

**6<sup>th</sup> International Conference on Base Editing,  
Prime Editing & Related Enzymes**



**Deaminet 2025, Hotel Zoso, Palm Springs, CA**

**January 22<sup>nd</sup>-24<sup>th</sup>, 2025**

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**Rémi Buisson**, University of California Irvine  
**Reuben Harris**, University of Texas Health San Antonio, HHMI  
**Catriona Jamieson**, University of California San Diego  
**Rahul Kohli**, University of Pennsylvania  
**Alexis Komor**, University of California San Diego  
**Audrone Lapinaite**, University of California Irvine  
**David Liu**, Broad Institute, Harvard University, HHMI  
**Branden Moriarity**, University of Minnesota  
**Matthew Weitzman**, Children's Hospital of Philadelphia

**With expert assistance from:**

**Lily Leader**, University of Texas Health San Antonio  
**Caren Myers**, University of Texas Health San Antonio

**Front Cover:**

Artwork created by Audrone Lapinaite with the assistance of DALL·E 2  
*Precision Genome and Transcriptome Editing: A Gustav Klimt-inspired piece that  
combines the art of molecular tools and the intricate beauty of nucleic acids,  
symbolizing innovation in genetic engineering.*

## WEDNESDAY, JANUARY 22

- 2:00 – 4:00 PM HOTEL REGISTRATION & CONFERENCE CHECK-IN (LOBBY)
- 4:30 – 6:20 PM **SESSION I (WOODSTOCK #1) – RNA editing & applications**
- Conveners:** **Catriona Jamieson, University of California San Diego, USA**  
**Chikdu Shivalila, WAVE Life Sciences, USA**
- 4:30 – 4:35 **Welcome Remarks - Reuben Harris, HHMI & UT Health San Antonio**
- 4:35 – 4:50 **Catriona Jamieson**, University of California San Diego, USA, “Stem cell pathways, aging, and cancer stem cell RNA editing”
- 4:50 – 5:05 **Yang Gao**, Rice University, USA, “Biochemical profiling and structural basis of ADAR1-mediated RNA editing”
- 5:05 – 5:20 **Helen Piontkivska**, Kent State University, USA, “ADAR editing: hidden dimension of viral infections and host outcomes”
- 5:20 – 5:35 **Chia-Ning Yang**, National Sun Yat-sen University, Taiwan, “Exploring ADAR1: structural mechanisms of pathogenic mutations and RNA editing defects”
- 5:35 – 5:50 **Benjamin Fixman**, University of Southern California, USA, “Validation of the APOBEC3A-mediated RNA single base substitution signature and proposal of novel APOBEC1, APOBEC3B, and APOBEC3G RNA signatures”
- 5:50 – 6:05 **Ayelet Lamm**, Technion Israel Institute of Technology, Israel, “A-to-I RNA editing enzyme’s subcellular localization can affect its function in *C. elegans*”
- 6:05 – 6:20 **Chikdu Shivalila**, WAVE Life Sciences, USA, “Expanding the therapeutic landscape for hepatic and extrahepatic RNA editing via endogenous ADAR enzymes”
- 6:30 – 8:00 PM **DINNER (ITALIAN THEME; FILLMORE ROOM)**  
**BAR AVAILABLE (DRINK TICKET, CASH, OR CREDIT CARD)**

## THURSDAY, JANUARY 23

7:30 – 8:30 AM BREAKFAST (THE KITCHEN)

8:30 – 10:00 AM **SESSION II (WOODSTOCK #1) – Clinical applications for precision genome engineering**

**Conveners:** **Joe Biedenkapp, Verve Therapeutics, USA**  
**David Liu, Broad Institute, Harvard University, HHMI, USA**

8:30 – 8:45 **Joe Biedenkapp**, Verve Therapeutics, USA, “Development of base editing medicines to durably lower LDL-C and reduce cardiovascular risk”

