA, USA

T-29 Local translation atlas revealed by APEX-Ribo-Seq

Kotaro Tomuro[1,2], Shintaro Iwasaki[1,2], Yuichi Shichino[1]
[1]RIKEN, Wako, Japan. [2]The University of Tokyo, Kashiwa, Japan

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Concurrent 4: Viral RNAs and Innate Immunity

Town and Country Ballroom A

Session Chair: Lena Steckelberg

T-30 Influenza A virus utilizes non-canonical cap-snatching to diversify viral RNAs

Adrian Toquero, David Gorrie, Lars Luscher, Swati Srivastava, Weifeng Gu, UC Riverside, Riverside, CA, USA

T-31 Structural insights into RNA-mediated enteroviral genome replication

Deepak Koirala, University of Maryland, Baltimore County, Baltimore, MD, USA

T-32 Discovery of regulatory RNA elements through viromic screening

C. Han Li[1,2], Soo-Jin Jung[1,2], Jennifer Jenny Seo[1,2], V. Narry Kim1,2
[1]Center for RNA Research, Seoul, Korea, Republic of. [2]Seoul National University, Seoul, Korea, Republic of

T-33 Genome-wide interrogation of SARS-CoV-2 protein-RNA interactions uncovers hidden regulatory sites

Joy Xiang[1], Karen Zhao[1], Laliv Tadri[1], Kurt Tamaru[1], Brian Yee[2], Katherine Rothamel[2], Jasmine Mueller[2], Assael Madrigal[2], Samuel Park[2], Rachael McVicar[3], Alex Clark[2], Ben Croker[2], Aaron Carlin[2], Sandra Leibel[2], Gene Yeo[2]
[1]University of California Riverside, Riverside, CA, USA. [2]University of California San Diego, La Jolla, CA, USA. [3]Sanford Burnham Prebys Medical Discovery Institute, La Jolla, CA, USA

T-34 Type I Interferon signalling causes a global remodelling of the cellular RNA-bound proteome
Louisa Iselin[1], Yana Demyanenko[2], Azman Embarc-Buh[1], Honglin Chen[3], Wael Kamel[1], Peter Simmonds[4], Shabaz Mohammed[2,4], Alfredo Castello[1]
[1]MRC-University of Glasgow Centre for Virus Research, Glasgow, United Kingdom. [2]Rosalind Franklin Institute, Didcot, United Kingdom. [3]Imperial College London, London, United Kingdom. [4]University of Oxford, Oxford, United Kingdom

T-35 MERS-CoV limits protein kinase R activation by antagonizing its condensation at viral double-stranded RNA puncta
Ebba K. Blomqvist[1,2], Nicole Bracci[3], Helena Winstone[3], J Monty Watkins[1,2], Susan Weiss[3], James M Burke[1]
[1]Wertheim UF Scripps, Jupiter, FL, USA. [2]Skaggs Graduate School, La Jolla, CA, USA. [3]University of Pennsylvania, Philadelphia, PA, USA

T-36 Cellular RNA interacts with MAVS to promote antiviral immunity
Nandn Gokhale, Cincinnati Children's Hospital Medical Center, Cincinnati, OH, USA

T-37 Y-Box binding protein 1 (YBX1) modulates RNA polymerase III transcripts to prevent autoimmunity
Tania Strilets[1], Mariano A. Garcia-Blanco[2]
[1]University of Texas Medial Branch, Galveston, TX, USA. [2]University of Virginia School of Medicine, Charlottesville, VA, USA

T-38 Subversion of Host DNA Transcription and Replication Machinery by a BSL-4 Model RNA Virus
Andrea Ascura, Stephen Clarke, Manuel Ascano
Vanderbilt University, Nashville, TN, USA

T-39 Alternatively Spliced Isoforms of IRF7 Differentially Regulate Innate Immune Signaling to Respond to Viral Infection
Asmita Panthi, Max Ferretti, Olivia Howard, Kristen Lynch
University of Pennsylvania, Philadelphia, PA, USA

Concurrent 5: Bioinformatics

Town and Country Ballroom C & D
Session Chair: Xiao Wang

T-40 Transcriptome-wide profiling of intron retention events using a powerful intron-encoded reverse transcriptase in RNA-seq
Li-Tao Guo, George Maio, SungHee Park, RNAConnect Inc, Branford, CT, USA

T-41 NanoQuartz: Single-Molecule Profiling of Transcriptome-wide RNA Dynamics

Junsoo Kim[1], Chae Young Kwon[1], Hanju Lee[1], Heena Jeong[1], Yongkuk Choi[2], Hyeshik Chang[1]

[1]Seoul National University, Seoul, Republic of Korea. [2]Catholic University of Korea College of Medicine, Seoul, Republic of Korea

T-42 Nanopore sequencing enables esophageal cancer early detection via RNA liquid biopsy

Vikas Peddu, Alexander Hill, Daniel Kim, University of California, Santa Cruz, USA

T-43 piRNA pathways in terrestrial slugs: Evolutionary insights from germline and somatic small RNA landscapes

Kateryna Nemesh[1], Tobiáš Ber[1], Josef Pasulka[1], Filip Horvat[1,2], Kristian Vlahovicek[2], Petr Svoboda[1]

[1]Institute of Molecular Genetics of the Czech Academy of Sciences, Prague, Czech Republic. [2]Bioinformatics Group, Division of Molecular Biology, Department of Biology, Faculty of Science, University of Zagreb, Zagreb, Croatia

T-44 Multi-omic lineage tracing predicts the transcriptional, epigenetic and genetic determinants of cancer evolution

Francesco Nicassio, Istituto Italiano di Tecnologia (IIT), Milan, Italy

T-45 Mapping snoRNA-target RNA interactions in an RNA binding protein-dependent manner with chimeric eCLIP

Zhuoyi Song[1], Bongmin Bae[2], Simon Schnabl[2], Fei Yuan[1], Thareendra De Zoysa[2], Maureen V Akinyi[1], Charlotte A Le Roux[1], Karine Choquet[3], Amanda J Whipple[2], Eric L Van Nostrand[1]

[1]Therapeutic Innovation Center & the Verna Marrs McLean Department of Biochemistry & Molecular Pharmacology, Baylor College of Medicine, Houston, TX, USA. [2]Department of Molecular & Cellular Biology, Harvard University, Cambridge, MA, USA. [3]Department of Biochemistry and Functional Genomics, Université de Sherbrooke, Sherbrooke, Québec, Canada

T-46 A comprehensive meta-analysis to test thermodynamic models for RNA binding protein specificity and function

Gabriel Tauber[1], Daniel Herschlag[1,2]

[1]Department of Biochemistry, Stanford University School of Medicine, Stanford, CA, USA. [2]Department of Chemical Engineering and Sarafan ChEM-H Institute, Stanford, CA, USA

T-47 ASTRO enables spatial exploration of whole transcriptome in archival FFPE tissues

Dingyao Zhang, Zhiyuan Chu, Yiran Huo, Zhiliang Bai, Rong Fan, Jun Lu, Mark Gerstein, Yale University, New Haven, CT, USA

