29TH ANNUAL MEETING OF THE RNA SOCIETY

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May 28th– June 2nd, 2024 Edinburgh, Scotland



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The 29th Annual Meeting of the RNA Society



May 28th– June 2nd, 2024

Edinburgh International Conference Centre Edinburgh, Scotland

MEETING ORGANIZERS

David Tollervey (Lead), University of Edinburgh, Scotland
Ben Blencowe, University of Toronto, Canada
Markus Bohnsack, University of Göttingen, Germany
Atlanta Cook, University of Edinburgh, Scotland
Yue Wan, Agency for Science, Technology and Research, Singapore



May 28th, 2024

Dear RNA friends and colleagues,

It is a great honor and pleasure to welcome you to RNA 2024. This year, we return to Edinburgh, where the Society's first meeting outside North America was held in 1999. In the past twenty-five years we have grown immensely as a society. Our science now includes areas that were only dreams back in 1999, such as the use of RNA as therapeutics and drug targets, and the ability to visualize large RNPs with cryo-EM. As the geographic diversity of our members has greatly expanded, our meetings now cycle between North America, Europe, and Asia.

One thing that remains unchanged is the incredible science and collegial spirit that characterizes our Annual Meeting. The meeting is shaped by its attendees, and so I thank all of you for attending and sharing your science. We look forward to an amazing five days of inspiring talks, great conversations at our poster sessions, renewing old friendships and making new ones. I encourage you to take advantage of the opportunities to build and strengthen your networks, meet the Editors of the **RNA** Journal, and discuss how we can make our Society even more welcoming at the DEI panel.

Finally, I want to express my immense gratitude to our organizers David Tollervey, Atlanta Cook, Ben Blencowe, Markus Bohnsack, and Yue Wan for their hard work in making this an amazing meeting.

Sandy

Sandra Wolin President, RNA Society

The RNA Society

Officers of the RNA Society FY 2024

President (2023-2024)

Sandra L. Wolin National Cancer Institute - NIH, USA

Past President (2021–2022) Maria Carmo-Fonseca Univ of Lisbon, Portugal

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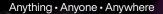
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Kristin Koutmou Univ of Michigan, USA

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Special thanks to Moderna, sponsor of the RNA Society Poster Presentation Prizes

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Cover image and image on page 5: "Edinburgh City Skyline" by Eddscape (132A North High Street, Musselburgh EH21 6AS, Scotland).

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Using metabolic RNA labelling and SLAMseq to track mobile extracellular RNA

Join Lexogen's Morning Session at the #RNA2024

🛗 May 29, 2024

• 7.45 am

Lomond Suite at EICC

Small treats with coffee are provided!



LEXOGEN

The RNA Experts

GENERAL MEETING GUIDELINES

All those partaking in RNA 2024 sessions, events and activities must be a registered meeting participant. Meeting badges must be warn by RNA 2024 attendees at all times.

Citation of abstracts presented during RNA 2024 (in bibliographies or other) is <u>strictly prohibited</u>. 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 hash tag of the 29th Annual Meeting of the RNA Society is **#RNA24.** Meeting participants are encouraged to share the amazing science they experience at RNA 2024 on social media platforms; however,

please respect the following rules when using

the #RNA24 hash tag on XTwitter, 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 <u>under any circumstance</u>.
- 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."



Abstracts can be found in the digital meeting program online. Login to **Oxford Abstracts** with the email address and password used when registering for the meeting.

Exhibitors

















NATIONAL ACADEMIES Sciences Engineering Medicine



PROGRAM SCHEDULE

TUESDAY, MAY 28

- 13:00 20:30 **Registration** Lennox Lobby
- 17:00 19:00 **Opening Session** Welcome Keynote 1: Jernej Ule, King's College London and Francis Crick Institute, United Kingdom Keynote 2: Narry Kim, Center for RNA Research, Institute for Basic Science, Seoul National University, Korea **Sponsored by BioNtech** *Pentland*
- 19:00 22:30 **Opening Reception** Lennox Lobby, Strathblane, Cromdale, Lammermuir, Conference Square (weather permitting)

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WEDNESDAY, MAY 29

07:45 – 08:45	Sponsored Seminar Breakfast Sponsored by Lexogen, Inc. Lomond Suite (Moorfoot)	
08:00 - 18:30	Registration Lennox Lobby	
09:00 – 10:30	Plenary Session 1: RNA Modification & Ed Sponsored by Oxford Nanopore Technolo Pentland Chair: Denis Lafontaine, U. Brussels - Belgiu	ogies
10:30 – 11:10	Coffee Break Lennox 2 & 3/Level -2, Strathblane Hall/Leve	el O
11:10 – 12:40	Plenary Session 2: Diseases and Therape Sponsored by BioNTech Chair: Polly Lei Lei Chen, National University Pentland	
12:40 - 14:00	Lunch Cromdale and Lammermuir/Level -2, Strathl	blane Hall/Level 0

WEDNESDAY, MAY 29 (continued)

- 12:40 14:00 Meetings Committee Lunch/Meeting Ochil
- 12:50 13:50 Sponsored Seminar Lunch Sponsored by BioNTech Lomond Suite (Moorfoot)



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14:00 – 15:30 Concurrent Session 1: New Technologies Sponsored by RNAConnect Chair: Evelina Tutucci, Vrije Universiteit Amsterdam Pentland

> Concurrent Session 2: Ribosome Synthesis Chair: Marlene Oeffinger, Montreal Clinical Research Institute Lennox 1

Concurrent Session 3: Transport and Localization Chair: Eric Lécuyer, IRCM Lomond Suite (Moorfoot)

- 15:30 16:10 **Coffee Break, sponsored by Pfizer** Lennox 2 & 3/Level -2, Strathblane Hall/Level 0
- 16:10 17:50 **Concurrent Session 4: Innate Immunity** Chair: Mary O'Connell, CEITEC Masaryk University *Pentland*

Concurrent Session 5: Cotranscriptional Events Chair: Xiaohua Shen, Tsinghua Unviersity Lomond Suite (Moorfoot)

Concurrent Session 6: circRNA and mitRNA Sponsored by Sanofi

Chair: Štěpánka Vaňáčová, Masaryk University, CEITEC Lennox 1

- 18:00 20:00 Mentoring Dinner Organizer: Nancy Greenbaum, Hunter College, CUNY Cromdale and Lammermuir/Level -2
- 18:00 20:00 Dinner (for all non-Mentoring Dinner attendees) Strathblane Hall/Level 0 / Lammermuir/Level -2
- 20:00 22:00 **Poster Session 1** Lennox 2 & 3

THURSDAY, MAY 30



- 07:45 08:45 Sponsored Seminar Breakfast Sponsored by Oxford Nanopore Technologies Lomond Suite (Moorfoot)
- 08:00 17:00 **Registration** Lennox Lobby
- 09:00 10:30 Plenary Session 3: Interconnected Gene Expression Processes Chair: Marina Rodnina, Max Planck Institute for Multidisciplinary Sciences Pentland
- 10:30 11:10 **Coffee Break** Lennox 2 & 3/Level -2, Strathblane Hall/Level 0
- 11:10 12:40 Concurrent Session 7: Translation Mechanisms Sponsored by Immagina Chair: Brian Zid, UC San Diego Pentland

Concurrent Session 8: RNA Degradation Sponsored by Lexogen Chair: Sutapa Chakrabarti, Freie Universität Berlin Lomond Suite (Moorfoot)

Concurrent Session 9: RNA Structure and Modeling, Sponsored by BioNTech

Chair: Qiangfeng Cliff Zhang, Tsinghua University Lennox 1

- 12:40 14:00 Lunch Cromdale and Lammermuir/Level -2, Strathblane Hall/Level 0
- 12:50 13:50 Sponsored Seminar Lunch Sponsored by Immagina Lomond Suite (Moorfoot)



- 14:00 16:00 **Poster Session 2** *Lennox 2 & 3*
- 16:00 17:00 Junior Scientists Social Platform 5