8:45 – 9:00 **Paula Rio**, CIEMAT/CIBERER/IIS-FJD, Spain, “Advancing hematopoietic stem cell gene therapy for Fanconi Anemia”

9:00 – 9:15 **Xiaoyi Li**, University of Washington, USA, “Chromatin context-dependent regulation and epigenetic manipulation of prime editing”

9:15 – 9:30 **Tiffany Carlaw**, University of British Columbia, Canada, “CRISPR/Cas9 base editing gene therapy of human Cystic Fibrosis models following topical application of lung-optimized lipid nanoparticles”

9:30 – 9:45 **Alexander Sousa**, Broad Institute and Harvard University, USA, “*In vivo* prime editing rescues alternating hemiplegia of childhood in mice”

9:45 – 10:00 **Donald Kohn**, University of California Los Angeles, USA, “Gene therapy for adenosine deaminase-deficient severe combined immune deficiency (ADA SCID)”

10:00 – 10:45 COFFEE BREAK (WOODSTOCK FOYER)

10:45 – 12:30 **SESSION III (WOODSTOCK #1) – Regulation of DNA editing & genome integrity**

**Conveners:** **Matthew Weitzman, Children’s Hospital of Philadelphia, USA**  
**Bingbing Wu, CorrectSequence Therapeutics, China,**

10:45 – 11:00 **Bingbing Wu**, CorrectSequence Therapeutics, China, “Clinical application of innovative transformer base editor (tBE)”

- 11:00 – 11:15 **Allie Dananberg**, Memorial Sloan Kettering Cancer Center, USA, “APOBEC3A bursting drives keratinocyte-associated gene expression programs in human cancer cells”
- 11:15 – 11:30 **Maria Ramos**, German Cancer Research Center (DKFZ), Germany, “APOBEC3B overexpression results in a clonal shift in a Her2-positive breast cancer mouse model”
- 11:30 – 11:45 **Linda Chelico**, University of Saskatchewan, Canada, “Differential effects of APOBEC3A, APOBEC3B, and APOBEC3H Haplotype I on DNA repair”
- 11:45 – 12:00 **Pedro Oretaga**, University of California Irvine, USA, “Unraveling the mechanism of APOBEC3B-mediated replication fork collapse”
- 12:00 – 12:15 **Shailja Pathania**, University of Massachusetts - Boston, USA, “BRCA2 deficiency induced APOBEC3A and APOBEC3B drive genomic instability upon replication stress”
- 12:15 – 12:30 **Lee Zou**, Duke University, USA, “CDK9 inhibition as a strategy to induce synthetic lethality in APOBEC3A-expressing cancer cells”
- 12:30 – 2:00 PM **LUNCH (SUMMER PICNIC THEME; FILLMORE ROOM)**
- 2:00 – 4:00** **SESSION IV (WOODSTOCK #1) – Epigenomic and genomic editing editing**
- Conveners:** **Shanhu Hu, Korro Bio, USA**  
**Audrone Lapinaite, University of California Irvine, USA**
- 2:00 – 2:15 **Shanhu Hu**, Korro Bio, USA, “Characterization of oligo-directed RNA editing with purified ADAR proteins”
- 2:15 – 2:30 **Shun-Qing Liang**, University of Minnesota, USA, “Genome-wide profiling of prime editor off-target sites using PE-tag”
- 2:30 – 2:45 **Pierre Billon**, University of Calgary, Canada, “One-pot DTECT enables rapid and efficient capture of genetic signatures for precision genome editing and clinical diagnostics”
- 2:45 – 3:00 **Yuan Wu**, University of Chicago, USA, “Precise genome editing with context-specific base editor”
- 3:00 – 3:15 **Alexis Komor**, University of San Diego, USA, “Engineering and evolving nucleic acid modifying enzymes”

