5th International Conference on Base Editing, Prime Editing & Related Enzymes

Deaminet 2024, San Diego, CA

January 17th-20th, 2024

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Audrone Lapinaite, Arizona State University
David Liu, Broad Institute, Harvard University, HHMI
Branden Moriarity, University of Minnesota
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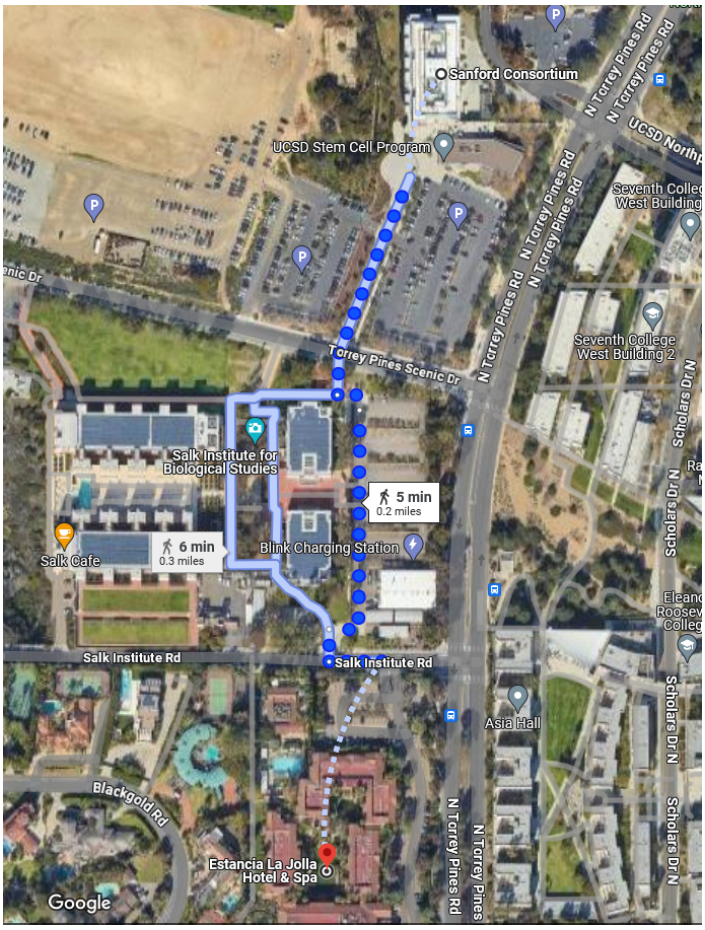
Front Cover:

Artwork created by Audrone Lapinaite with the assistance of DALL·E 2

Walking Routes from Estancia Hotel to Duane Roth Auditorium:



WEDNESDAY, JANUARY 17

2:00 – 4:30 PM	REGISTRATION @ ESTANCIA HOTEL
4:00	ESTANCIA HOTEL - CHECK-IN (some rooms may be available before this official check-in time)

5-10 MIN WALK TO UCSD

4:30 – 6:20 PM	**SESSION I – Advances in Gene Editing Tools for Precision Clinical Applications (Duane Roth Auditorium, Sanford Consortium for Regenerative Medicine, UCSD)**
Conveners:	**Andrew Bellinger, Verve Therapeutics** **Peter Chen, Prime Medicine**
4:30 – 4:35	**Welcome Remarks - Reuben Harris, HHMI & UT Health San Antonio**
4:35 – 4:50	Virtual: **David Liu**, Broad Institute, Harvard University, HHMI, USA, "Recent developments in prime editing"
4:50 – 5:05	**Reilly Mach**, Scripps Research Institute, USA, "Engineering SpCas9 towards compatibility with fully chemically modified sgRNA"
5:05 – 5:20	**Jia Chen**, Shanghai Tech University, China, "Therapeutic base editing for β-thalassemia"
5:20 – 5:35	**Mallory Evanoff**, University of California San Diego, USA, "Illuminating contributions of mutations accumulated in ABE7.10 development - their roles in DNA editing efficiency, specificity, and protein stability"
5:35 – 5:50	**Andrew Bellinger**, Verve Therapeutics, USA, "First-in-human trial of VERVE-101 demonstrates proof-of-concept for durable LDL cholesterol lowering with *in vivo* base editing of the *PCSK9* gene"
5:50 – 6:05	**Mark Osborn**, University of Minnesota, USA, "Precise exon deletion to restore type VII collagen in recessive dystrophic epidermolysis bullosa"
6:05 – 6:20	**Peter Chen**, Prime Medicine, USA, "Advancing prime editors towards clinical evaluation in patients"