16:00 Free evening

FRIDAY, MAY 31

07:45 – 08:45 Sponsored Seminar Breakfast Sponsored by Sanofi Lomond Suite (Moorfoot)

sanofi

- 08:00 18:30 **Registration** Lennox Lobby
- 09:00 10:30 Plenary Session 4: RNP Assembly Sponsored by BioNTech Chair: Sebastian Klinge, Rockefeller University Pentland
- 10:30 11:10 **Coffee Break** Lennox 2 & 3/Level -2, Strathblane Hall/Level 0
- 11:10 12:40 Concurrent Session 10: Poly(A) and tRNA Processing Sponsored by Oxford Nanopore Technologies Chair: Michaela Müller-McNicoll, Goethe University Frankfurt/ Max-Planck-Institute for Biophysics Lomond Suite (Moorfoot)
 - **Concurrent Session 11: Bacterial and Viral RNAs** Chair: Sander Granneman, University of Edinburgh *Lennox 1*

Junior Scientists Career Panel: Weighing your Career Options: BigPharma versus StartUp and University versus Research Institute Organized by the RNA Society Junior Scientist Group Pentland

- 12:40 14:00 Lunch Cromdale and Lammermuir/Level -2, Strathblane Hall/Level 0
- 12:45 13:45 Sponsored Seminar Lunch Sponsored by RNAConnect Lomond Suite (Moorfoot)



- 14:00 15:00 **Plenary Session 5: RNA-protein Interactions** Chair: Henning Urlaub, MPI Multidisciplinary Sciences *Pentland*
- 15:00 16:00 DEI Panel: Creating and Preserving a Welcoming Environment Organized by the RNA Society DEI Committee Pentland

16:00 - 16:40

Coffee Break Sponsored by Pfizer Lennox 2 & 3/Level -2, Strathblane Hall/Level 0

16:40 - 18:30

Concurrent Session 12: Splicing Mechanisms

Chair: Sebastian Fica, The University of Oxford Lomond Suite (Moorfoot)

Concurrent Session 13: Bioinformatics, Transcriptomics and Genomics Sponsored by Oxford Nanopore Technologies Chair: Xinshu (Grace) Xiao, University of California, Los Angeles Lennox 1

Concurrent Session 14: Modification and Editing 2 Chair: Tom Suzuki, University of Tokyo Pentland

- 18:30 20:00 **Dinner** Cromdale and Lammermuir/Level -2, Strathblane Hall/Level 0
- 18:30 20:00 Board of Directors Dinner/Meeting Ochil
- 20:00 22:00 Poster Session 3 Sponsored by BioNTech Lennox 2 & 3

SATURDAY, JUNE 1

- 08:30 18:00 **Registration** Lennox Lobby
- 09:00 10:30 Plenary Session 7: RNP Condensates Chair: Karsten Weis, ETH Zurich Pentland
- 10:30 11:10 **Coffee Break** *Cromdale/Level -2, Strathblane Hall/Level 0*
- 11:10 12:40 Plenary Session 8: Translation Regulation Sponsored by BioNTech Chair: Fátima Gebauer, Center for Genomic Regulation -CRG Pentland
- 12:40 14:00 Lunch Cromdale and Lammermuir/Level -2, Strathblane Hall/Level 0

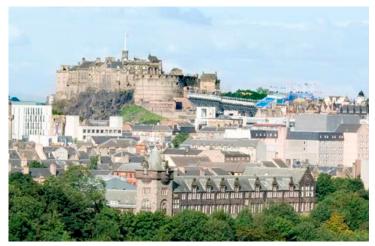
SATURDAY, JUNE 1 (continued)

14:00 – 15:30	Plenary Session 9: Splicing Regulation Chair: Kristen Lynch, University of Pennsylvania Pentland
15:30 - 16:00	Coffee Break Sponsored by Pfizer Cromdale/Level -2, Strathblane Hall/Level 0
16:00 – 17:00	Closing Session Keynote 3: Reinhard Lührmann, Max Planck Institute for Multidisciplinary Sciences Chair: David Tollervey, Edinburgh University Sponsored by BioNTech Pentland
17:00 – 18:00	Awards Ceremony and Closing Remarks Pentland
19:00 - 23:30	Closing Dinner/Dance

Join fellow scientists for the 2024 Scottish Stroll Dinner and Ceilidh Dance! National Museum of Scotland

SUNDAY, JUNE 2

Conference concludes



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View of Edinburgh's castle



INVITATION TO MEMBERSHIP

The RNA Society gathers worldwide experts in all things RNA. Since 1993, 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, IncRNA, 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 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 A DO LAND

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.





Visit the **RNA** journal booth to view a copy of the May Special Issue on mRNA modifications.

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

presentation Wednesday morning

2024 RNA SOCIETY AWARD WINNERS

THE RNA SOCIETY LIFETIME ACHIEVEMENT IN SCIENCE AWARD



Jennifer Doudna

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) and Marlene Belfort (2023).

Congratulations to Jennifer Doudna, the Li Ka Shing Chancellor's Chair and a Professor in the Departments of Chemistry and of Molecular and Cell Biology at the University of California, Berkeley. She is an HHMI Investigator, the Founder, President & Chair of the Innovative Genomics Institute at UC Berkeley and UCSF, and a senior investigator at the Gladstone Institute. She is an elected member of the National Academy of Sciences, the National Academy of Medicine, and the National Academy of Inventors, of the Academy of Arts and Sciences, AAAS, a foreign member of the Royal Society, and a member of the Pontifical Academy of Science, and a Fellow of the American Association for Cancer Research, and the American Society for Microbiology. She holds honorary doctorates from 11 colleges and universities, including her alma maters of Pomona College and Harvard University. She is a 2020 laureate of the Nobel Prize in Chemistry.

THE RNA SOCIETY LIFETIME ACHIEVEMENT IN SERVICE AWARD

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



Ute Kothe

(2022), and Benoît Chabot (2023).

Congratulations to **Ute Kothe**, Professor at the University of Manitoba, Canada, Head of the Department of Chemistry, and the incoming Dean of the Division of Extended Education. Kothe and her lab are world leaders in identifying the molecular and structural features that allow different types of RNAs to fulfill diverse functions. Kothe has been elected into the College of the Royal Society in Canada, received a RiboClub Blue Jacket award, and was awarded the Canadian Society for Molecular Biosciences (CSMB) Jeanne Manery Fisher Memorial Lecture.

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

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), and Amanda Hargrove (2023).



at ETH Zurich, Switzerland, since 2017. She investigates RNA cleaving and degrading machineries involved in gene regulation and RNA processing. Jonas is active in the RNA community in Switzerland and has been recognized by the University of Berne for her efforts to ensure equal opportunity for women in research.

Congratulations to **Stefanie Jonas,** an Assistant Professor in the Institute of Molecular Biology and Biophysics

Stefanie Jonas





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**.

THE RNA SOCIETY MID-CAREER AWARD

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), and Nicholas Ingolia (2023).



Chase Beisel

Congratulations to **Chase Beisel**, Professor in the Helmholtz Institute for RNA-based Infection Research and the Julius Maximilians University of Würzburg. Beisel has applied his combined training in RNA biology and engineering to CRISPR-Cas bacterial immune systems. His group has worked to elucidate the functional diversity of these versatile immune systems while translating insights into new and improved technologies spanning genome editing and molecular recording to tailored-spectrum antimicrobials and molecular diagnostics. Beisel has co-founded the start-up companies, Locus Biosciences and Leopard Biosciences.

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), and Jinwei Zhang (2023).



Chun Kit Kwok

Congratulations to **Chun Kit Kwok,** Associate Professor in the Department of Chemistry and State Key Laboratory of Marine Pollution at City University of Hong Kong. Kwok investigates the function and binding partners of rG4s in coding and non-coding genes and explores structural adaptations of RNA in response to environmental cues in animals and plants. Kwok has been a member of the RNA Society since 2012, co-chaired the RNA Structure and Folding session of the RNA Society meetings in 2021 and 2023 and initiated the Hong Kong RNA Club (an RNA Society-sponsored RNA Salon site).