T-48 A foundation language model to decipher diverse regulation of RNAs
Hanwen Zhou[1,2], Yue Hu[3], Yulong Zheng[2], Jiefu Li[2], Jielong Peng[2], Jiang Hu[4], Yun Yang[4], Guoqing Zhang[2], Zefeng Wang[1,2]
[1]School of Life Science, Guangming Advanced Research Institute, Southern University of Science and Technology, Shenzhen, Guangdong, China. [2]Bio-Med Big Data Center, Chinese Academy of Sciences Key Laboratory of Computational Biology, Shanghai Institute of Nutrition and Health, University of Chinese Academy of Sciences, Chinese Academy of Sciences, Shanghai, China. [3]School of Medicine, Department of Pharmacy, University of North Carolina at Chapel Hill, Chapel Hill, North Carolina, USA. [4]CirCode Biomedicine Inc., Shanghai, China

T-49 Exploring the splicing landscape of the Cyanidiales reveals crucial insights into both the mechanisms underlying evolutionary intron loss and spliceosomal complexity
Viktor Slat[1], Martha Stark[2], Stephen Rader[2]
[1]University of British Columbia, Vancouver, BC, Canada. [2]University of Northern British Columbia, Prince George, BC, Canada

Concurrent 6: RNA Structure, Folding and Modeling

Sponsored by Sanofi
Town and Country Ballroom B
Session Chair: Katie Eichhorn

T-50 RNA structural patterns at 3' splice sites altered by SF3B1 K700E mutation
Austin Herbert, Abigail Hatfield, Alexandra Randazza, Valeria Miyamoto, Katie Palmer, Lela Lackey, Clemson University, Clemson, SC, USA

T-51 Functional insights into regulatory RNA structure with critical roles in vitro and in vivo in murine norovirus
Tanja Hann, Arya Okten, Renata Filler, Craig Wilen, Anna Marie Pyle, Yale University, New Haven, USA

T-52 Decoding lncRNA structure beyond sequence through AI
Nicolás Aira, Mercedes Castro Figueroa, Uciel Chorostecki
Department of Biomedical Sciences, Universitat Internacional de Catalunya, Barcelona, Spain

T-53 Direct measurement of RNA G-quadruplex folding topologies by multi-site DMS probing
Rebekah Rothacher[1], Bryan Guzman[2], Daniel Dominguez[2], Anthony Mustoe[1]
[1]Baylor College of Medicine, Houston, TX, USA. [2]UNC, Chapel Hill, NC, USA

T-54 Characterization of 3D RNA structural features in DMS reactivity
Sanduni Deenalattha, Chris Jurich, Bret Lange, Darren Armstrong, Kaitlyn Nein, Joseph Yesselman, University of Nebraska - Lincoln, Lincoln, NE, USA

T-55 Serum stable RNA origami nanodevices with 2'-FY-modification for sensing and targeting in vivo
Emil Kristoffersen[1], Nikolaj Zwergius[1], Nestor Vallina[2], Nicolas Glück[3], Amanda Stange[1], Lasse Desdorf[1], Laia Civit[1], Cody Geary[4], Jørgen Kjems[1], Julian Valero[1], Ebbe Andersen[1]
[1]Aarhus University, Aarhus, Denmark. [2]Danish Technical University, Kgs. Lyngby, Denmark. [3]University of Tübingen, Tübingen, Germany. [4]University of Heidelberg, Heidelberg, Germany

T-56 Naturally ornate RNA homo-oligomeric complexes
Rachael Kretsch[1], Yuan Wu[1], Svetlana Shabalina[2], Hyunbin Lee[1], Grace Nye[1], Eugene Koonin[2], Alex Gao[1], Rhiju Das[1], Wah Chiu[1]
[1]Stanford University, Stanford, CA, USA. [2]National Institutes of Health, Bethesda, MD, USA

T-57 Cryo-EM structure of a natural RNA nanocage
Xiaobin Ling[1], Dmitrij Golovenko[1], Jianhua Gan[2], Jinbiao Ma[2], Andrei A. Korostelev[3], Wenwen Fang[3]
[1]Umass Chan Medical School, Worcester, Massachusetts, USA. [2]Fudan University, Shanghai, China. [3]Umass Chan Medical School, Worcester, USA

T-58 Structure of a hibernating archaeal ribosome with a divergent active site
Amos Nissley, Yekaterina Shulgina, Roan Kivimae, Blake Downing, Petar Penev, Jillian Banfield, Dipti Nayak, Jamie Cate, University of California, Berkeley, Berkeley, CA, USA

T-59 RNA structuromics: Perturbing bacterial ribosome assembly at single-nucleotide resolution
Kai Sheng, Scripps Research Institute, San Diego, California, USA

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THURSDAY, MAY 29

Plenary Session 2: RNA and Disease

Thursday, May 29, Town and Country Ballroom C& D
Session Chair: Paul Donlin-Asp
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T-60 RNA splicing regulation of T cell exhaustion
Yuxi Ai, Beatrice Zhang, Joshua Schoenfeld, Maxim Maron, Jahan Rahman, Simon Hogg, Charlotte Ariyan, Benjamin Greenbaum, Santosha Vardhana, Omar Abdel-Wahab, Memorial Sloan Kettering Cancer Center, New York, NY, USA

T-61 Integrative CRISPR Screens and RNA-Omics Discover an Essential Role for PUF60-3' Splice Site Interactions in Cancer Progression
Alexandra Tankka, Corina Antal, Gene Yeo, UCSD, La Jolla, CA, USA

T-62 Dysregulated RNA splicing propels tumorigenesis and presents therapeutic targets in lung cancer
Yufang Bao[1], Yueren Yan[2], Ning Wang[3], Zefeng Wang[4], Yongbo Wang[1]
[1]Department of Cellular and Genetic Medicine, School of Basic Medical Sciences, Fudan University, Shanghai, China. [2]Department of Thoracic Surgery, Fudan University Shanghai Cancer Center, Shanghai, China. [3]Shanghai Institute of Nutrition and Health, Chinese Academy of Sciences, Shanghai, China. [4]School of Life Science, Southern University of Science and Technology, Shenzhen, Guangdong, China

T-63 Regulated intron retention directs the timely usage of transcripts during cardiac maturation
Subhashis Natua, Ishita Purwar, Sandip Chorghade, Diptatanu Das, Auinash Kalsotra, University of Illinois, Urbana-Champaign, Urbana, Illinois, USA

T-64 Alternative start codon selection shapes mitochondrial adaptation during evolution, homeostasis, and disease
Jimmy Ly[1], Yi Fei Tao[1], Ekaterina Khalizeva[1], Matteo Di Bernardo[1], Christopher Giuliano[1], Sebastian Lourido[1], Mark Fleming[2], Iain Cheeseman[1]
[1]Whitehead Institute and MIT, Cambridge, MA, USA. [2]Boston Children's Hospital, Boston, MA, USA

T-65 Codon-dependent regulation of gene expression during dengue virus infection
Luciana Castellano[1], Ryan McNamara[1], Horacio Pallares[1], Andrea Gamarnik[2], Diego Alvarez[3], Ariel Bazzini[1,4]
[1]Stowers Institute for Medical Research, Kansas City, Missouri, USA. [2]Leloir Institute Foundation, IIBBA-CONICET, Buenos Aires, Ciudad Autonoma de Buenos Aires, Argentina. [3]Instituto de Investigaciones Biotecnológicas, CONICET, Universidad Nacional de San Martin, San Martin, Buenos Aires, Argentina. [4]Department of Molecular and Integrative Physiology, University of Kansas Medical Center, Kansas City, Kansas, USA