5-10 MIN WALK TO ESTANCIA

6:30 – 8:00 PM	DINNER @ ESTANCIA HOTEL

THURSDAY, JANUARY 18

7:30 – 8:30 AM BREAKFAST @ ESTANCIA HOTEL

5-10 MIN WALK TO UCSD

8:30 – 10:15 AM **SESSION II – RNA Editing and CRISPR Screens Providing Biological Insights and Advancing Therapies (Duane Roth Auditorium, Sanford Consortium for Regenerative Medicine, UCSD)**

Conveners: **Catriona Jamieson, University of California San Diego**
Alexis Komor, University of California San Diego
Gerard Platenburg, ProQR Therapeutics

8:30 – 8:45 **Catriona Jamieson,** University of California San Diego, USA, "Malignant deaminase activation fuels cancer stem cell generation"

8:45 – 9:00 **Tajinder Ubhi**, University of Toronto, Canada, "APOBEC3C and APOBEC3D promote DNA replication stress resistance in pancreatic cancer cells"

9:00 – 9:15 **Weixin Tang**, University of Chicago, USA, "Directed evolution of an adenine base editor with increased context compatibility"

9:15 – 9:30 **Eugene Yeo**, University of California San Diego, USA, "Development of methods that leverage RNA-based editing for fundamental studies of RNA processing"

9:30 – 9:45 **Erez Levanon**, Bar-Ilan University, Israel, "What can we learn from endogenous RNA editing?"

9:45 – 10:00 **Lisa (Qishan) Liang**, University of California San Diego, USA, "High-sensitivity *in situ* capture of endogenous RNA-protein interactions in fixed cells and primary tissues"

10:00 – 10:15 **Gerard Platenburg**, ProQR Therapeutics, Netherlands & USA, "Axiomer™, an RNA editing technology to address liver-originated disorders and beyond"

10:15 – 10:45 COFFEE BREAK @ UCSD

10:45 – 12:30 **SESSION III – Rewards and Risks of DNA Editing (Duane Roth Auditorium, Sanford Consortium for Regenerative Medicine, UCSD)**

Conveners: **Ayan Banerjee, Beam Therapeutics**
Matthew Weitzman, Children's Hospital of Philadelphia

10:45 – 11:00	**Ayan Banerjee**, Beam Therapeutics, USA, “BEAM-302: targeting AATD-related liver and lung disease with base editing”
11:00 – 11:15	**Philip Barbulescu**, University of Toronto, Canada, “The CTLH E3 ligase complex degrades UNG2 through FAM72A to promote mutagenic DNA repair during antibody diversification”
11:15 – 11:30	**Mia Petljak**, New York University, USA, “Mechanisms of APOBEC3 mutagenesis in human cancer cells”
11:30 – 11:45	**Alberto Ciccia**, Columbia University, USA, “Functional interrogation of nucleotide variants of the DNA damage response using optical base editing screens”
11:45 – 12:00	**Frank van Gemert**, Netherlands Cancer Institute (NKI), Netherlands, “ADARp150 prohibits whole genome duplication”
12:00 – 12:15	**Hideko Isozaki**, Harvard University, USA, “APOBEC3A drives tumor evolution through activation of ERVs in non-small cell lung cancer”
12:15 – 12:30	**Xiaojiang Chen**, University of Southern California, USA, “Molecular mechanism for regulating APOBEC3G function by the non-catalytic domain”
12:30 – 2:00 PM	LUNCH @ UCSD
2:00 – 4:00	**SESSION IV – The RNA Editing Toolbox: From Fundamental Biology to Therapeutic Applications (Duane Roth Auditorium, Sanford Consortium for Regenerative Medicine, UCSD)**
Conveners:	**Brian Booth, Shape Therapeutics** **Chris Brown, Korro Bio** **Rémi Buisson, University of California Irvine**
2:00 – 2:15	**Brian Booth**, Shape Therapeutics, USA, “~95% RNA editing in the brain with ADAR guide RNAs delivered by systemic injection”
2:15 – 2:30	**Cem Nass Kebapcioglu**, Institute of Clinical Physiology, National Research Council (IFC-CNR), Italy, “Fine-tuning site-directed RNA editing: controlled gRNA synthesis with T7 RNA polymerase”
2:30 – 2:45	**Ruslan Afasizhev**, Boston University, USA, “Structures of mitochondrial RNA editing complexes from trypanosomes”
2:45 – 3:00	**Inge van der Werf**, University of California San Diego, USA, “Increased ADAR1-related editing events in pediatric acute myeloid leukemia near exon junctions”