- 3:15 – 3:30 **Axel Vera**, Massachusetts Institute of Technology, USA, “Cell-permeable anti-CRISPR proteins for precision genome editing”
- 3:30 – 3:45 **Bei Yang**, ShanghaiTech University, China, “Structural visualization of DdCBE in action and optimization of its editing precision”
- 3:45 – 4:00 **David Liu**, Broad Institute and Harvard University, USA, “Mutation-specific, mutation-agnostic, and disease-agnostic therapeutic genome editing”
- 4:15 – 6:00 PM POSTER SESSION I (ODD #'S) WITH REFRESHMENTS  
(DRINK TICKET, CASH, OR CREDIT CARD)  
FILLMORE FOYER AND ENCORE
- 6:30 – 8:00 PM DINNER – Free time to enjoy Palm Springs’ restaurants

## FRIDAY, JANUARY 24

7:30 – 8:30 AM BREAKFAST (THE KITCHEN)

8:30 – 10:15 AM **SESSION V (WOODSTOCK #1) – AIDing editing & novel applications**

**Conveners:** **Rahul Kohli, University of Pennsylvania, USA**  
**Zhi-Yi Sun, New England Biolabs, USA**

8:30 – 8:45 **Kevin McBride**, MD Anderson Cancer Center, USA, “UNG-RPA interaction governs the choice between high-fidelity and mutagenic uracil repair”

8:45 – 9:00 **Nathaniel Wesley**, Pairwise Plants, USA, “New adenosine DNA deaminases for adenine base editing”

9:00– 9:15 **Feilong Meng**, Shanghai Institute of Biochemistry and Cell Biology, China, “Mechanisms of transcription-coupled AID deamination”

9:15 – 9:30 **Jana Ridani**, Institut de Recherches Cliniques de Montréal, Canada, “Comparative proteomics of AID/APOBEC3 family identifies mechanisms tethering AID to chromatin”

9:30 – 9:45 **Christian Loo**, University of Pennsylvania, USA, “DNA Deaminase-based true epigenetic and genetic sequencing of ultra-low input DNA”

9:45 – 10:00 **Mason McCrury**, University of Arkansas, USA, “*BCL2* promoter secondary structures serve as recognition sites for AID”

10:00 – 10:15 **Chris Mullally**, New England Biolabs and UT Health San Antonio, USA, “Functional characterization of bacterial anti-deaminases”

10:15 – 10:45 COFFEE BREAK (WOODSTOCK FOYER)

10:45 – 12:30 **SESSION VI (WOODSTOCK #1) – Understanding, improving, and inhibiting editing mechanisms**

**Conveners:** **Kyle Franks, Maxcyte, USA**  
**Alexis Komor, University of California San Diego, USA**

10:45 – 11:00 **Kyle Franks**, Maxcyte, USA, “Advancing base editing with MaxCyte high-efficiency electroporation”



- 11:00 – 11:15 **Ingrun Alseth**, Oslo University, Norway, “ADA2 is a lysosomal deoxyadenosine deaminase acting on DNA regulating TLR9-mediated immune sensing of DNA”
- 11:15 – 11:30 **Steven Roberts**, University of Vermont, USA, “Mutagenic potential of APOBEC3A orthologs”
- 11:30 – 11:45 **Tyler Daniel**, University of Pennsylvania, USA, “Orthogonal and multiplexable genetic perturbations with an engineered prime editor and a diverse RNA array”
- 11:45 – 12:00 **Isaac Witte**, Broad Institute and Harvard University, USA, “Continuous evolution of CRISPR-associated transposases for efficient, RNA-programmed gene insertion into the human genome”
- 12:00 – 12:15 **Vyacheslav Filichev**, Massey University, New Zealand, “DNA-based inhibitors of APOBEC3: mimicking the highest-energy transition state of cytosine deamination”
- 12:15 – 12:30 **Lulu Yin**, University of Minnesota, USA, “Structural basis for broad substrate selectivity of the double-stranded DNA deaminase toxin BaDTF3”
- 12:30 – 2:00 PM **LUNCH (MEDITERRANEAN THEME; FILLMORE ROOM)**
- 2:00 – 4:00 **SESSION VII (WOODSTOCK #1) – Deaminases in cancer**
- Conveners:** **Rémi Buisson**, University of California Irvine, USA  
**Walraj Gosal**, Biomodal, UK
- 2:00 – 2:15 **Walraj Gosal**, Biomodal, UK, “Simultaneous single cell sequencing of genetic and epigenetic bases”
- 2:15 – 2:30 **Susan Baserga**, Yale University, USA, “The cytidine deaminase APOBEC3A regulates nucleolar function to promote cell growth and ribosome biogenesis”
- 2:30 – 2:45 **Francisco Sanchez-Rivera**, Massachusetts Institute of Technology, USA, “Probing gene-variant-context interactions with multiplexed base and prime editing”
- 2:45 – 3:00 **Silvo Conticello**, ISPRO of Florence, Italy, “Mechanisms of extrachromosomal DNA formation in bladder cancer”

