Abstracts of papers presented
at the 2025 Cold Spring Harbor Asia Conference

SYSTEMS BIOLOGY OF GENE REGULATION & GENOME EDITING

October 20–October 24, 2025

Arranged by

Len Pennacchio, *Lawrence Berkeley National Laboratory*
Alexander Stark, *Research Institute of Molecular Pathology*
Zhiping Weng, *University of Massachusetts Chan Medical School*
Wei Xie, *Tsinghua University*

Cold Spring Harbor Conferences Asia
Cold Spring Harbor Laboratory

SYSTEMS BIOLOGY OF GENE REGULATION & GENOME EDITING

Monday, October 20 – Friday, October 24, 2025

Monday	7:00 pm	**1** Gene Regulation in Development
Tuesday	9:00 am	**2** Regulatory Elements
Tuesday	12:00 pm	**Flash Talks**
Tuesday	2:00 pm	**Poster Session**
Tuesday	7:00 pm	**3** Functional Genomics
Wednesday	9:00 am	**4** Epigenetic Mechanisms
Wednesday	1:30 pm	*Visit to Old Suzhou**
Wednesday	7:00 pm	**5** Gene Regulation in Disease
Thursday	9:00 am	**6** Emerging Technologies
Thursday	2:00 pm	**7** Transcription Factors and Complexes
Thursday	5:00 pm	*Cocktails and Banquet*
Friday	9:00 am	**8** AI and Genomic Predictions

Oral presentation sessions are located in the CSHA Auditorium
Poster session is in the Lake Front Hall.
Cocktail social hour is held outside in the Suz Garden.
Old Suzhou visits depart from the CSHA lobby
**optional tour requires additional fee.*

Meal locations and times are as follows:
Lunch: Main Cafeteria 12:00pm - 1:30pm
Dinner: Main Cafeteria 6:00pm - 7:30pm
Banquet: Suz Garden 6:00pm

More information will be available at CSHA office.
(Map at the end of this abstract book)

PROGRAM

MONDAY, October 20—7:00 PM

Opening Remarks

SESSION 1 GENE REGULATION IN DEVELOPMENT

Chairperson: **Zhiping Weng,** University of Massachusetts
Chan Medical School, Worcester, Massachusetts, USA

Ultra-long-range gene regulation in fly neurons
Jenisha Khadka, Pascual Justine, Marion Solbach, Hani Sahar, Dorier Julien, Maria Cristina Gambetta [20’+10’]
Presenter affiliation: University of Lausanne, Lausanne, Switzerland. 1

From organoid genetics to mosaic genetics
Bon-Kyoung Koo [20’+10’]
Presenter affiliation: Institute for Basic Science, Yuseong-gu, South Korea. 2

Epitranscriptomic regulation of human primordial germ cells
Jin Zhang, Di Chen [10’+5’]
Presenter affiliation: Zhejiang University, Haining, China. 3

Decoding life's history with evolving DNA methylome
Shou-Wen Wang [10’+5’]
Presenter affiliation: Westlake University, Hangzhou, China. 4

TUESDAY, October 21—9:00 AM

SESSION 2 REGULATORY ELEMENTS

Chairperson: **Maria Cristina Gambetta,** University of Lausanne, Lausanne, Switzerland

SINE retrotransposons link replication timing with higher-order genome organization by recruiting H2B monoubiquitination at genebody
Jafar Sharif, Meiji Kit-Wan Ma, Ryo Onishi, Haruhiko Koseki [20'+10']
Presenter affiliation: RIKEN Center for Integrative Medical Sciences (IMS), Yokohama, Japan. 5

An expanded registry of candidate cis-regulatory elements for studying transcriptional regulation
Jill E. Moore, The Registry of cCRE WG: ENCODE Phase IV, Zhiping Weng [20'+10']
Presenter affiliation: UMass Chan Medical School, Worcester, Massachusetts. 6

Functional genomics in the pangenome era
Ting Wang [20'+10']
Presenter affiliation: Washington University School of Medicine, St. Louis, Missouri. 7

Break

Mapping and modeling cell landscapes at single-cell level
Guoji Guo [10'+5']
Presenter affiliation: Center for Stem Cell and Regenerative Medicine, Hangzhou, China. 8