Keynote 3: Matt Disney

Town and Country Ballroom C & D
Introduced by Zefeng Wang

K-3 The druggable transcriptome project: From chemical probes to precision medicines
Matt Disney, The Herbert Wertheim UF Scripps Institute for Biomedical Innovation & technology, Jupiter, fl, USA

Plenary Session 3: RNA Therapeutics I

Sponsored by Sanofi
Town and Country Ballroom C & D
Session Chair: Kristopher Brannan

T-66 Reversal of myotonic dystrophy with artificial RNA enzymes targeting CUG repeat expansions
Miaowei Mao[1], Tong Wei[2], Zefeng Wang[2]
[1]Shanghai Institute of Immunity and Infection, Chinese Academy of Sciences, Shanghai, China. [2]Southern University of Science and Technology, Shenzhen, China

T-67 From missense to antisense: Splicing modulation therapies for POLR3-Related leukodystrophies
Benoît Chabot[1,2], Lulzim Shkreta[3,2], Aurélie Delannoy[1]
[1]FMSS-MicrobiologyUniversité de Sherbrooke, Sherbrooke, Quebec, Canada. [2]The Quebec DePTAQ Network for RNA Therapeutics, Sherbrooke, Quebec, Canada. [3]Université de Sherbrooke, Sherbrooke, Quebec, Canada

T-68 3´-end stabilization increases cellular half-life and improves potency of mRNA therapeutics
Joshua Zimmer, Brian Fritz, Valeri Taruno, Marissa Licata, Joseph Chan, Groves Dixon, Adriana Jones, David Reid, Eckhard Jankowsky, Alicia Bicknell
Moderna, Cambridge, MA, USA

T-69 RNA-only delivery for site-specific transgene addition to the human genome by retrotransposon-protein mediated DNA synthesis
Kathleen Collins, UC Berkeley, Berkeley, CA, USA

Concurrent 7: The Current and Future State of RNA Medicines

Town and Country Ballroom A
Panel hosted by the RNA Society Junior Scientists Group

Concurrent 8: RNA Therapeutics II

Town and Country Ballroom C & D
Session Chair: Alicia Bicknell

T-70 Exogenous RNA surveillance by proton-sensing TRIM25
Myeonghwan Kim[1,2], Youngjoon Pyo[1,2], Seong-In Hyun[1,2], Minseok Jeong[1,2], Yeon Choi[1,2], V. Narry Kim[1,2]
[1]Institute for Basic Science, Seoul, Korea, Republic of. [2]Seoul National University, Seoul, Korea, Republic of

T-71 A Novel Circular RNA Vaccine Platform for Chikungunya
Daniel L. Kiss[1,2], Nada Bejar[1], Daniel R. Boutz[3], Murilo T.D. Bueno[1], Kathrina Castillo[1], Tulsi Ram Damase[1], Elizabeth A. Davis[1,4], Wataru Horikawa[1], Andrew P. Horton[3], Shaunak Kar[3], Sana Koubaa Kharrat[1], Honyi Li[1], Chiara Mancino[5,6], Amanda Mareth[7], Brooke Mitchell[7], Jessica A. Plante[7], Ankita Rao[1], Rachel Reyna[7], Chotiwat Seephetdee[1], Thomas Segall-Shapiro[3], Vrutant V. Shah[1], Raghav Shroff[3], Trinh T. Tat[1], Xiaoxiao Wang[1], Qing Yan[1], Kristopher W. Brannan[1], Jimmy Gollihar[3,8], Kenneth Plante[7], Francesca Taraballi[5,6], Scott Weaver[7], John P. Cooke[1,2]
[1]Center for RNA Therepeutics; Houston Methodist Research Institute, Houston, TX, USA. 2Deparment of Cardiovascular Sciences; Houston Methodist Research Institute, Houston, TX, USA. [3]Center for Infectious Diseases; Houston Methodist Research Institute, Houston, TX, USA. [4]Deparment of Cardiovascular Sciences, Houston Methodist Research Institute, Houston, tx, USA. [5]Center for Musculoskeletal Regeneration; Houston Methodist Research Institute, Houston, TX, USA. [6]Orthopedics and Sports Medicine; Houston Methodist Hospital, Houston, TX, USA. [7]World Reference Center for Emerging Viruses and Arboviruses; University of Texas Medical Branch, Galveston, TX, USA. [8]The Laboratory of Antibody Discovery & Accelerated Protein Therapeutics, Dept. of Pathology & Genomic Medicine; Houston Methodist Research Institute, Houston, TX, USA

T-72 The long non-coding RNA Lnc-RAINY regulates genes involved in radiation susceptibility through DNA:DNA:RNA triplex-forming interactions and has tumor therapeutic potential in lung cancers
Ivan Martinez, Emily Westemeier-Rice
West Virginia University, Morgantown, WV, USA

T-73 Chemically and topologically modified branched mRNA with enhanced translation capacity
Hongyu Chen[1,2], Dangliang Liu[1,2], Abhishek Aditham[1,2], Jianting Guo[1,2], Jiahao Huang[1,2], Franklin Kostas[1,2], Kamal Maher[1,2], Mirco Friedrich[1,2,3,4], Ramnik Xavier[2,5], Feng Zhang[1,2,3], Xiao Wang[1,2]
[1]Massachusetts Institute of Technology, Cambridge, MA, USA. [2]Broad Institute of MIT and Harvard, Cambridge, MA, USA. [3]Howard Hughes Medical Institute, Cambridge, MA, USA. [4]Deutsches Krebsforschungszentrum, Heidelberg, Germany. [5]Massachusetts General Hospital, Boston, MA, USA

T-74 Programmable RNA-sensing elements for targeted activation of mRNA platforms
Kristopher Brannan, Ricardo Noriega, Vrutant Shah, Thy Nguyen, Martin Requena
Houston Methodist Research Institute, Houston, Texas, USA

T-75 Complementation of a human disease phenotype by intercellular mRNA transfer
Gal Haimovich, Sandipan Dasgupta, Anand Govindan-Ravi, Jeffrey E. Gerst
Weizmann Institute of Science, Rehovot, Israel

T-76 Small molecule recognition of positive-sense viral RNA regulatory structures to inhibit translation
TinTin Luu[1], Josie van de Klashorst[2], Kanika Chopra[3], Shinya Suzuki[2], Amanda Hargrove[1]
[1]University of Toronto, Mississauga, ON, Canada. [2]Duke University, Durham, NC, USA. [3]Transylvania University, Lexington, KY, USA

Concurrent 9: Training Future Scientists Through RNA

Town and Country Ballroom B
Session Chair: Suzanne Lee

T-77 Exploring gene expression changes in response to cellular stress via a scalable, modular and investigative lab suitable for introductory biology students
Angie Hilliker, University of Richmond, Richmond, VA, USA