Cell Research

Cell Discovery

2022 Impact Factor 44.1 (Clarivate Analytics, 2023)



Editor Emeritus: Gang Pei Editor-in-Chief: Dangsheng Li

Published in association with Center for Excellence in Molecular Cell Science, Chinese Academy of Sciences and the Chinese Society for Cell Biology

Cell Research is a premium international life science journal with a broad scope in basic molecular and cell biology. The journal publishes original research results that are of unusual significance or broad conceptual or technical advances in all areas of life sciences, as well as authoritative reviews and sharply focused research highlights.

www.nature.com/cr

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Cell Discovery is an open access international journal that publishes results of high significance and broad interest in all areas of molecular and cell biology. The basic bar of acceptance is comparable to the major sister journals of Cell/Nature/Science. It is established in 2015 as a sister journal of Cell Research.

www.nature.com/celldisc

2022 Impact Factor 33. Clarivate Analytics, 2023

Cell Discovery





Engineered poly(A)-surrogates for translational regulation and therapeutic biocomputation in mammalian cells Cell Research (2024) 34:31-46; https://doi.org/10.1038/s41422-023-00896-y



Hypoxia induces mitochondrial protein lactylation to limit oxidative phosphorylation

Featured Papers



Cell Research (2024) 34:13-30: https://doi.org/10.1038/s41422-023-00864-6

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Structural basis of nucleosome deacetylation and DNA linker tightening by Rpd3S histone deacetylase complex Cell Research (2023) 33:790-801; https://doi.org/10.1038/s41422-023-00869-1



Lin28a maintains a subset of adult muscle stem cells in an embryonic-like state Cell Research (2023) 33:712-726; https://doi.org/10.1038/s41422-023-00818-v

Cathepsin B S-nitrosylation promotes ADAR1-mediated editing of its own mRNA transcript via an ADD1/MATR3 regulatory axis Cell Research (2023) 33:546-561. https://doi.org/10.1038/s41422-023-00812-4

SPRINGER NATURE

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 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) and Wendy Gilbert (2023).



Shobha Vasudevan

Congratulations to **Shobha Vasudevan**, Associate Professor at Massachusetts General Hospital, Harvard Medical School, in Boston, USA, where she investigates post-transcriptional regulation of gene expression in quiescent cancer cells. Vasudevan has been a vocal advocate for increasing diversity, equity, inclusion, and accessibility at Harvard. Vasudevan has served as the inaugural chair of the RNA Society Diversity, Equity and Inclusion Committee since 2021 and in this role has spearheaded efforts to enhance resources on the RNA Society website, organize DEI panel discussions at our annual meeting, expand RNA Society global access, and increase the visibility of the RNA Society to undergraduate students interested in RNA research.

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) and Sara Olson (2023).

Congratulations to **Jason Stagno,** Senior Associate Scientist in the lab of Dr. Yun-Xing Wang at the National Cancer Institute, Center for Cancer Research, in Frederick, Maryland, USA. Stagno is an expert in elucidating the structure of RNA and the proteins that bind



it, and has been an author on over 30 publications including lead author on a seminal study capturing the adenine riboswitch bound by its ligands. While Stagno has been a central member of the Wang lab since 2014 and a member of the RNA Society since 2015, his long career as an RNA scientist date back to his doctoral studies in the lab of Hartmut Luecke at the University of California, Irvine, where he worked in collaboration with Ruslan Aphasizhev on the role of TUTases in RNA editing.

Jason Stagno

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) and Sezen Meydan (2023).



Mariela Cortés López

Congratulations to **Mariela Cortés López**, a postdoctoral researcher in the laboratory of Dan-Avi Landau at the Weill Cornell Medical College in New York, USA. Cortés López started her research career at the Universidad Nacional Autónoma de México. She was a graduate student at the Institute of Molecular Biology in Mainz, Germany, under the mentorship of Julian König. In her current work, Cortés López is applying single cell, long-read sequencing to genotype myelodysplastic syndrome patient cells for mutations in key splicing factors, simultaneously identifying the effects of these mutations on pre-mRNA splicing events.

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) and Doug Turner (2023).



Phillip D. Zamore

Congratulations to **Phillip D. Zamore,** chair of the RNA Therapeutics Institute at University of Massachusetts Chan Medical School, Worcester, MA and a Howard Hughes Medical Institute Investigator. Zamore's research focuses on small RNA silencing pathways and has resulted in more than 170 publications and fundamental insights into the biology of small RNAs. He has mentored over 50 postdoctoral research associates and graduate students, many of whom have continued on to their own successful careers running their academic labs as well as at biotech companies. His mentoring extends to his participation in the Student National Medical Association Mentorship Program and his impact is reflected in a Broadening Experiences in Scientific Training (BEST) grant from the National Insti-

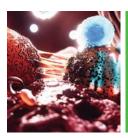
tutes of Health (USA) and the Dean's Award for Research Mentoring and Commitment to Student Professional Development (U Mass).

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



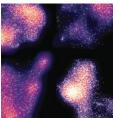
2005, the RNA Society/Scaringe Award was given to the student author(s) of the best paper published during the previous year in *RNA* the official journal of the RNA Society, as selected by the Editors. The winners of the 2004 and 2005 awards were Stefano Marzi and Ramesh Pillai, respectively. In 2006, 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.



AACR American Association for Cancer Research 2024 SCIENTIFIC CONFERENCES

Presenting the most significant research on cancer etiology, prevention, diagnosis, and treatment









Bladder Cancer: Transforming the Field May 17-20, 2024 | Charlotte, NC

Conference Cochairs: Lars Dyrskøjt Andersen, Donna E. Hansel, Dan Theodorescu, and Tahlita C. M. Zuiverloon

Expanding and Translating Cancer Synthetic Vulnerabilities June 10-13, 2024 | Montreal, Quebec, Canada

Conference Cochairs: Kimberly Stegmaier, E. Alejandro Sweet-Cordero, Michael Erb, and Kris C. Wood

Fourth AACR International Meeting Advances in Malignant Lymphoma:

Maximizing the Basic-Translational Interface for Clinical Application In Cooperation with the International Conference on Malignant Lymphoma (CML) In Association with *Blood Cancer Discovery* June 19 - 22, 2024 | Philadelphia, PA Conference Cochairs: Francesco Bertoni*, Christopher R. Flowers, Ari, M. Melnick, Laura Pasqualucci, and Margaret A. Shipp "International Conference on Malignant Lymphoma (CML) Representative

Advances in Pediatric Cancer Research In Collaboration with the AACR Pediatric Cancer Working Group (PCWG)

September 5-8, 2024 | Toronto, ON, Canada Conference Cochairs: Alejandro Gutierrez, Cynthia E. Hawkins, Andrea A. Hayes, and Gilles Vassal

Pancreatic Cancer September 15-18, 2024 | Boston, MA Conference Cochairs: Peter J. Allen, Stephanie K.

Dougan, Michael A. (Tony) Hollingsworth, and Alec C. Kimmleman

Learn more and register a AACR.org/Calendar 17th AACR Conference on the Science of Cancer Health Disparities in Racial/Ethnic Minorities and the Medically Underserved In Association with the AACR Minorities in Cancer Research Council

September 21 - 24, 2024 | Los Angeles, CA Conference Cochairs: Moon S. Chen, Melissa B. Davis, Carmen E. Guerra, Ruben A. Mesa, Jasmine Plummer and Susan M. Shinagawa

Tumor Immunology and Immunotherapy In Association with the AACR Cancer Immunology Working Group (CIMM)

October 18-21, 2024 | Boston, MA Conference Cochairs: Yvonne Y. Chen, Sergio Quezeda, Robert D. Schreiber, and Fernando Vidal-Vanaclocha

EORTC-NCI-AACR Symposium on Molecular Targets and Cancer Therapeutics

October 23–25, 2024 | Barcelona, Spain Conference Cochairs: E.G. Elisabeth de Vries, Tim F. Greten, and Timothy A. Yap

Liquid Biopsy: From Discovery to Clinical Implementation

November 13-16, 2024 | San Diego, CA Conference Cochairs: Catherine Alix-Panabières, Luis A. Diaz, Jr., Maximilian Diehn, Y.M. Dennis Lo, and Klaus Pantel

RNAs as Drivers, Targets, and Therapeutics in Cancer November 14-17, 2024 | Bellevue, WA

Conference Cochairs: Howard Y. Chang, Joshua T. Mendell, Anastasia Khvorova, and V. Narry Kim

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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), and Jonas Tholen (2023).