- 3:00 – 3:15 **Yuqing Feng**, York University, Canada, “FAM72A promotes UNG2 degradation and mutagenesis in human cancer cells”
- 3:15 – 3:30 **Deborah Casswell**, The Francis Crick Institute, UK, “APOBEC3B driven mechanisms of targeted cancer therapy resistance”
- 3:30 – 3:45 **Samuel Gould**, Massachusetts Institute of Technology, USA, “Prospective profiling of resistance to transcriptional CDK inhibitors with tiling base editing mutagenesis”
- 3:45 – 4:00 **Reuben Harris**, HHMI and UT Health San Antonio, USA, “APOBEC mutagenesis and carcinogenesis are exacerbated by chemical mutagens”
- 4:15 – 6:00 PM **POSTER SESSION II (EVEN #'S) WITH REFRESHMENTS (DRINK TICKET, CASH, OR CREDIT CARD) FILLMORE FOYER AND ENCORE**
- 6:30 – 8:00 PM **AWARDS DINNER (SALMON OR BEEF; FILLMORE ROOM) BAR AVAILABLE (DRINK TICKET, CASH, OR CREDIT CARD)**

**SATURDAY, JANUARY 25**

TRAVEL DAY – NO MEETING EVENTS

## Poster Presentation List (alphabetical by last name of presenter)

1. **Jonuelle Acosta**, Department of Biology, MIT, Cambridge, MA, USA, “Multiplexed *in vivo* analysis of cancer-associated genetic variants using high-throughput base editing”
2. **Lene Alsøe**, Oslo University Hospital, Oslo, Norway, “Uracil base excision repair as tumour enabler in DNA cytidine deaminase expressing mice”
3. **Meirui An**, Broad Institute of MIT and Harvard, Cambridge, MA, USA, “*In vivo* base editing extends lifespan of a humanized mouse model of prion disease”
4. **Ondine Atwa**, Department of Biology, MIT, Cambridge, MA, USA, “Exploring oncogenic chromatin regulation with precision genome editing”
5. **Chris Belica**, University of Minnesota, Minneapolis, USA, “Characterization and development of novel APOBEC3B-binding nanobodies as multifunctional tools”
6. **Katia Capitani**, Core Research Laboratory, ISPRO, Florence, Italy, “Harnessing MMEJ for precise DNA cassette integration using CRISPR/Cas”
7. **Diego Detres**, Department of Biology, MIT, Cambridge, MA, USA, “Mapping pathogenic genetic variants in disordered proteins using high-throughput gene editing”
8. **Mallory Evanoff**, UCSD, La Jolla, USA, “Directed evolution reversion analysis produces minimally mutated adenine base editor variants with improved efficiency and precision”
9. **Harshita Gupta**, Department of Biochemistry & Structural Biology, University of Texas Health San Antonio, USA, “Murine models for immunotherapy of APOBEC3 mutated tumors”
10. **Kevyn Hart**, Department of Microbiology, Immunology and Molecular Genetics, UCLA, Los Angeles, U.S.A., “Suppressing APOBEC3 in lentiviral producer cells to maximize transgene fidelity”
11. **Michael Hollander**, Department of Chemistry and Biochemistry, UCSD, La Jolla, USA, “Prime editing optimization for a rare *PSEN1* mutation in Alzheimer’s disease”
12. **Jane Isquith**, Sanford Stem Cell Institute, UCSD, La Jolla, USA, “A dynamic equilibrium of innate immune deaminases and deregulation in hematopoietic malignancies”
13. **Grace A. Johnson**, Department of Biology, MIT, Cambridge, MA, USA, “Systematic discovery of genetic variants that impact cancer immune surveillance using high-throughput base editing”
14. **Farzana Kabir**, Department of Medicinal Chemistry, University of Minnesota, USA, “Computational design and experimental characterization of APOBEC3A DNA cytidine deaminase proteins with enhanced stability”
15. **Lindsay E. Lathrop**, Department of Molecular and Medical Pharmacology, David Geffen School of Medicine, UCLA, Los Angeles, USA, “Development of non-