T-78 Empowering undergraduate research through a course-based approach: The superlab experience at Haverford College
Amy Cooke, Haverford College, Haverford, PA, USA

T-79 A CURE laboratory course for student exploration in research at the chemistry-biology interface using fluorogenic RNA aptamers
Catherine Eichhorn, University of Nebraska - Lincoln, Lincoln, NE, USA

T-80 Increasing access to undergraduate research experiences at Loyola Marymount University through an RNA-centric course-based undergraduate research experience in an Advanced Biochemistry Lab Course
Sandhya Krishnan[1], Lisa Corwin[1], Kathryn Mouzakis[2]
[1]University of Colorado Boulder, Boulder, CO, USA. [2]Loyola Marymount University, Los Angeles, CA, USA

T-81 The RNA hero's journey – A storytelling framework for RNA education
Belén Moro, Science As Stories, Barcelona, Catalunya, Spain

T-82 Enhancing RNA education and scientific development through a collaborative structure-function course-based research experience
Megan Filbin[1], Janet Filbin[2]
[1]Metropolitan State University of Denver, Denver, CO, USA. [2]University of Colorado, Denver, Denver, CO, USA

T-83 The Toxic RNA Lab: Expanding undergraduate research opportunities through Curricular Undergraduate Research Experiences
Jeremy Sanford, John Tamkun, Guido Bordignon
University of California Santa Cruz, Santa Cruz, CA, USA

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FRIDAY, MAY 30

Plenary Session 4: Translation Mechanisms

Town and Country Ballroom C & D
Session Chair: Sezen Meyden

T-84 The mechanism of mRNA activation
Riley Gentry[1], Nicholas Ide[1], Victoria Comunale[1], Erik Hartwick[1,2], Colin Kinz-Thompson[1,3], Ruben Gonzalez, Jr.[1]
[1]Columbia University, New York, NY, USA. [2]University of Colorado Boulder, Boulder, CO, USA. [3]Rutgers University-Newark, Newark, NJ, USA

T-85 eIF1 and eIF5 dynamically control translation start site fidelity
Rosslyn Grosely[1], Carlos Alvarado[1], Sydney McGuire[2], Niseema Pachikara[2], Oliver Nicholson[2], Ivaylo Ivanov[3], Jody Puglisi[1], Tom Dever[3], Chris Lapointe[2]
[1]Stanford University, Stanford, CA, USA. [2]Fred Hutchinson Cancer Center, Seattle,
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WA, USA. [3]Eunice Kennedy Shriver National Institute of Child Health and Human Development National Institutes of Health, Bethesda, MD, USA

T-86 Investigating a role for DDX6 in regulating the co-translational assembly of protein complexes
Joseph Waldron[1], James Ettles[1], Pauline Herviou[1], Tobias Schmidt[1], Sarah Gillen[1], Jonathan Bohlen[2], Ania Wilczynska[1], Martin Bushell[1]
[1]CRUK Scotland Institute, Glasgow, United Kingdom, [2]Gene Center at the Ludwig Maximillian University of Munich, Munich, Germany

T-87 How do cells distinguish between a functional translation pause and a harmful pathological stall?
Sounak Saha, Christopher Hawk, Hong Jin
University of Illinois Urbana Champaign, Urbana, Illinois, USA

T-88 Single-molecule imaging of protein-mRNA interactions in live cells reveals ZNF598 as a limiting factor in disassembling collided ribosomes
Ana De La Cruz, Bin Wu
Johns Hopkins University, Baltimore, MD, USA

T-89 Translational control of transcripts with allele specific expression during mouse embryo development
Dayea Park, Can Cenik, University of Texas at Austin, Austin, Texas, USA

Keynote 4: Ling-Ling Chen

Town and Country Ballroom C & D
Introduced by Jørgen Kjems

K-4 Biogenesis, function and application of circular RNAs
Ling-Ling Chen
CAS Center for Excellence in Molecular Cell Science, Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences, Shanghai, China

Concurrent 10: RNA Processing Events

Town and Country Ballroom A
Session Chair: Jeff Chao

T-90 Large-scale tethered screen of RNA-binding proteins reveals novel regulators of poly(A) site selection

Pratibha Jagannatha[1], Yoseop Yoon[2], Samuel Landry[1], Jack Naritomi[1], Lijun Zhan[3], Sara Olson[3], Xintao Wei[3], Lena Street[4], Liang Liu[2], Joshua Jeong[2], Jack Reid[2], Lindsey Soles[2], Elijah Rosales[1], Vicky Chen[1], Shuhao Xu[1], Avery Pong[1], Marko Jovanovic[4], Brenton Graveley[3], Yongsheng Shi[2], Gene Yeo[1]
[1]University of California, San Diego, La Jolla, CA, USA. [2]University of California, Irvine, Irvine, CA, USA. [3]Institute for Systems Genomics, UConn Health, Farmington, CT, USA. [4]Columbia University, New York, NY, USA

T-91 Cytoplasmic mRNA decay by anti-viral nuclease RNase L promotes transcriptional repression

Xiaowen Mao[1], Sherzod Tokamov[1], Felix Pahmeier[2], Jinyi Xu[3], Azra Lari[1], Eva Harris[2], Britt Glaunsinger[1,4]
[1]Department of Plant and Microbial Biology, University of California, Berkeley, Berkeley, CA, USA. [2]Division of Infectious Diseases and Vaccinology, School of Public Health, University of California, Berkeley, Berkeley, CA, USA. [3]School of Basic Medical Sciences, Shanghai Medical College, Fudan University, Shanghai, China. [4]Howard Hughes Medical Institute, Berkeley, CA, USA

T-92 Composition and RNA binding specificity of metazoan RNase MRP

Yuan Liu[1], Shiyang He[1], Kawon Pyo[1], Shanshan Zheng[2], Meijuan Chen[1], Sihem Cheloufi[1], Nikolai Slavov[2], William F Marzluff[3], Jernej Murn[1]
[1]UC Riverside, Riverside, CA, USA. [2]Northeastern University, Boston, MA, USA. [3]University of North Carolina, Chapel Hill, NC, USA

T-93 dFORCE reveals the multimodal timing of pre-mRNA processing *in vivo*

AJ Sethi[1,2,3], Marco Guarnacci[1], Azusa Hayashi[1], Madhu Kanchi[1], Takayuki Nojima[4], Eduardo Eyras[1,2,3], Rippei Hayashi[1]
[1]The Shine-Dalgarno Centre for RNA Innovation, The John Curtin School of Medical Research, Australian National University, Canberra, ACT, Australia. [2]The Centre for Computational Biomedical Sciences, The John Curtin School of Medical Research, Australian National University, Canberra, ACT, Australia. [3]EMBL Australia Partner Laboratory Network at the Australian National University, Canberra, ACT, Australia. [4]Research Centre for Systems Immunology, Medical Institute of Bioregulation, Kyushu University, Fukuoka, Kyūshū, Japan

T-94 Less is more: Converting IscB and Cas9 into versatile RNA-guided RNA editors by switching off their DNA-binding activity

Chengtao Xu, Xiaolin Niu, Haifeng Sun, Ailong Ke
Yale University, New Haven, CT, USA