Jennifer Porat



Arnaud Vanden Broeck

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) and Charles Bou-Nader (2023).

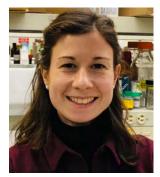
Congratulations to the winners of the 2024 RNA Society/ Scaringe Young Scientist Awards: Graduate Student **Jennifer Porat,** in the lab of Mark Bayfield at York University in Toronto, Ontario, Canada, for work on eukaryotic RNA modification enzymes Trm1 and Bmc1, and Postdoctoral Fellow **Arnaud Vanden Broeck,** in the lab of Sebastian Klinge at The Rockefeller University in New York, USA, for his work toward understanding how both the small (40S) and large (60S) subunits of the human ribosome get assembled and how these are coordinated with maturation of the ribosomal RNA.

THE ECLIPSE AWARD FOR INNOVATION ECLIPSEBIO

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 award-ed 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



Morghan Lucas



Giulia Biancon

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).

Congratulations to the winners of the 2024 Eclipse Award for Innovation in High-Throughput Biology: Graduate Student **Morghan Lucas** from the Novoa laboratory at the Centre for Genomic Regulation in Barcelona, Spain, for using direct RNA nanopore sequencing (DRS) for the simultaneous determination of RNA base identity and the presence of base modifications to help uncover the true diversity of the RNA epitranscriptome, and **Giulia Biancon**, a member of the Halene lab at Yale University, New Haven, USA, for her use of eCLIP to study the binding of mutant RNA splicing factor U2AF identified in a number of blood cancers.

THE RNA SOCIETY MODERNA AWARD FOR BIOMEDICAL INNOVATION IN RNA

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.



Raman Bahal

Congratulations to the inaugural recipient of this award, **Raman Bahal,** Associate Professor in the Department of Pharmaceutical Sciences at the University of Connecticut, USA. Bahal develops next-generation synthetic nucleic acids and delivery methods to target DNA and RNA for genomic engineering and to modulate RNA expression and/or function in cancer cells and for the treatment of metabolic disorders. Bahal's independent research has resulted in several patents and ~50 publications. GENE TOOLS, LLC www.gene-tools.com

O=P-N

A Morpholino oligo works like sequence-specific masking tape, blocking a section of RNA.

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ORAL PRESENTATIONS LISTING

Keynote 1: Jernej Ule

Tuesday, May 28, 17:20–18:10, Pentland

Session Chair: Ben Blencowe

K-1 RNA multivalency enables homeostatic co-regulation of LCD-containing proteins Rupert Faraway, Neve Costello Heaven, Holly Digby, Oscar Wilkins, Charlotte Capitanchik, Urška Janjoš, Klara Kuret, Jure Rebselj, Rhys Dore, Ira Iosub, <u>Jernej Ule</u>

Keynote 2: Narry Kim

Tuesday, May 28, 18:10-19:00, Pentland

Session Chair: Yue Wan

K-2 Viral and cellular strategies for RNA stability control Narry Kim

Plenary 1: Modification and Editing 1

Wednesday, May 29, 9:00-10:30, Pentland

Session Chair: Denis Lafontaine

T-1 Targeted pseudouridylation identifies a novel Ψ - Ψ codon-anticodon pairing in nonsense suppression and translational recoding $\underline{Yi$ Pan, Yi-Tao Yu

T-2 SNORA81-guided ribosomal RNA pseudouridylation modulates the translation of a specific subset of cancer-associated genes

Laurence Faucher-Giguère. Gabrielle Deschamps-Francoeur, Etienne Fafard-Couture, Taha Azad, Michelle Scott, Sherif Abou Elela

T-3 A single molecule detection of tRNA modifications by signal alignment of nanopore sequencing data

<u>Ryo Noguchi</u>, Qiuyu Wang, Yosei Hanzawa, Takayuki Ohira, Bhaskar Dasgupta, Hiroki Ueda, Tsutomu Suzuki

T-4 m6A sites in the coding region trigger translation-dependent mRNA decay You Zhou, Miona Ćorović, Peter Hoch-Kraft, Mikhail Mesitov, Anke Busch, Christoph Dieterich, Martin Hengesbach, <u>Kathi Zarnack</u>, Julian König

T-5 Metabolic regulation of modified RNA in physiology and pathology Akiko Ogawa, Satoshi Watanabe, Kenji Inaba, Fan-Yan Wei

T-6 Molecular basis for capping of bacterial RNAs by Np4N alarmones and removal of the Np4 caps

Ashok Nuthanakanti, Wenqian Duan, Abhishek Kaushik, Rose Levenson-Palmer, Nikita Vasilyev, Maria Ariza Mateos, Evgeny Nudler, Joel Belasco, <u>Alexander Serganov</u>

Plenary 2: Diseases and Therapeutics

Wednesday, May 29, 11:10-12:25, Pentland

Session Chair: Polly Lei Lei Chen

T-8 The functional diversity and application potential of CRISPR-Cas12a2 systems Chase Beisel

T-9 Measuring the functional impact of 5'UTR variants in human disease. <u>Srikar Krishna Gopinath,</u> Ethan Strayer, Wilder Wohns, Haejeong Lee, Tami Gjorgjeiva, Jonathan Pritchard, Monkol Lek, Antonio Giraldez

T-10 Molecular mechanisms of the ZFP36-family RNA binding proteins in T lymphocytes Martin Turner

T-11 Genome-wide screen identifies cellular factors regulating exogenous mRNAs Myeonghwan Kim, Youngjoon Pyo, Yeon Choi, V. Narry Kim

T-7 Novel technologies to target RNA G-quadruplexes (rG4s) and control rG4mediated gene expression Chun Kit Kwok

Concurrent 1: New Technologies

Wednesday, May 29, 14:00-15:30, Pentland

Session Chair: Evelina Tutucci

T-12 Selection of enzyme inhibiting aptamers by ultrahigh-throughput microfluidic screening

Claire Husser, Janis Hötzel, Roger Cubi, Beatrix Suess, Michael Ryckelynck

T-13 Integrated analysis of tRNA sequence, modification, and charging by nanopore sequencing

Laura White, Aleksandar Radakovic, Marcin Sajek, Kezia Dobson, Kent Riemondy, Jack Szostak, Jay Hesselberth

T-14 Thioadenosine tRNAs as more reactive acyl carriers in ribosomal translation Alexandra Kent, Jacob Robins, Isaac Knudson, Jessica Vance, Alanna Schepartz, Scott Miller, Jamie Cate l

T-15 REAP-seq enables pooled CRISPR screening of RNA binding protein regulators Rui Zhang

T-16 INSCRIBE: High-sensitivity in situ capture of endogenous RNA-protein interactions in fixed cells and primary tissues

<u>Qishan Liang</u>, Tao Yu, Eric Kofman, Pratibha Jagannatha, Kevin Rhine, Brian Yee, Kevin Corbett, Gene Yeo

T-17 Full droplet characterization of RNA/protein condensates by diffusion NMR Mihailo Novakovic, Nina Han, Yinan Ni, Leonidas Emmanouilidis, Frederic Allain

Concurrent 2: Ribosome Synthesis

Wednesday, May 29, 14:00-15:30, Lennox 1

Session Chair: Marlene Oeffinger

T-18 IGS38s ncRNA from human rDNA spacer regulates 45s rRNA transcription and rDNA chromatin organization

Kanwal Tariq, Jaclyn Quin, Stefanie Böhm, Signe Skog, Neus Visa, Anita Öst, Ann-Kristin Östlund Farrants

T-19 Formation of the dense fibrillar component of the nucleolus and condensateaided ribosomal RNA modification

Koceila Meznad, Manisha Deogharia, Ludivine Wacheul, Christiane Zorbas, Denis L.J. Lafontaine, <u>U. Thomas Meier</u>

T-20 Uncovering the architecture and function of the human rixosome complex in ribosome synthesis