3:00 – 3:15 **Junwei Shi**, University of Pennsylvania, USA, “Decoding cancer vulnerability with inducible split-engineered base editors”

3:15 – 3:30 **Bailey Wong**, University of California Davis, USA, “RNA sequences that enable ADAR editing from a SELEX library bearing 8-azanebularine”

3:30 – 3:45 **Nina Papavasiliou**, German Cancer Research Center (DKFZ), Germany, “AID/APOBEC catalysed base editing: balancing deamination activity vs sequence specificity”

3:45 – 4:00 **Chris Brown**, Korro Bio, USA, “Harnessing endogenous ADAR for oligo-directed RNA editing”

5-10 MIN WALK TO ESTANCIA

4:15 – 6:00 PM POSTER SESSION I WITH REFRESHMENTS @ ESTANCIA

6:30 – 8:00 PM DINNER @ ESTANCIA

FRIDAY, JANUARY 19

7:30 – 8:30 AM BREAKFAST @ ESTANCIA

5-10 MIN WALK TO UCSD

8:30 – 10:15 AM **SESSION V – New Deaminases and Biotechnologies (Duane Roth Auditorium, Sanford Consortium for Regenerative Medicine, UCSD)**

Conveners: **Walraj Gosal, Biomodal**
Rahul Kohli, University of Pennsylvania
Yi Sun, New England Biolabs

8:30 – 8:45 **Walraj Gosal**, Biomodal, Cambridge, UK, “Discriminating 5-mC and 5-hmC at single-base resolution”

8:45 – 9:00 **Chris Belica**, University of Minnesota, USA, “A real-time biochemical assay for quantitative analyses of APOBEC-catalyzed DNA deamination”

9:00– 9:15 **Xue (Sherry) Gao**, University of Pennsylvania, USA, “A split and inducible adenine base editor for precise *in vivo* base editing”

9:15 – 9:30 **Ian Reddin**, University of Southampton, UK, “Identification of GRHL3 as a novel regulator of APOBEC3A expression using single cell sequencing, spatial transcriptomics and RNA interference”

9:30 – 9:45	**Richard Chahwan**, University of Zurich, Switzerland, “Modular cytosine base editing promotes epigenomic and genomic modifications”
9:45 – 10:00	**Kevin Zhao**, Qi Biodesign, USA, “Discovery of deaminase functions by structure-based protein clustering”
10:00 – 10:15	**Yi Sun**, New England Biolabs, USA, “Discovery of novel cytosine deaminases enables powerful new tools for methylome analysis”
10:15 – 10:45	COFFEE BREAK @ UCSD
10:45 – 12:30	**SESSION VI – Additional Frontiers in Editing (Duane Roth Auditorium, Sanford Consortium for Regenerative Medicine, UCSD)**
Conveners:	**Branden Moriarity, University of Minnesota** **Aaron Hummel, Pairwise**
10:45 – 11:00	**Aaron Hummel**, Pairwise, USA, “From better salads to more corn: CRISPR is bringing innovation across the agricultural landscape”
11:00 – 11:15	**Nathaniel A. Wesley**, Pairwise, USA, “Precision genome editing in commodity and consumer crops”
11:15 – 11:30	**Brian Burger**, Genus Plc, USA, “Gene editing for disease resistance in livestock”
11:30 – 11:45	**Richard Sherwood**, Brigham and Women’s Hospital and Harvard Medical School, USA, “Joint genotypic and phenotypic outcome modeling improves base editing variant effect quantification”
11:45 – 12:00	**Abby Green**, Washington University, USA, “Disruption of DNA replication dynamics by APOBEC3A”
12:00 – 12:15	**Kyle Jancola**, University of Wisconsin - Madison, USA, “Identification of functional variants affecting DNA repair pathways”
12:15 – 12:30	**Ludmil Alexandrov**, University of California San Diego, USA, “The mutagenic activity of APOBEC deaminases in human precancer”
12:30 – 2:00 PM	LUNCH @ UCSD