Concurrent 11: Splicing Mechanisms and Regulation

Town and Country Ballroom C & D
Session Chair: Ruixue Wan

T-95 Splicing fidelity influences the fate of mRNA molecules
Eraj Khokhar, Kaitlyn Brokaw, Nida Javeed, Zachary Kartje, Ayush Kumar, Sanabria Valeria, Jonathan Watts, Athma Pai
UMass Chan Medical School, Worcester, MA, USA

T-96 SENA1: A Novel Intrinsically Disordered Protein That Repairs Splicing of Distorted Branch Point Sequences
Shinichi Nakagawa[1], Kotaro Tsuboyama[2], Yukihide Tomari[2]
[1]Hokkaido University, Sapporo, Hokkaido, Japan. [2]The University of Tokyo, Tokyo, Tokyo, Japan

T-97 Intron-mediated delays in gene expression control ~24-hour circadian rhythms
Ye Yuan, Amanda Linskens, Swathi Yadlapalli, University of Michigan, Ann Arbor, MI, USA

T-98 Mammalian aging involves genome-wide splicing degeneration leading to functional decline
Sirui Zhang, Alexander Tyshkovskiy, Vadim Gladyshev
Brigham and Women's Hospital, Harvard Medical School, Boston, MA, USA

T-99 Mechanistic insights into catalysis of the U12-type spliceosome
Rui Bai[1,2], Han Guo[1,2], Yaping Ge[1], Ting Luo[1,2], Ruixue Wan[1,2]
[1]School of Life Sciences, Key Laboratory of Structural Biology of Zhejiang Province, Westlake University, Hangzhou, China. [2]Institute of Biology, Westlake Institute for Advanced Study, Hangzhou, China

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Plenary Session 5: Alternative Splicing

Town and Country Ballroom C & D
Session Chair: Yongbo Wang

T-100 Decoding the pre-mRNA structurome in alternative splicing regulation
Jianhui Bai, Kongpan Li, Zhipeng Lu, University of Southern California, Los Angeles, CA, USA

T-101 Systematic discovery of cell type-specific alternative splicing determinants using massively parallel reporter assays
Xi Dawn Chen[1,2], Maile Jim[1,2], Mounica Vallurupalli[1], Kai Cao[1], Andrea Navarro Torres[1], Yifan Zhang[1], David Wollensak[1], Qiyu Gong[1], Jing Sun[1,2], Anisha Laumas[1], Jennifer Roth[1], Todd Golub[1], Fei Chen[1]
[1]Broad Institute of MIT and Harvard, Cambridge, MA, USA. [2]Harvard University, Boston, MA, USA

T-102 The ultraconserved poison exons of SRSF3 and TRA2ß are essential for pluripotent cells
Nathan Leclair[1,2], Mattia Brugiolo[3], Isha Walawalker[3], Ryan Englander[3], Mallory Ryan[3], Caleb Heffner[4], Justin McDonough[3], William Skarnes[3], Steve Murray[4], Olga Anczukow[3,5]
[1]The Jackson Laboratory for Genomic Medicine, The Jackson Laboratory for Genomic Medicine, CT, USA. [2]Graduate Program in Genetics and Development, UConn Health, Farmington, CT, USA. [3]The Jackson Laboratory for Genomic Medicine, Farmington, CT, USA. [4]The Jackson Laboratory, Bar Habor, ME, USA. [5]Department of Genetics and Genome Sciences, UConn Health, Farmington, CT, USA

T-103 A conserved poison microexon for neuronal longevity
Sika Zheng[1], Lin Lin[1], Wei Jiang[2], Peter Stoilov[3], Liang Chen[2]
[1]Center for RNA Biology and Medicine, University of California, Riverside, CA, USA. [2]Department of Quantitative and Computational Biology, University of Southern California, Los Angeles, CA, USA. [3]Department of Biochemistry and Cancer Institute, Robert C. Byrd Health Sciences Center, West
Virginia University, Morgantown, WV, USA

T-104 Structural and functional basis for selective transcriptomic effects of anti-tumor SF3B1 inhibitors
Suzanne Mays[1], Sophie Bonnal[1], Marat Pavlyukov[1], Federica Battistini[2], Andrew MacRae[1], Modesto Orozco[2], Vladimir Pena[3], Juan Valcarcel[1,4,5]
[1]CRG, Barcelona, Spain. [2]IRB, Barcelona, Spain. [3]ICR, London, United Kingdom. [4]UPF, Barcelona, Spain. [5]ICREA, Barcelona, Spain

Plenary 6: RNA and Neuroscience

Town and Country Ballroom C & D
Session Chair: Ezgi Hacisuleyman

T-105 Live single-transcript imaging reveals a global shift in particle dynamics during neuronal development
Aileen-Diane Bamford[1,2,3], Gilles Gut[2], Tim-Oliver Buchholz[3], Ryoko Okamoto[2], Barbara Treutlein[2], Franka Voigt[1]

[1]University of Zurich, Department of Molecular Life Sciences, Zurich, Switzerland. [2]ETH Zurich, Department for Biosystems Science and Engineering, Basel, Switzerland. [3]Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland

T-106 Activity-dependent local regulation of Camk2a mRNA confers persistent supply of CaMKIIα at the postsynaptic dendritic spine
Dong-Woo Hwang[1], Sulagna Das[2], Robert H. Singer[1]
[1]Albert Einstein College of Medicine, Bronx, NY, USA. [2]Emory University School of Medicine, Atlanta, GA, USA

T-107 An RNA binding protein functions as a key coordinator of cellular metabolism and neuronal function
Jordan Goldy, Heath Dunlop, Kenneth Moberg, Anita Corbett
Emory University, Atlanta, Georgia, USA

T-108 Investigating tissue-specific consequences of neuropathy-causing RNA exosome mutations in drosophila
Lauryn Higginson[1], Alex Cerda[1], Kevin He[2], Mayra Rodriguez[1], Guillaume Chanfreau[2], Derrick Morton[1]
[1]University of Southern California, Los Angeles, CA, USA. [2]University of California, Los Angeles, Los Angeles, CA, USA

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SATURDAY, MAY 30

Plenary Session 7: RNA Surveillance and Degradation

Town and Country Ballroom C & D
Session Chair: Derrick Morton

T-109 Multiple RNA quality control checkpoints safeguard the biogenesis of small nuclear RNAs
Tiantai Ma, Claire Huntington, Jens Lykke-Andersen
UCSD, La Jolla, California, USA

T-110 Deciphering the code: codons, codon-codon interactions, amino acids, and peptide bonds regulate mRNA stability
Haejeong Lee, Damir Musaev, Charles Vejnar, Srikar Krishna, Ethan Strayer, Jean-Denis Beaudoin, Mario Abdelmessih, Antonio Giraldez
Yale University, New Haven, CT, USA
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T-111 Structural and functional insights into the MTR4-NRDE2-CCDC174 Complex establish a direct link between mRNA splicing surveillance and RNA degradation
Sebastian Falk, Toni Manolova, Max Perutz Labs, Vienna, Austria