Jacob Gordon, Alan Warren, Robin Stanley

T-21 SURF2 is a MDM2 antagonist in triggering the p53 dependent nucleolar stress response

Sophie Tagnères, Paulo Espirito Santo, Julie Radermecker, Dana Rinaldi, Carine Froment, Manon Bongers, Quentin Provost, Solemne Capeille, Nick Watkins, Julien Marcoux, Pierre-Gleizes, Virginie Marcel, Célia Plisson-Chastang, <u>Simon Lebaron</u>

T-22 Removal of Rps26 from small ribosomal subunits during salt stress leads to metabolic reprogramming in *Saccharomyces cerevisiae*

Fiona Fitzgerald, Mindi Klaus, Katrin Karbstein

T-23 Compositionally distinct 5.8S-L rRNA ribosomes function in translation of differential mRNAs in S. cerevisiae

Christian Trahan, Amal Seffouh, Ludivine Wacheul, Malik Chaker-Margot, Denis Lafontaine, Joaquin Ortega, <u>Marlene Oeffinger</u>

Concurrent 3: Transport and Localization

Wednesday, May 29, 14:00–15:30, Lomond Suite (Moorfoot)

Session Chair: Eric Lecuyer

T-24 Mapping RNA-protein interactions with subcellular resolution using colocalization CLIP

Soon Yi, Sashi Singh, Kathryn Rozen-Gagnon, Joseph Luna

T-25 Identification of the sequence elements and protein factors dictating RNA localization to the mitochondria Furgan Fazal

T-26 mRNA translation in proximity to forming autophagosomes promotes sustained autophagy

Yunping Xue, Nicholas Valentino, Derrick Gibbings

T-27 Molecular mechanisms and functions of RNA nuclear detention Kai Wu, Guangnan Li, Peng Tang, Yunfan Luo, <u>Yu Zhou</u>

T-28 Conditional mitochondrial mRNA Localization: Connecting mitochondrial composition to growth and metabolism

Yuko Sugiyama, Ximena Garcia Arceo, Tatsuhisa Tsuboi, Brian Zid

T-29 Fluorescent nucleoside analogues from single-molecule applications to live cell imaging of RNA

<u>Byron Purse</u>

Concurrent 4: Innate Immunity

Wednesday, May 29, 16:10-17:50, Pentland

Session Chair: Mary O'Connell

T-30 A novel Pol III dependent dual activity tRNA gene can activate the cellular innate immune system by a pathway that is suppressible by the SSB/La protein Alan Kessler, Sandy Mattijssen, Jack Prochnau, Sergei Gaidamakov, James Iben, Gennady Margolin, Ryan Dale, Markus Hafner, Rich Maraia

T-31 LGP2 Controls MDA5 Translocation on dsRNA to Activate Antiviral Signalling Xiao-Peng Han, Jun Cheng, Qiong Wu, Shu-Rui Wu, <u>Jiaquan Liu</u>

T-32 MDA5 proofreads viral dsRNA via a dynamic ATP-dependent overtwisting mechanism

<u>Salina Quack.</u> Pim America, Misha Klein, Alba Herrero del Valle, Rahul Singh, Quinte Smitskamp, Flavia Stal Papini, Chase Broedersz, Yorgo Modis, David Dulin

T-33 dsRNA recognition drives interferon silencing during early embryonic development

Jeroen Witteveldt, Hendrik Marks, Alasdair Ivens, Sara Macias

T-34 Aberrant accumulation of mitochondrial double-stranded RNAs activates PKR and potentiates proinflammatory functions of monocytes in Childhood Sjögren's Disease

Jimin Yoon, Daesong Jang, Myung-Chul Kim, Joon Paek, Rehae Miller, Rudy Alvarado, Yoosik Kim, Seunghee Cha

T-35 RNase L-induced antiviral condensates sequester subgenomic Flavivirus RNAs and re-establish host RNA decay

Monty Watkins, James Burke

T-36 mRNA deadenylation machinery selectively targets interferon mRNAs to regulate antiviral immunity

<u>Rachel Braun</u>, Max Ferretti, Jesse Miller, Jae Seung Lee, Lauren Castellana, Kanupriya Whig, Lenka Dohnalová, Hélène Descamps, Alex Huber, Peter Hewins, Mark Dittmar, Zienab Etwebi, Thomasina Cook, David Schultz, Perry Blackshear, Kellie Jurado, Christoph Thaiss, Kristen Lynch, Sara Cherry

Concurrent 5: Cotranscriptional Events

Wednesday, May 29, 16:10–17:50, Lomond Suite (Moorfoot)

Session Chair: Xiaohua Shen

T-37 Mechanisms and consequences of RNA duplex formation within the exit channel of RNA polymerase

Junqiao Zhu, Michael Palo, Robert Landick, Aaron Hoskins

T-38 Deep mutational scanning of hepatitis B virus unveils ribosome stalling as the underlying mechanism for cis-preferential binding of the viral polymerase to its genomic RNA transcript

Yingpu Yu, Maximilian Kass, Mengyin Zhang, Noor Youssef, Catherine Freije, Kelly Brock, Lauren Aguado, Leon Seifert, Sanjana Venkittu, Xupeng Hong, Amir Shlomai, Ype de Jong, Debora Marks, Charles Rice, <u>William Schneider</u>

T-39 EIF4A3-mediated transcriptional surveillance safeguards accurate elongation Yantao Hong, Guanwen Li, Xiaohua Shen

T-40 Co-transcriptional structure tracking detects dynamic base pairing of nascent RNA *in vivo*

Leonard Schärfen, Isaac W. Vock, Mathew D. Simon, Karla M. Neugebauer

T-41 Promoter-proximal convergent antisense transcripts (PCATs): a new player in the transcriptional activation of protein coding genes

<u>Rui Sousa-Luís,</u> Marta Furtado*, Pedro Prudêncio*, Sue Mei Tan-Wong*, Inna Zucher*, Rosina Savisaar, Noélia Custódio, Sandra Martins, Gwendal Dujardin, Nick Proudfoot, Maria Carmo-Fonseca

T-42 Mechanisms of transcription attenuation and condensation of RNA polymerase II by RECQ5 helicase

Marek Sebesta, Karel Skubnik, William Morton, Marek Kravec, Katerina Linhartova, Veronika Klapstova, Jiri Novacek, Karel Kubicek, Vitezstav Bryja, Robert Vacha, <u>Richard Stefl</u>

T-43 Mapping of actively transcribing human RNA polymerase III reveals new regulatory elements in tRNA transcription

Jan Mikołajczyk, Tomasz Turowski

Concurrent 6: circRNA and mitRNA

Wednesday, May 29, 16:10-17:50, Lennox 1

Session Chair: Štěpánka Vaňáčová

T-44 An endogenous cluster of target-directed miRNA degradation sites induces decay of distinct miRNA families

<u>Nicholas Hiers.</u> Lu Li, Tianqi Li, Peike Sheng, Conner Traugot, Yuzhi Wang, Michael Yao, Mingyi Xie

T-45 RNA structural determinants of Alu-mediated backsplicing

Justin Waldern, Catherine Gianetti, Kevin Weeks, Alain Laederach

T-46 Systematic study of RNA binding proteins that enhance circular RNA translation Qianyun Lu, Siqi Wang, <u>Yanwen Ye</u>, Yun Yang, Zefeng Wang

T-47 Cross-kingdom RNAi in the fungal-tomato interaction

An-Po Cheng, Lorenz Oberkofler, Florian Dunker, Nathan Johnson, Arne Weiberg

T-48 RNA splicing factor mutations drive widespread aberrant canonical and cryptic circular RNA biogenesis in leukemia

<u>Mike Fernandez.</u> Meiling Jin, Qiong Jia, Yiming Wu, Kevyn Hart, Emilee Bargoma, Joseph Pangallo, Robert Bradley, Omar Abdel-Wahab, Zhenyu Jia, Ren-Jang Lin, Lili Wang

T-49 Neurodevelopmental disorder-relevant Argonaute1 mutant narrows the RNA-binding channel and lets 3' \rightarrow 5' exonucleases convert miRNAs to unusually short tinyRNAs