CRISPR-mediated live imaging revealing chromatin status and enhancer interactions
Haifeng Wang [10'+5']
Presenter affiliation: Tsinghua University, Beijing, China. 9

Diabetes recovery by rapid insulin expression switch of a delta cell subtype in Zebrafish
Jo Graesslin [10'+5']
Presenter affiliation: Max Delbrück Center for Molecular Medicine, Berlin, Germany; Humboldt-Universität zu Berlin, Berlin, Germany. 10

TUESDAY, October 21—12:00 PM

FLASH TALKS

***Cellist*—Accurate, scalable and cross-platform cell identification for high-resolution spatial transcriptomics**
Dongqing Sun, Lele Zhang, Tong Han, Qiu Wu, Peng Zhang, Chenfei Wang
Presenter affiliation: Tongji Hospital, Shanghai, China. 11

Drivers of pro-regenerative cell state activation in zebrafish heart regeneration
Emese Ratkai, Jan P. Junker
Presenter affiliation: Max Delbrück Center for Molecular Medicine in the Helmholtz Association, Berlin, Germany. 12

CRISPR-Taiji perturb-seq deciphers the first comprehensive genotype-phenotype landscape of aneuploidy
Hugang Feng, Daqi Deng, Rashmi Dahiya, Libin Wang, Peter Ly, Samra Turajlic
Presenter affiliation: The Francis Crick Institute, London, United Kingdom. 13

Establishing polycomb regulatory landscapes in human early development
Xiaoyu Hu, Chuanxin Zhang, Bofeng Liu, Fangnong Lai, Shuiying Ma, Qizhe Shao, Ling Liu, Xukun Lu, Guanling Yu, Hui Liu, Zhen Yang, Ning Wang, Zili Lin, Lijuan Wang, Han Zhao, Keliang Wu, Zijiang Chen, Wei Xie
Presenter affiliation: Tsinghua University, Beijing, China. 14

Catalytic activity of METTL1 contributes to METTL1 dependency in paediatric cancers
Pei Y. Liu, Steven He, Alice Salib, Priyank Rawat, Wenxin Hu, Chelsea Mayoh, Wong Marie, Greg M. Arndt, Ian Street, Mohamed Fared, Antoine de Weck, Paul G. Ekert
Presenter affiliation: Children's Cancer Institute, UNSW, Sydney, NSW, Australia. 15

A draft mouse graph pangenome reference accelerates genomic analyses
Juan F. Macias-Velasco, John E. Garza, Wenjin Zhang, Wanying Wu, Zheng Xu, Derek A. Albracht, Hang Su, Yang E. Li, Ting Wang
Presenter affiliation: Washington University School of Medicine, St. Louis, Missouri. 16

N^6-methyladenosine on L1PA Governs the Trans-silencing of LTR and restrains the rolling back to totipotent state in naïve human embryonic stem cells
Xuehao Zhu, Zhanhe Chang, Weide Xiao, Jun Liu, Yixuan Wang, Shaorong Gao, Yawei Gao
Presenter affiliation: China; Shanghai East Hospital, School of Life Sciences and Technology, Tongji University, Shanghai, China. 17

TUESDAY, October 21—2:00 PM

POSTER SESSION

***Cellist*—Accurate, scalable and cross-platform cell identification for high-resolution spatial transcriptomics**
Dongqing Sun, Lele Zhang, Tong Han, Qiu Wu, Peng Zhang, Chenfei Wang
Presenter affiliation: Tongji Hospital, Shanghai, China. 11

Drivers of pro-regenerative cell state activation in zebrafish heart regeneration
Emese Ratkai, Jan P. Junker
Presenter affiliation: Max Delbrück Center for Molecular Medicine in the Helmholtz Association, Berlin, Germany. 12

CRISPR-Taiji perturb-seq deciphers the first comprehensive genotype-phenotype landscape of aneuploidy
Hugang Feng, Daqi Deng, Rashmi Dahiya, Libin Wang, Peter Ly, Samra Turajlic
Presenter affiliation: The Francis Crick Institute, London, United Kingdom. 13