T-112 Identification of human pathways acting on nuclea non-coding RNAs using the mirror forward genetic approach
Rui Che[1,2], Monireh Panah[1,2], Bhoomi Mirani[1,2], Krista Knowles[1,2], Anastacia Ostapovich[3], Debarati Majumdar[1,2], Xiaotong Chen[1], Joseph DeSimone[1], William White[1], Megan Noonan[1], Hong Luo[1], Andrei Alexandrov[1,2]
[1]Clemson University Dept. of Genetics and Biochemistry, Clemson, SC, USA. [2]Clemson University Center for Human Genetics, Greenwood, SC, USA. [3]Yale University Dept. of Molecular Biophysics and Biochemistry, New Haven, CT, USA

T-113 The Drosha homolog Rnt1 regulates protein-coding genes by directly cleaving a range of mRNAs
Lee-Ann Notice[1], Mathieu Catala[2], Sherif Abou Elela[2], Ambro van Hoof[1]
[1]The University of Texas MD Anderson Cancer Center UTHealth Houston Graduate School of Biomedical Sciences, Houston, TX, USA. [2]Université de Sherbrooke, Sherbrooke, Québec, Canada

T-114 Cell Type- and Factor-Specific NMD
Kun Tan, Jonathan Sebat, Miles Wilkinson
University of California San Diego, La Jolla, CA, USA

Plenary Session 8: RNA Protein Interactions

Sponsored by Sanofi
Town and Country Ballroom C & D
Session Chair: Daniel Dominguez

T-115 A Deep Dive into the Landscape of Arthropod RNA Binding Proteins
Zaydah de Laurent[1], Wael Kamel[1], Yana Demyanenko[2,3], Rozeena Arif[1], Alexandra Wilson[4], Shabaz Mohammed[2,3], Alain Kohl[5], Benjamin Brennan[1], Alfredo Castello[1]
[1]MRC-University of Glasgow, Centre for Virus Research, Glasgow, United Kingdom. [2]Department of Chemistry, University of Oxford, Oxford, United Kingdom. [3]The Rosalind Franklin Institute, Didcot, United Kingdom. [4]Veterinary Research Institute, Emerging Viral Diseases, Department of Experimental Biology, Faculty of Science, Masaryk University, Brno, Czech Republic. [5]Liverpool School of Tropical Medicine, Pembroke, United Kingdom

T-116 Structural mechanism of LINE-1 target-primed reverse transcription
George Ghanim[1], Hongmiao Hu[2], Jerome Boulanger[2], Thi Hoang Duong Nguyen[2]
[1]Princeton University, Princeton, New Jersey, USA. [2]MRC LMB, Cambridge, United Kingdom

T-117 The DND1-NANOS3 Ribonucleoprotein Complex controls germline development by suppressing the expression of a network of genes by binding a high-information-content cis-acting element in mRNA 3' untranslated regions
Masataka Suzawa[1], Ahsan Polash[1], Chen Qiu[2], Alexis Jacob[1], Wataru Horikawa[3], Eugene Valkov[3], Traci Hall[2], Masashi Yamaji[4], Markus Hafner[1]
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T-118 Dynamic remodeling of long-range flavivirus RNA interactions by host translation initiation factors
Michael Palo, Betty Ha, Christopher Lapointe, Carlos Alvarado, John Janetzko, Jan Carette, Joseph Puglisi, Elisabetta Viani Puglisi
Stanford University School of Medicine, Stanford, CA, USA

T-119 Unraveling the hypoxia-dependent regulations of RNA-protein interactions
Arne Praznik, Max-Delbrück-Centrum, Berlin, Berlin, Germany

T-120 Local destabilization of 16S rRNA drives functional adaptation in chimeric ribosomes
Tushar Raskar[1], Alan Costello[2], James Fraser[1], Ahmed Badran[3]
[1]University of California, San Francisco, San Francisco, California, USA. [2]National Institute for Bioprocessing Research, Dublin, Ireland. [3]The Scripps Research Institute, San Diego, California, USA

Concurrent 12: RNA Condensates

Town and Country Ballroom C & D
Session Chair: Maria Hondele

T-121 RNA multivalency plays a key role in biomolecular condensate properties both in vivo and in vitro
Sierra Cole[1,2], Christine Roden[3], Amy Gladfelter[2]
[1]UNC-Chapel Hill, Chapel Hill, NC, USA. [2]Duke University, Durham, NC, USA. [3]University of Montreal, Montreal, Canada

T-122 Controlling intermolecular base pairing in Drosophila germ granules by mRNA folding and its implications in fly development

Siran Tian[1], Hung Nguyen[2,3], Ziqing Ye[1,4], Silvi Rouskin[5], D. Thirumalai[3], Tatjana Trcek[1]
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T-123 HS-AFM Unveils Stepwise Condensation Dynamics in RNA-Mediated LLPS
SM Neaz Mahmud, Noriyuki Kodera, Hanae Sato, Nano Life Science Institute (WPI-NanoLSI), Kanazawa University, Kanazawa, Ishikawa, Japan

T-124 Investigating the role of the neuroprotective RNA chaperone RBM3 in stress granules
Silvia Scalzitti[1], Henri Niskanen[2], Denes Hnisz[2], Florian Heyd[1]
[1]Laboratory of RNA Biochemistry, Institute of Chemistry and Biochemistry, Freie Universität Berlin, Berlin, Germany. [2]Department of Genome Regulation, Max Planck Institute for Molecular Genetics, Berlin, Germany

T-125 Condensates containing phosphorylated SR proteins expose RNA at their surfaces and enhance splicing in vitro
Noémie Kociolek, Rajika Arora, Jianning Jiang, Anuradha Bhat, Timo Greter, Maria Escura Pérez, Tamara Kazeeva, Antoine Cléry, Frédéric Allain
ETH Zürich, Institute of Biochemistry, Zürich, Switzerland

T-126 Tag with Caution - How most tags influence biomolecular condensation in vivo and in vitro
Kerstin Dörner[1], Michelle Jennifer Gut[1], Daan Overwijn[1], Fan Cao[2], Matej Siketanc[1], Stephanie Heinrich[1], Nicole Beuret[1], Timothy Sharp[1], Kresten Lindorff-Larsen[2], Maria Hondele[1]
[1]Biozentrum, University of Basel, Basel, Switzerland. [2]University of Structural Biology and NMR Laboratory & the Linderstrøm-Lang Centre for Protein Science, Department of Biology, University of Copenhagen, Copenhagen, Denmark

T-127 Immunofluorescent probes for live-cell RNA imaging
Hasan Al Banna[1], Kimberley Berg[2], Tasnia Sadat[1], Naba Krishna Das[1], Roshan Paudel[3], Victoria D'Souza[2], Deepak Koirala[1]
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Concurrent 13: Ribosome Biogenesis

Town and Country Ballroom A
Session Chair: Yoon-Mo Yang

T-128 ZNHIT6 interacts with NPM1 to coordinate snoRNP biogenesis with other nucleolar processes
Md Lutfur Rahman, Homa Ghalei, Emory University School of Medicine, Atlanta, GA, USA

T-129 Protein determinants of RNase MRP specificity and function
Eric Smith[1,2], Jimmy Ly[1,2], Sofia Haug[1,2], Iain Cheeseman[1,2]
[1]Whitehead Institute for Biomedical Research, Cambridge, MA, USA.
[2]Massachusetts Institute of Technology, Cambridge, MA, USA