<u>Andrew Savidge.</u> Huaqun Zhang, Cameron Divoky, Audrey Kehling, Jackson Secor, Kotaro Nakanishi

T-50 Exploring the small RNA epitranscriptome using direct RNA sequencing

Morghan Lucas, Anya Fefilova, Anna Delgado-Tejedor, Leszek Pryszcz, Ivan Milenkovic, Alexane Ollivier, Eva Maria Novoa

Plenary 3: Interconnected Gene Expression Processes

Thursday, May 30, 9:00-10:30, Pentland

Session Chair: Marina Rodnina

T-51 TRIM28 prevents the export of retrotransposon RNAs via an unproductive interaction with NXF1

Nicole Blümel, Florian Richter, Irena Slišković, Kathi Zarnack, Michaela Müller-McNicoll

T-52 Regulation of the multifunctional RNA helicase DHX15 in different gene expression processes

Indira Memet, Nidhi Kanwal, Nicolai Krogh, Nicolas Lemus-Diaz, Chairini Thomé, Luisa Welp, Athanasia Mizi, Philipp Hackert, Argyris Papantonis, Henning Urlaub, Henrik Nielsen, Markus T. Bohnsack, <u>Katherine E. Bohnsack</u>

T-53 Divergent fates for new and old mRNA following acute changes in gene expression

Mostafa Zedan, Alexandra Schürch, Stephanie Heinrich, Pablo Gomez-Garcia, Sarah Khawaja, Karsten Weis

T-54 Stress adaptive protein synthesis is mediated through spatial-temporal control of CK2 kinase

Shaoni Mukhopadhyay, Amy Lee

T-55 eIF2A regulates cell migration without overtly affecting translation

Jennifer Jungfleisch, Neus Mestre-Farràs, Nadia Halidi, Fátima Gebauer

T-56 mRNA initiation and termination are spatially coordinated

Ezequiel Calvo-Roitberg, Christine Carroll, Sergey Venev, GyeungYun Kim, Steven Mick, Job Dekker, Ana Fiszbein, <u>Athma Pai</u>

Concurrent 7: Translation Mechanisms

Thursday, May 30, 11:10–12:40, Pentland

Session Chair: Brian Zid

T-57 Structural pathway of human translation initiation: from 43S pre-initiation complex assembly to multi-step remodeling of the 48S initiation complex towards subunit joining

Valentyn Petrychenko, Sung-Hui Yi, David Liedtke, Bee-Zen Peng, Marina V Rodnina, Niels Fischer

T-58 Modeling alternative translation initiation sites in plants reveals evolutionarily conserved cis-regulatory codes in eukaryotes

Ting-Ying Wu, Ya-Ru Li, Kai-Jyun Chang, Jhen-Cheng Fang, Daisuke Urano, Ming-Jung Liu

T-59 Delineating the mechanism of repeat-associated non-AUG translation initiation in C9orf72 ALS

<u>Rosslyn Grosely.</u> Christopher Lapointe, Shizuka Yammada, Antonio Puglisi, Michael Palo, Carlos Alvarado, Aaron Gitler, Joseph Puglisi

T-60 Tracking transcription-translation coupling in real-time

Nusrat Qureshi, Olivier Duss

T-61 The RNA helicase HrpA splits collided ribosomes in E. coli

Annabelle Campbell, Hanna Esser, Roland Beckmann, Rachel Green, Allen Buskirk

T-62 Dissecting the translation elongation phase through ultra-long tracking of individual ribosomes

Maximilian Madern*, Sora Yang*, Marvin Tanenbaum

Concurrent 8: RNA Degradation

Thursday, May 30, 11:10-12:40, Lomond Suite (Moorfoot)

Session Chair: Sutapa Chakrabarti

T-63 XRN1-mediated cellular mRNA degradation feeds alphavirus replication

<u>Vincenzo Ruscica</u>, Louisa Iselin, Ryan Hull, Chen Honglin, Samyukta Narajanan, Josmi Joseph, Natasha Palmalux, Azman Embarc-Buh, Zaydah Rolande De Laurent, Joseph Hughes, Connor Hughes, Marko Noerenberg, Wael Kamel, Manuel Garcia-Moreno, Catia Igreja, David Robertson, Shabaz Mohammed, Vicent Pelechano, Ilan Davis, Alfredo Castello

T-64 Yeast elongation factor 3 homolog New1 protects specific mRNAs from no-go decay

Max Müller, Marie-Luise Winz

T-65 Polyamine transport via a PARK9 homolog facilitates ribosome stalling-induced mRNA decay

Chloe Wohlenberg, Parissa Monem, Joshua Arribere

T-66 Deciphering the role of the SMG1:SMG8:SMG9 complex during the first authentication step in NMD

Sabrina Kueckelmann, Volker Boehm, Jan-Wilm Lackmann, Sophie Theunissen, Marek Franitza, Kerstin Becker, Niels H. Gehring

T-67 Structural basis of ribosomal 30S subunit degradation by RNase R

Lyudmila Dimitrova-Paternoga, Sergo Kasvandik, Bertrand Beckert, Sander Granneman, Tanel Tenson, Daniel Wilson, <u>Helge Paternoga</u>

T-68 Quantitative tests of Pumilio-mediated mRNA decay

Gabriel Tauber, Abby Thurm, Scott Grote, Silvi Rouskin, Daniel Herschlag

Concurrent 9: RNA Structure and Modeling

Thursday, May 30, 11:10–12:40, Lennox 1

Session Chair: Qiangfeng Cliff Zhang

T-69 The delicate balance of RNA structure: Tracking secondary structure and topology of viral genomic RNAs through 2 years of SARS-CoV-2 evolution Roland G Huber, Louis DeFalco Jr, Siwy Ling Yang, Yue Wan

T-70 Poly(UG) RNA forms distinct quadruplex structures involved in gene silencing and phase separation

Saeed Roschdi, Craig Bingman, Eric Montemayor, Samuel Butcher

T-71 Discovering regulatory RNA structure in the murine norovirus (MNV) genome Tanja Hann, Han Wan, Madison Strine, Madeleine Mankowski, Arya Ökten, Craig Wilen, Anna Marie Pyle T-72 The three-dimensional structure of an exonuclease-resistant viral RNA reveals common molecular strategies to evade host degradation

Jeanine Gezelle, Jayden McDonald, Sophie Korn, Zhen Gong, Matt Cronin, Wayne A Hendrickson, Brian Wimberly, Anna-Lena Steckelberg

T-73 RNA structure prediction and design with large language model-based deep learning methods

<u>Yu Li</u>

T-74 Developing next-generation synthetic nucleic acid-based RNA therapeutics Raman Bahal

Plenary 4: RNP Assembly

Friday, May 31, 09:00-10:30, Pentland

Session Chair: Sebastian Klinge

T-75 Assembly mechanism of Integrator's RNA cleavage module Kevin Sabath, Chunhong Qiu, <u>Stefanie Jonas</u>

T-76 The fission yeast methylphosphate capping enzyme Bmc1/Bin3 promotes telomerase assembly and U6 2'-O-methylation through catalytic-independent functions Jennifer Porat, Viktor Slat, Moaine El Baidouri, Jorg Grigull, Jean Marc Deragon, Stephen Rader, Mark Bayfield

T-77 Changes in cellular environment modulate EJC composition Elizabeth Abshire, Hana Cho, Lynne Maquat

T-78 Molecular basis of human polyA polymerase recruitment by mPSF Sofia Todesca, Felix Sandmeir, Achim Keidel, Elena Conti

T-79 A molecular switch orchestrates the export of human messenger RNA <u>Ulrich Hohmann</u>, Max Graf, Ulla Schellhaas, Belén Pacheco-Fiallos, Laura Fin, Daria Riabov-Bassat, Thomas Pühringer, Michael-Florian Szalay, László Tirián, Dominik Handler, Julius Brennecke, Clemens Plaschka

T-80 The R2TP chaperone mediates co-translational channeling of quaternary structure formation

Manon Philippe, Soha Salloum, Héloïse Chassé, Serge Urbach, Hugues Parinello, Séverine Boulon, Edouard Bertrand, <u>Céline Verheggen</u>

Concurrent 10: Poly(A) and tRNA Processing

Friday, May 31, 11:10–12:40, Lomond Suite (Moorfoot) Session Chair: Michaela Müller-McNicoll

T-81 Genomic landscape of regulated alternative polyadenylation

Yajing Hao, Xiang-Dong Fu

T-82 A novel pathway of mRNA 3'-end formation independent of cleavage factors

Keaton Barr, Kevin He, Samuel DeMario, Angel Arce Quintor, Camille Killeen, <u>Guillaume Chanfreau</u>

T-83 Polyadenylation of mRNAs encoding secreted proteins by TENT5 family of enzymes is essential for gametogenesis in mice.