Establishing polycomb regulatory landscapes in human early development
Xiaoyu Hu, Chuanxin Zhang, Bofeng Liu, Fangnong Lai, Shuiying Ma, Qizhe Shao, Ling Liu, Xukun Lu, Guanling Yu, Hui Liu, Zhen Yang, Ning Wang, Zili Lin, Lijuan Wang, Han Zhao, Keliang Wu, Zijiang Chen, Wei Xie
Presenter affiliation: Tsinghua University, Beijing, China. 14

Catalytic activity of METTL1 contributes to METTL1 dependency in paediatric cancers
Pei Y. Liu, Steven He, Alice Salib, Priyank Rawat, Wenxin Hu, Chelsea Mayoh, Wong Marie, Greg M. Arndt, Ian Street, Mohamed Fared, Antoine de Weck, Paul G. Ekert
Presenter affiliation: Children's Cancer Institute, UNSW, Sydney, NSW, Australia. 15

A draft mouse graph pangenome reference accelerates genomic analyses
Juan F. Macias-Velasco, John E. Garza, Wenjin Zhang, Wanying Wu, Zheng Xu, Derek A. Albracht, Hang Su, Yang E. Li, Ting Wang
Presenter affiliation: Washington University School of Medicine, St. Louis, Missouri. 16

N^6-methyladenosine on L1PA Governs the Trans-silencing of LTR and restrains the rolling back to totipotent state in naïve human embryonic stem cells
Xuehao Zhu, Zhanhe Chang, Weide Xiao, Jun Liu, Yixuan Wang, Shaorong Gao, Yawei Gao
Presenter affiliation: China; Shanghai East Hospital, School of Life Sciences and Technology, Tongji University, Shanghai, China. 17

Identify transcription factor direct and indirect binding sites using ChIP-exo
Yahui Bai, Silin Zhong
Presenter affiliation: The Chinese University of Hong Kong, Hong Kong, China. 18

Predicting and designing mouse tissue-specific enhancers with deep learning
Shenzhi Chen, Vincent Loubiere, Jacob Schreiber, Ethan Hollingsworth, Evgeny Z. Kvon, Alexander Stark
Presenter affiliation: Research Institute of Molecular Pathology, Vienna, Austria; Vienna BioCenter PhD Program, Vienna, Austria. 19

Gastrula-premarked posterior enhancer primes posterior tissue development through cross-talk with TGF-β signaling pathway
Yingying Chen, Fengxiang Tan, Qing Fang, Lin Zhang, Jiaoyang Liao, Penglei Shen, Yun Qian, Mingzhu Wen, Rui Song, Yonggao Fu, He J. Xu, Ran Wang, Cheng Li, Zhen Shao, Jinsong Li, Naihe Jing, Xianfa Yang
Presenter affiliation: Guangzhou National Laboratory, Guangzhou, China. 20

Systematic detection of uniparental disomy through Mendelian inheritance error analysis in postnatal and prenatal trio-exome sequencing
Ting Xu, Xinyi Lu, Xiaoyan Huo, Huili Liu, Yongguo Yu, Yanjie Fan
Presenter affiliation: Xinhua Hospital affiliated to Shanghai Jiao Tong University School of Medicine, Shanghai, China. 21

RNA regulation in anti-tumor immunotherapy—From multi-dimensional omics to novel therapeutic strategies
Dali Han
Presenter affiliation: China National Center for Bioinformation, Beijing, China. 22

Cisformer—A scalable cross-modality generation framework for decoding transcriptional regulation at single-cell resolution
Luzhang Ji, Qihang Zou, Ke Tang, Chenfei Wang
Presenter affiliation: Tongji University, Shanghai, China. 23

How to infer miRNA activity from single-cell transcriptomes
Panagiotis Kalogeropoulos, Jialin Zheng, Vaishnovi Sekar, Inna Biryukova, Marc Friedländer
Presenter affiliation: Stockholm University, Stockholm, Sweden. 24

Dissection of cell-fate transition in direct lineage reprogramming from human fibroblast to renal tubular epithelial cells
Shuhan Kong, Ruth Röck, Zengyan Yang, Francesca Solinas, Antonia Ibel, Soeren Lienkamp, Michael Kaminski
Presenter affiliation: Charité Universitätsmedizin Berlin, Berlin, Germany; Max Delbrück Center for Molecular Medicine in the Helmholtz Association, Berlin, Germany. 25