T-130 A DEAD-box-ATPase mediated checkpoint avoids RNA misfolding
Zahrat El Oula Hassoun[1], Xin Liu[2], Emma Irbe[1], Katrin Karbstein[1]
[1]Vanderbilt University, Nashville, Tennessee, USA. [2]Boston Children's Hospital, Boston, USA

T-131 NMD3 and TIF6 gate the release of defective 60S ribosomal subunits into translation
Ruta Chitale[1], Kaoling Guan[2], Shilpa Rao[2], Can Cenik[2], David Taylor[1,2], Arlen Johnson[1,2]
[1]Interdisciplinary Life Sciences Graduate Program, The University of Texas at Austin, Austin, Texas, USA. [2]Department of Molecular Biosciences, The University of Texas at Austin, Austin, Texas, USA

T-132 Evolutionary origins of archaeal and eukaryotic RNA-guided RNA modification in IS110 transposons
Chance Meers[1], Hugo Vaysset[2], Jean Cury[2], Aude Bernheim2, Samuel Sternberg[1]
[1]Columbia University, New York City, New York, USA. [2]Institut Pasteur, Paris, France

T-133 Mapping and engineering RNA-controlled architecture of the multiphase nucleolus
Sofia Quinodoz[1,2], Lifei Jiang[1], Aya Abu-Alfa[1], Troy Comi[1], Hongbo Zhao[1], Qiwei Yu[1], Lennard Wiesner[1], Jordy Botello[1], Anita Donlic[1], Elizabeth Soehalim[1], Prashant Bhat[3,4], Christiane Zorbas[5], Ludivine Wacheul[5], Andrej Košmrlj[1], Denis Lafontaine[5], Sebastian Klinge[6], Clifford Brangwynne[1,2]
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T-134 Subcellular-specific RNA structural remodeling revealed by RAID-MaP
Ritwika Bose, Joshua Riback, Furqan Fazal, Anthony Mustoe
Baylor College of Medicine, Houston, TX, USA

Concurrent 14: RNA Transport and Localization

Town and Country Ballroom B

Session Chair: Dorothy Lerit

T-135 LENG8 mediates RNA nuclear retention

Lusong Tian, Yoseop Yoon, Liang Liu, Lindsey Soles, Marielle Valdez, Joshua Jeong, Jack Reid, Yongsheng Shi, Department of Microbiology and Molecular Genetics, School of Medicine, Universityof California, Irvine, Irvine, Irvine, CA, USA

T-136 Structures and mRNP remodeling mechanism of the TREX-2 complex

Yihu Xie[1], Bradley Clarke[1], Dongqi Xie[2], Beatriz Fontoura[2], Yi Ren[1]

[1]Vanderbilt University, Nashville, TN, USA. [2]University of Texas Southwestern Medical Center, Dallas, TX, USA

T-137 Profiling the transcriptome composition and dynamics of nuclear speckles using SLAM-RT&Tag

Nadiya Khyzha[1], Kami Ahmad[1], Steven Henikoff[1,2]

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T-138 Polysomes and mRNA control the biophysical properties of the eukaryotic cytoplasm

Vamshidhar R Gade[1], Stephanie Heinrich[1], Matteo Paloni[2], Pablo A. Gómez-García[1], Ajla Dzanko[1], Alexandra Oswald[1], Désirée Marchand[1], Alessandro Barducci[3], Karsten Weis[1]

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T-139 PUS7 cytoplasmic localization directs a pseudouridine-mediated cellular stress response

Minli Ruan[1], Sean Engels[2], Matthew Burroughs[2], Dylan Bloch[3], Oleksandra Fanari[3], Stuart Akeson[3], Daniel Eyler[1], Xiaoyan Li[1], Chase Weidmann[1], Sara Rouhanifard[3], Miten Jain[3], Lydia Contreras[2], Kristin Koutmou[1]

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T-140 Motor transport and ribosome anchoring kinetically control mitochondrial mRNA localization

Surbhi Sharma[1], Xuemei Wang[1], Madeline Rasband[1], Prabha Chupal[2], Trinh Tat[3], Jen Yun Chang[1], Eric Van Nostrand[1], Daniel Kiss[3], Aidan Brown[2], Furqan M Fazal[1]

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T-141 Determinants of RNA localization to centrosomes

Dorothy Lerit, Emory University School of Medicine, Atlanta, GA, USA

Concurrent 15: lncRNAs and circRNAs

Town and Country Ballroom C & D
Session Chair: Tony Mustoe

T-142 Theta ribozymes: Making the cut in tRNA maturation
Kasimir Kienbeck[1], Lukas Malfertheiner[2], Susann Zelger-Paulus[1], Silke Johannsen[1], Christian von Mering[2], Roland K. O. Sigel[1]
[1]Department of Chemistry, University of Zurich, Zurich, Switzerland. [2]Department of Molecular Life Sciences, University of Zurich, Zurich, Switzerland

T-143 Splicing factor SRSF3 coordinates with mutant SF3B1 to drive cryptic circRNA biogenesis
Mike Fernandez[1], Meiling Jin[1], Yiming Wu[1], Kevyn Hart[1], Eric Wang[2,3], Iannis Aifantis[2], Ren-Jang Lin[1], Lili Wang[1]
[1]City of Hope, Duarte, CA, USA. [2]NYU School of Medicine, New York, NY, USA. [3]The Jackson Laboratory for Genomic Medicine, Farmington, CT, USA

T-144 A conserved circular RNA-protein interaction regulates antiviral defense across species
Jie Min[1], Weihong Liang[1], Wei Liu[1], Xiao-Peng Xiong[2], Jennifer Li[3], Jian-Liang Li[4], Ranjan Perera[1], Rui Zhou[1]
[1]Johns Hopkins University School of Medicine, Johns Hopkins All Children's Hospital, St. Petersburg, FL, USA. [2]Sanford Burnham Prebys Medical Discovery Institute, La Jolla, CA, USA. [3]Brown University, Providence, RI, USA. 4National Institute of Environmental Health Sciences, Durham, NC, USA

T-145 The molecular mechanism of HERV-H RNA in maintaining stem cell identity
Wenkai Yi[1], Shanxin Lyu[1], Qianwen Xie[1,2,3], Jie Chen[1], Haorui Zhu[1], Wei Jin[4], Wenju Sun[2], Ligang Fan[2], Furong Ju[1,3], Xiaomin Zhou[1], Yarui Diao[5], Zhongjun Zhou[4], Chun-Kit Kwok[1], Jian Yan[1,2,3]
[1]City University of Hong Kong, Hong Kong, China. [2]Northwest University, Xi'an, China. [3]The City University of Hong Kong Shenzhen Research Institute, Shenzhen, China. [4]The University of Hong Kong, Hong Kong, China. 5Duke University Medical Center, Durham, NC, USA

T-146 Free tRNA introns act as novel complementarity-dependent regulatory RNAs
Paolo L. Sinopoli[1], Regina T. Nostramo[1], Sara Metcalf[1], Alicia Bao[1,2], Lauren M. Peltier[1,3], Anita K. Hopper[1]
[1]The Ohio State University, Columbus, Ohio, USA. [2]Present Address: Thomas Jefferson University, Philadelphia, Pennsylvania, USA. [3]Present Address: The University of Toledo, Toledo, Ohio, USA