alloreactive CAR T cells from iPSCs”

16. **Qishan Liang**, Department of Cellular and Molecular Medicine, University of California San Diego, La Jolla, USA, “INSCRIBE: *in situ* mapping of RNA-protein interactions in fixed cells and primary tissues”
17. **Pei-Jung Lu**, Institute of Clinical Medicine, College of Medicine, National Cheng Kung University, Tainan, Taiwan, “Targeting ADAR1: protein expression strategies and allosteric inhibitor development”
18. **Kimberly Manning**, Cancer Biology Program, University of Pennsylvania, Philadelphia, USA, “APOBEC3 mutagenesis: possible missing link in modeling head and neck cancer immunogenicity *in vivo*”
19. **Tessa Morin**, University of British Columbia, Vancouver, Canada, “Engineering a precise and high-activity TadA for therapeutic base editing”
20. **Andrew Nelson**, Merkin Institute of Transformative Technologies in Healthcare, Broad Institute of Harvard and MIT, Cambridge, USA, “Adenine base editing rescues dravet syndrome in mice”
21. **Paul Russell**, Revvity Discovery Limited, Cambridge, UK, “Revvity’s Pin-point Platform: a flexible, modular base editing system”
22. **Brandon B. Schuldt**, Department of Medicinal Chemistry, University of Minnesota, Minneapolis, MN, United States, “Development of second-generation small molecule fragment ligands targeting APOBEC3B”
23. **Cheshta Shandilya**, ICGEB, Trieste, Italy, “Dissecting the role of E6AP catalytic activity in HPV transformed cells”
24. **Teresa Sposito**, Moores Cancer Center and Sanford Stem Cell Institute, Department of Medicine, UCSD, La Jolla, USA, “Exploring ADAR1 dependencies in breast cancer brain metastases”
25. **Inge Van der Werf**, Sanford Stem Cell Institute, Division of Regenerative Medicine, Department of Medicine, UCSD, La Jolla, California, USA, “The malignant role of APOBEC3 in RNA splicing of hematopoietic stem and progenitors”
26. **Keisuke Yamada**, Bioengineering Graduate Group, University of Pennsylvania, Philadelphia, USA, “Peptide-assisted delivery of CRISPR-Cas genome and base editors into primary cells”
27. **Stephen Yu**, Department of Brain and Cognitive Sciences, McGovern Institute for Brain Research, Massachusetts Institute of Technology, Cambridge, US, “Using cytosine base editors to generate non-human primate disease models”
28. **Jojo Zhu**, College of Arts and Sciences, University of Pennsylvania, Philadelphia, PA, USA, “Simultaneous profiling of cytosine base modifications and chromatin states using DNA deaminase and engineered methyltransferase”