2:00 – 4:00	**SESSION VII – Nucleic Acid Deaminases: Insights into Mechanisms, Functions, Disease Relevance, and Advances in Base Editing Technologies (Duane Roth Auditorium, Sanford Consortium for Regenerative Medicine, UCSD)**
Conveners:	**Ian Harding, Wave Life Sciences** **Audrone Lapinaite, Arizona State University**
2:00 – 2:15	**Ian Harding**, Wave Life Sciences, USA, "Building a therapeutic A-to-I RNA editing platform through oligonucleotide chemistry optimization"
2:15 – 2:30	**Avantika Gupta**, Memorial Sloan Kettering Cancer Center, USA, "APOBEC3 enzymes drive therapeutic resistance in breast cancer"
2:30 – 2:45	**Rommie Amaro**, University of California San Diego, USA, "APOBEC3B structure, dynamics, mechanisms, and druggability"
2:45 – 3:00	**Quinn Cowan**, University of California San Diego, USA, "Development and characterization of multiplexed orthogonal base editing systems"
3:00 – 3:15	**Audrone Lapinaite**, Arizona State University, USA, "Understanding the molecular mechanism of DNA adenine base editors (ABEs) to improve their precision and expand their targeting scope"
3:15 – 3:30	**Christopher Collins**, Washington State University & University of Vermont, USA, "Investigating the role of acetylation in post-translational regulation of APOBEC3A"
3:30 – 3:45	**Caterina Baccioni**, Institute of Clinical Physiology, National Research Council (IFC-CNR), Italy, "Unraveling the role of ADARs in SARS-CoV-2 Infection"
3:45 – 4:00	**Ambrocio Sanchez**, University of California Irvine, USA, "Mesoscale DNA features impact APOBEC3A and APOBEC3B deaminase activity and shape tumor mutational landscapes"

5-10 MIN WALK TO ESTANCIA

4:15 – 6:00 PM POSTER SESSION II WITH REFRESHMENTS @ ESTANCIA

6:30 – 8:00 PM DINNER & AWARDS @ ESTANCIA

SATURDAY, JANUARY 20

TRAVEL DAY – NO MEETING EVENTS

Poster Presentations (alphabetical by last name of presenter)

1. **Giada Agostini,** Core Research Laboratory, ISPRO, Florence, Italy, “APOBEC3A-dependent editing on the *DDOST* transcript triggers formation of an early stop codon”
2. **Rachel Anderson,** UC San Diego, USA, **“**Validation of hits from CRISPRi screen elucidating the mechanisms of cytosine base editing”
3. **Jessica Becerra**, Fred Hutchinson Cancer Center, USA, “APOBEC mediated survival of drug-tolerant persister cells and their role in acquired resistance to EGFR inhibitors in lung cancer”
4. **Mac Kevin Braza**, UC San Diego, USA, “Full-length APOBEC3B active site opening mechanism”
5. **Allison Cafferty**, University of Minnesota, “Utilization of nanobodies for the detection and knockdown of APOBEC3B”
6. **Alex Chadwick**, Verve Therapeutics, USA, “Off-target assessment of VERVE-101, an investigational *in vivo* base editing medicine targeting *PCSK9* for the treatment of heterozygous familial hypercholesterolemia”
7. **Xiaoyu Chen**, Arizona State University, USA, “Understanding precision genome editing tools: molecular basis of efficient DNA deamination by ABE8e”
8. **Yanjun Chen**, UT Health San Antonio, USA, **“**A rabbit monoclonal antibody for specific detection of human APOBEC3A”
9. **Jeff Cheng**, UC Davis, USA, “Repurposing an RNA-editing enzyme, ADAR, for DNA base editing”
10. **Brenda Delamonica**, Stony Brook University, USA, “APOBEC and AID evolution in bat species”
11. **Jessica Devenport**, Washington University School of Medicine, USA, “APOBEC3A promotes ovarian cancer metastasis”
12. **Hongyuan Fei**, Chinese Academy of Sciences, College of Advanced Agricultural Sciences, University of Chinese Academy of Sciences, China, "Discovery of deaminase functions by structure-based protein clustering"
13. **Dylan Fingerman**, Washington University School of Medicine, USA, “Molecular mechanisms of tolerance of APOBEC3A mediated damage during replication”
14. **Sifeng Gu**, UC San Diego, USA**, “**Elucidating cytosine base editing mechanisms through CRISPRi screens”
15. **Natalia Gurule**, Revvity, USA, “Development of a versatile aptamer-based Pin-point™ base editing system with type V CRISPR-Cas effectors”
16. **Adam K. Hedger,** University of Massachusetts Chan Medical School, RNA Therapeutics Institute, USA, “Improving APOBEC3 oligonucleotide inhibitors: optimized placement of chemical modifications to improve potency, stability, and cellular inhibition”
17. **Jane Isquith**, UC San Diego, USA, **“**Hallmarks of APOBEC3 mutagenesis in normal, pre-leukemic, and myeloproliferative neoplasm cell populations”