Concurrent 16: miRNA and siRNA

Town and Country Ballroom A
Session Chair: Sebastian Falk

T-147 Distinct SUMOylation 'hot spots' in piRNA biogenesis and function
Mikhail Trostnikov[1], Maheshwaran Natarajan[1], Hannah Holmes[1], Katalin Fejes Tóth[2], Alexei Aravin[2], Maria Ninova[1]
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T-148 Determine the mechanism for piRNA degradation
Benjamin Pastore, Hannah Hertz, Wen Tang, Ohio State University, Columbus, Ohio, USA

T-149 Dynamics of miR-34a in human Argonaute2
Rubin Dasgupta[1], Walter Becker[2], Katja Petzold[1]
[1]Uppsala University, Uppsala, Sweden. [2]University of Sydney, Sydney, Australia

T-150 Structural basis for gene silencing by siRNAs in humans
Luca Gebert, Sucharita Sarkar, Ian MacRae, The Scripps Research Institute, La Jolla, CA, USA

T-151 A menagerie of endogenous site architectures mediates mammalian target-directed miRNA degradation
Daniel Lin[1,2], Maile Jim[1,2,3], Lara Elcavage[1,2,3], Michelle Frank[1,2,3], Lianne Blodgett[1,2,3], Elena Slobodyanyuk[1,2,3], Katya Khalizeva[1,3], Peter Wang[1,2,3], David Bartel[1,2,3]
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Concurrent 17: Diverse RNA Processes

Town and Country Ballroom B
Session Chair: Colin Wu

T-152 Protein-primed DNA homopolymer synthesis by anantiviral reverse transcriptase
Samuel Sternberg, Columbia University, New York, NY, USA. Howard Hughes Medical Institute, New York, NY, USA

T-153 RNA-coupled CRISPR screens uncover ZNF207 as a novel regulator of LMNA aberrant splicing linked to progeria

Jeongjin Kim, Amit Behera, Shreya Kordale, Arun Damodaran, Thomas Gonatopoulos-Pournatzis, RNA Biology Laboratory, Center for Cancer Research (CCR), National Cancer Institute (NCI), National Institutes of Health (NIH), Frederick, MD, USA

T-154 Translation of fragmented transcripts induces innate immunity and cell death

Agnes Karasik[1], Hernan Lorenzi[1], Andrew DePass[1], Nicholas Guydosh[2]
[1]NIH, Bethesda, MD, USA. [2]NIH, Bethesda, DC, USA

T-155 Noncanonical activity of tRNA genes for interferon signaling utilizes selective RNA Pol III terminators and is suppressible by the La protein/SSB

Alan Kessler, Sandy Mattijssen, Gennady Margolin, Alex Vassilev, Markus Hafner, Rich Maraia, NIH, Bethesda, USA

T-156 A new noncanonical biogenesis pathway generates a germline enriched miRNA family in *C. elegans*

Rima Sakhawala[1,2], Karl-Frédéric Vieux[1], Dustin Haskell[3], Guoyun Yu[1], Anna Zinovyeva[3], Katherine McJunkin[1]
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NOTES

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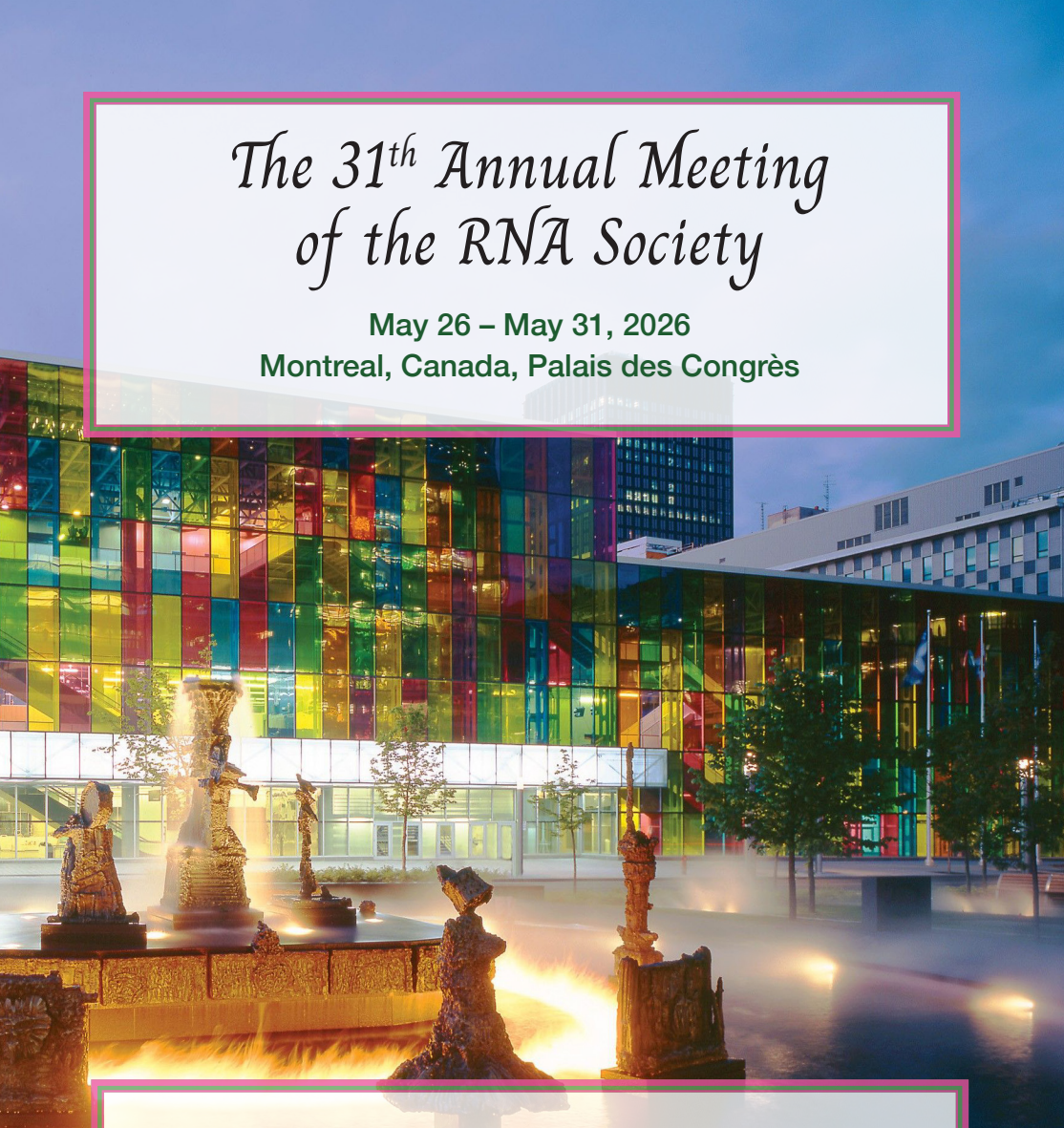

MEETING ORGANIZERS

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Anita Corbett, Emory University, USA
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