<u>Michał Brouze.</u> Agnieszka Czarnocka-Cieciura, Olga Gewartowska, Monika Kusio-Kobiałka, Kamil Jachacy, Marcin Szpila, Bartosz Tarkowski, Jakub Gruchota, Paweł Krawczyk, Seweryn Mroczek, Ewa Borsuk, Andrzej Dziembowski

T-84 Molecular basis of human tRNA 3'-processing

Arjun Bhatta, Bernhard Kuhle, Ryan Yu, Katja Ditter, Hauke Hillen

T-85 Structural and mechanistic insights into activation of the human RNA ligase RTCB by Archease

<u>Janina Lara Gerber,</u> Suria Morales Guzmán, Lorenz Worf, Petra Hubbe, Jürgen Kopp, Jirka Peschek

T-86 Modifications in the T arm of tRNA globally determine tRNA maturation, function and cellular fitness

<u>Sarah Schultz,</u> Christopher Katanski, Mateusz Halucha, Noah Pena, Richard Fahlman, Tao Pan, Ute Kothe

Concurrent 11: Bacterial and Viral RNAs

Friday, May 31, 11:10-12:40, Lennox 1

Session Chair: Sander Granneman

T-87 RNA thermometers are widespread upstream of ABC transporter genes in bacteria

Alina Tong, Samantha Shaffer, Elisha Tong, Michael Hannani, Danna Santiago, Adrian Ferré-D'Amaré, Michael Abdelsayed, Luiz F M Passalacqua

T-88 Nucleobase-mediated general acid catalysis in the MTR1 alkyl transferase ribozyme

<u>Timothy J. Wilson</u>, Lin Huang, Erika McCarthy, Solen Ekesan, Nan-Sheng Li, Joseph Piccirilli, Darrin York, David M. J. Lilley

T-89 Direct testing of twister ribozyme cleavage activity from over a thousand organisms reveals broad tolerance of RNA structural imperfections

Lauren McKinley, McCauley Meyer, Aswathy Sebastian, Ben Chang, Kyle Messina, Istvan Albert, Philip Bevilacqua

T-90 Salmonella sRNAs drive the decision between active stress resistance and persister cell dormancy

Sayema Naaz, Glen Borchert

T-91 Epstein-Barr virus non-coding RNA steers ribosomes into virus-favorable translation

Nara Lee

T-92 Characterization of the molecular factors regulating the interactions between HIV-1 gRNA and Pr55Gag for viral particle assembly

Lisa Welker, Julien Batisse, Florine Santier, Jean-Christophe Paillart, Roland Marquet, Salvatore Chiantia, Marc Ruff, Serena Bernacchi

Plenary 5: RNA-protein Interactions

Friday, May 31, 14:00–15:00, Pentland

Session Chair: Henning Urlaub

T-93 RNA-binding proteins and glycoRNAs form domains on the cell surface for cell-penetrating peptide entry

Jonathan Perr, Andreas Langen, Karim Almahayni, Gianluca Nestola, Peiyuan Chai, Charlotta Lebedenko, Regan Volk, Reese Caldwell, Malte Spiekermann, Helena Hemberger, Namita Bisaria, Konstantinos Tzelepis, Eliezer Calo, Leonhard Möckl, Balyn Zaro, Francisco Sánchez-Rivera, Diego Détres, Ryan Flynn

T-94 The FXR1 network acts as signaling scaffold for actomyosin remodeling

Xiuzhen Chen, Mervin Fansler, Urška Janjoš, Jernej Ule, Christine Mayr

T-95 Molecular basis for nuclear pA+ RNA fate determination

Andrii Bugai, Ulrich Hohmann, Ana Ines de Oliveira Lorenzo, Max Graf, Laura Fin, Laszlo Tirian, Jerome Rouviere, Yuhui Dou, Lis Jakobsen, Jens Skorstengaard Andersen, Julius Brennecke, Clemens Plaschka, Torben Heick Jensen

T-96 Structural and biochemical analyses of an RNA chaperone complex

Hyeyeon Nam, Justin Deme, Marco Boccitto, Soyeong Sim, Susan Lea, Sandra Wolin

Concurrent 12: Splicing Mechanisms

Friday, May 31, 16:40–18:30, Lomond Suite (Moorfoot)

Session Chair: Sebastian Fica

T-97 Two major classes of 5' splice site Matthew Parker, Carey Metheringham, Sebastian Fica, Geoffrey Barton, <u>Gordon Simpson</u>

T-98 Structural basis of the U12-dependent intron recognition Jiangfeng Zhao. Daniel Peter, Irina Brandina, Xiangyang Liu, Wojciech Galej

T-99 Myelodysplastic syndrome mutations in the U2 snRNP protein SF3B1 alter branchpoint recognition

Andrey Damianov, Chia-Ho Lin, Jian Zhang, James Manley, Douglas Black

T-100 Structure and Function of Fyv6 in 3' Splice Site selection during pre-mRNA splicing

Natalie Zeps, Katherine Senn, Karli Lipinski, Amory Griffin, Max Wilkinson, Aaron Hoskins

T-101 FAM32A and Prp18 regulation of NAGNAG alternative splicing reveals molecular basis for stable docking of competing 3[']-splice sites during the catalytic stage of splicing

Marco Preußner, Gwendal Dujardin, Rui Sergio de Sousa Luis, George-Valentin Datcu, Maria Carmo-Fonseca, Nicholas Proudfoot, Florian Heyd, <u>Sebastian Fica</u>

T-102 Structural basis of U12-type intron engagement by the fully assembled human minor spliceosome

Rui Bai, Meng Yuan, Pu Zhang, Kui Xu, Yigong Shi, Ruixue Wan

T-103 3D genome organization around nuclear speckles drives mRNA splicing efficiency

<u>Prashant Bhat.</u> Amy Chow, Benjamin Emert, Olivia Ettlin, Sofia Quinodoz, Mackenzie Strehle, Yodai Takei, Alex Burr, Isabel Goronzy, Allen Chen, Wesley Huang, Jose Lorenzo Ferrer, Elizabeth Soehalim, Say-Tar Goh, Tara Chari, Delaney Sullivan, Mario Blanco, Mitchell Guttman

Concurrent 13: Bioinformatics, Transcriptomics and Genomics

Friday, May 31, 16:40–18:30, Lennox 1

Session Chair: Xinshu (Grace) Xiao

T-104 Single-molecule approaches to quantitative epitranscriptomics Meni Wanunu

T-105 Endogenous labeling empowers accurate detection of m6A from single long reads of direct RNA sequencing

Wenbing Guo, Zhijun Ren, Xiang Huang, Jialiang He, Jie Zhang, Zehong Wu, Yang Guo, Zijun Zhang, Yixian Cun, <u>Jinkai Wang</u>

T-106 Long-read RNA-seq demarcates cis- and trans-directed alternative RNA splicing

Giovanni Quinones-Valdez, Kofi Amoah, Xinshu Xiao

T-107 Discovery of RNA tertiary structures across the human transcriptome David Qiu, Jeffrey Ehrhardt, Kevin Weeks

T-108 Streamlined iCLIP (siCLIP): A refined fluorescent iCLIP protocol to define protein-RNA interactions

Fiona Haward, Manon Tourbez, Joshua Mareschal, Aida Cardona, Christopher R Sibley

T-109 RiboGen generates diverse and realistic ncRNA sequences with generative large language models