18. **Fumiaki Ito**, USC/UCLA, USA, “Structural basis of HIV-1 Vif-mediated antagonism of APOBEC3H”
19. **Shyanne King,** University of Washington, USA, “Investigating APOBEC3 enzyme regulation in cancer”
20. **Sanjana Korpal**, UC San Diego, USA, “Evaluating the base editing activity of ABE7.10”
21. **Lisa (Qishan) Liang**, UC San Diego, USA, “High-sensitivity *in situ* capture of endogenous RNA-protein interactions in fixed cells and primary tissues”
22. **Christian Loo**, University of Pennsylvania, USA, “Direct, non-destructive localization of DNA modifications leveraging a DNA deaminase”
23. **Liyuan Ma**, Massachusetts General Hospital/Harvard, USA, “Optimization of prime editing towards *in vivo* mutation correction”
24. **Mason McCrury**, University of Arkansas for Medical Sciences, USA, “AID binds DNA secondary structures from the *BCL2* promoter”
25. **Emily McNutt**, New England Biolabs, USA, “Characterizing the promiscuity of *E. coli* adenosine deaminase”
26. **Clare Morris**, UC San Diego, USA, “Computational evaluation of novel allosteric small molecule interactions with A3Bctd”
27. **Joseph Peterson**, University of Minnesota, USA, “*In vivo* correction of genetically humanized patient-specific Fanconi anemia mutations using digital editing technologies”
28. **Paige Policelli,** University of Southampton, UK, “Friendly fire: Identification of *cis*- and *trans*-acting elements involved in the regulation of the genome-editing enzyme, *APOBEC3A”*
29. **Aditya Radhakrishnan**, Shape Therapeutics, Inc, USA, “Advancing the safety profile of ADAR-mediated programmable RNA editing”
30. **Jana Ridani,** IRCM/McGill, Canada, “Comparative proteomics to identify factors regulating the function of AID”
31. **Irene Schwartz**, Max Perutz Labs University of Vienna, Austria, “Cellular degradation mechanism of cancer-associated APOBEC3 deaminases”
32. **Rebekah Silva**, New England Biolabs, USA, “Loading the bases: DNA hypermodifications from bacteriophage”
33. **Anne Timmerman**, Amsterdam UMC, Netherlands, “Control of human Anelloviruses by cytosine to uracil genome editing”
34. **Mackenzie Wyllie**, University of Minnesota, USA, “The role of cytidine sugar conformation in APOBEC3 selectivity for DNA binding and deamination”
35. **Lulu Yin,** University of Minnesota, USA, “Structural basis for a broad sequence selectivity of the single-stranded DNA deaminase toxin SsdA”
36. **Stephen Yu**, MIT, USA, “Development of adenosine base editing for correcting the most common Mecp2 mutations found in Rett syndrome patients”
37. **Margo Coxon**, Washington State University, USA, "Development and Characterization of Multiplexed Orthogonal Base Editing Systems