Skyler Kramer, Lyndon Coghill, Dong Xu, Donald Burke

T-110 Single-cell temporal dynamics reveals the relative contributions of transcription and degradation to cell-type specific gene expression in zebrafish embryos

Lior Fishman, Avani Modak, Gal Nechooshtan, Talya Razin, Florian Erhard, Aviv Regev, Jeffrey Farrell, Michal Rabani

Concurrent 14: Modification and Editing 2

Friday, May 31, 16:40–18:30, Pentland

Session Chair: Tom Suzuki

T-111 Hepatitis C virus RNA is 5' capped with flavin adenine dinucleotide (FAD)

Anna Sherwood, Lizandro Rivera-Rangel, Line Ryberg, Helena Larsen, Klara Anker, Rui Costa, Cathrine Vågbø, Eva Jakljevič, Long Pham, Carlota Fernandez-Antunez, Gabriele Indrisiunaite, Agnieszka Podolska-Charlery, Julius Grothen, Nicklas Langvad, Nicolas Fossat, Anna Offersgaard, Amal Al-Chaer, Louise Nielsen, Anna Kuśnierczyk, Christina Sølund, Nina Weis, Judith Gottwein, Kenn Holmbeck, Sandro Bottaro, Santseharay Ramirez, Jens Bukh, Troels Scheel, Jeppe Vinther

T-112 RNA Modification by m5C - Lessons From RNA Viruses

Inna Ricardo-Lax, Georgia McClain, Nadia Houerbi, Stephan Bluethgen, Lauren Aguado, Yingpu Yu, Pradeep Ambrose, Charles Rice

T-113 Distinct interactomes of ADAR1 nuclear and cytoplasmic protein isoforms and their responses to Interferon induction

<u>Dragana Vukić,</u> Anna Cherian, Rita Bong, Salla Keskitalo, Leena Yadav, Liam Keegan, Markku Varjosalo, Mary O'Connell

T-114 Dimerization of ADAR1 modulates site specificity of RNA editing.

<u>Vinod Rajendra,</u> Allegra Mboukou, Serafina Messmer, Marjorie Catala, Carine Tisné, Therese Mandl, Pierre Barraud, Michael Jantsch

T-115 A tRNA synthetase serves as a substrate selection factor for a tRNA modification enzyme

Philipp Throll, Luciano Dolce, Palma Rico Lastres, Katharina Arnold, Laura Tengo, Shibom Basu, Stefanie Kaiser, Robert Schneider, <u>Eva Kowalinski</u>

T-116 Structures of mitochondrial RNA editing complexes

<u>Ruslan Afasizhev</u>, Shiheng Liu, Yun-Tao Liu, Andres Vacas, Jane Lee, Clinton Yu, Lan Huang, Liye Zhang, Inna Afasizheva, Z. Hong Zhou

T-117 Charting a Future for Sequencing RNA and Its Modifications: A National Academies Report

Brenda Bass, Taekjip Ha, Trisha Tucholski, Nicholas Adams, Juan Alfonzo, Jeffrey Baker, Susan Baserga, Lydia Contreras, Markus Hafner, Sarath Chandra Janga, Patrick Limbach, Julius Lucks, Mary Majumder, Nicole Martinez, Kate Meyer, Keith Nykamp, Tao Pan

Plenary 7: RNP Condensates

Saturday, June 1, 9:00-10:30, Pentland

Session Chair: Karsten Weis

T-118 The localization and organization of RNA around nuclear speckles Li Wen, Sneha Paul, Mauricio Arias, Xiaoshu Wang, Jiacheng Zhang, Susan Liao, Xingi Fan, Anna Perez, Oded Regev, Jingyi Fei

T-119 Nuclear Speckles Streamline the Genome via an RNA code Lisa Martina, Michał Małszycki, İbrahim Ilık, Tuğçe Aktaş

T-120 Investigating the role of intron RNP topology in facilitating splicing Om Mattagajasingh, Srivathsan Adivarahan, Pascal Raymond, <u>Daniel Zenklusen</u>

T-121 Dissecting altered stress granule biology in U2AF1-mutant myeloid malignancies

<u>Giulia Biancon,</u> Emma Busarello, Matthew Cheng, Simone Sidoli, Jennifer VanOudenhove, Domitilla Baccon, Hannah Maul-Newby, Anthony Khong, Matthew Walter, Karla Neugebauer, Roy Parker, Toma Tebaldi, Stephanie Halene

T-122 The role of cellular condensate maturation in gene expression Felix Räsch, Pablo García, Karsten Weis

T-123 The stress granule-nucleating G3BPs reinforce the translation program of the integrated stress response Jarrett Smith, David Bartel

Plenary 8: Translation Regulation

Saturday, June 1, 11:10–12:40

Session Chair: Fátima Gebauer

T-124 Multiplexed Assays of Human Disease-relevant UTR Mutations Reveal Major Determinants of RNA Stability and translatability

Yun-Lin Wang, Jia-Ying Su, Yu-Tung Hsieh, Wei-Ping Li, Yu-Chi Chang, Hung-Lun Chiang, Yen-Ling Ko, YoonSoon Kang, Yen-Tsung Huang, <u>Chien-Ling Lin</u>

T-125 Systematic Identification of Downstream ORFs and their Biological Functions

Cameron Berry, Ariel Bazzini

T-126 Translation of non-canonical ORFs within 'long non-coding RNAs' contributes to neuronal differentiation

Andreas Kosteletos, Eilidh Ward, Erica Harris, Karl Norris, Mark Handly, Mary O'Connell, David Westhead, Guillaume Hautbergue, Juan Fontana, James Poulter, Julie Aspden

T-127 RIOK3 mediates the degradation of ubiquitylated 40S ribosomes <u>Frances Diehl</u>, Zixuan Huang, Jingdong Cheng, Rachel Green

T-128 The yeast Pby1 decapping co-factor fine-tunes translation by glutaminylating the essential elongation factor eEF1A

Claudine Gaudon-Plesse, Nathalie Ulryck, Marc Graille, Bertrand Seraphin

T-129 "Metabolic tuning": Differential NTPase affinity drives translation shut down in yeast

Katherine Bexley, Michaela Ristova, Stefan Bresson, Andrei Chabes, David Tollervey

Plenary 9: Splicing Regulation

Saturday, June 1, 14:00–15:30, Pentland

Session Chair: Kristen Lynch

T-130 Exon-resolution perturbation coupled to single cell transcriptomics reveals global-regulatory functions of microexons during neuronal differentiation <u>Steven Dupas</u>, Shaghayegh Farhangmehr, Kevin Brown, Jason Moffat, Benjamin J. Blencowe

T-131 The ribosomal protein L22 binds the MDM4 pre-mRNA and promotes exon skipping to activate p53 upon nucleolar stress

Jennifer Jansen, Katherine E. Bohnsack, Susanne Böhlken-Fascher, Markus T. Bohnsack, Matthias Dobbelstein

T-132 RNPS1 in PSAP complex controls periodic pre-mRNA splicing over the cell cycle Kazuhiro Fukumura, Akio Masuda, Jun-ichi Takeda, Kinji Ohno, <u>Akila Mayeda</u>

T-133 IRF7 alternative splicing: its regulatory mechanism and role in modulating type 1 interferon response

Asmita Panthi, Max Ferretti, Olivia Howard, Simon Boudreault, Kristen Lynch

T-134 Deep indel mutagenesis reveals the regulatory and therapeutic architecture of alternative exons

Pablo Baeza-Centurión, Belén Miñana, Andre Faure, Michael Thompson, Sophie Bonnal1, Ben Lehner, Juan Valcarcel

T-135 An ancient competition for the conserved branchpoint sequence influences physiological and evolutionary outcomes in splicing

Karen Larissa Pereira de Castro, Robert E. E. Johnson, Jose Abril, Liao Kuo-Chieh3, Haiping Hao, John Paul Donohue, William Russel, Samuel W. Fagg

Keynote 3: Reinhard Lührmann

Saturday, June 1, 16:00–17:00, Pentland

Session Chair: David Tollervey

K-3 Structural insights into the cascade of snRNP remodeling steps leading to the formation of a catalytically activated spliceosome Reinhard Lührmann



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