Behavioral improvement through in vivo base editing in a mouse model of Snijders Blok-Campeau syndrome
Kan Yang, Weike Li, Yanbo Cheng, Yixiao Geng, Zhankui Xu, Yiting Yuan, Tanying Zhang, Zhenghui Li, Ruochuan Xu, Chenxi Lin, Wenxin Wang, Wenxiu Yang, Jiashuo Wen, Xinyi Zhang, Jie Li, Fei Li, Tianlin Cheng, Zilong Qiu
Presenter affiliation: Fudan University, Shanghai, China. 26

Multiplexed genetic manipulation and neural disease modelling by split-Cas9-knock-in mice
Weike Li, Xinyi Zhang, Zhili Liu, Yinuo Liu, Cheng Zhang, Feng Gao, Junying Chen, Ying Lu, Chao Song, Wanling Peng, Tianlin Cheng
Presenter affiliation: Fudan University, Shanghai, China. 27

Reprogramming of H3K36me2 guides lineage-specific post-implantation de novo DNA methylation
Xukun Lu, Lijuan Wang, Bofeng Liu, Xiaoyu Hu, Zhengmao Wang, Ling Liu, Guang Yu, Lijun Dong, Feng Kong, Qiang Fan, Yu Zhang, Wei Xie
Presenter affiliation: Shandong University, Jinan, China; Tsinghua University, Beijing, China. 28

Adapting prime editing in *Escherichia coli* and its application to *Staphylococcus aureus* genome editing
Seong Hyeok Ma, Junho Cho, Sang Sun Yoon
Presenter affiliation: Yonsei University College of Medicine, Seoul, South Korea; Graduate School of Medical Science, Seoul, South Korea. 29

Deep learning for understanding the mechanisms of cross-resistance in malignant melanoma
Ken Murakami, Anna Obenauf, Alexander Stark
Presenter affiliation: Research Institute of Molecular Pathology, Vienna, Austria. 30

Studying cis-regulatory heterogeneity in single-cells at allelic resolution
Veronika Petrova, Muqing Niu, Thomas Vierbuchen, Emily S. Wong
Presenter affiliation: Victor Chang Cardiac Research Institute, Sydney, Australia; University of New South Wales, Sydney, Australia. 31

The gene body associated epigenetic mark H2Bub regulates higher-order genome organization by antagonizing DNMT1-dependent DNA methylation
Jafar Sharif, Shu-Lan Sun, Kayoko Katsuyama, Haruhiko Koseki
Presenter affiliation: IMS, RIKEN, Yokohama, Japan. 32

Unraveling the mechanisms underlying tissue-specific transcription during *Drosophila* metamorphosis
Aleksandra A. Evdokimova, Tatyana D. Kolesnikova, Veit Schubert, Nadezhda E. Vorobyeva
Presenter affiliation: Institute of Gene Biology RAS, Moscow, Russia. 33

CRANE—A Self-adaptive algorithm for noise elimination in single-cell perturbation analysis using graph-structured pattern recognition
Jun Cao, Xiaoyue Wang
Presenter affiliation: Institute of Clinical Medicine and Peking Union Medical College Hospital, Beijing, China. 34

Spatial single cell transcriptomic analysis informs the developmental hierarchy of DICER1 Syndrome-associated cancer
Felix K. Kommoss, Joyce Yu Han Zhang, Branden J. Lynch, Shary Y. Chen, Janine Senz, Lesley S. Hill, T. Michael Underhill, David G. Huntsman, Yemin Wang
Presenter affiliation: University of British Columbia, Vancouver, Canada; British Columbia Cancer Research Institute, Vancouver, Canada; Vancouver Coastal Health Research Institute, Vancouver, Canada. 35

chromIDEAS reveals epigenetic dynamics via multi-dimensional clustering of chromatin states
Liu Yang, Shan Liu, Ting Lu, Shaokang Mo, Bin Qi, Kuangyu Yen
Presenter affiliation: Chinese Academy of Medical Sciences & Peking Union Medical College, Tianjin, China; Southern Medical University, Guangzhou, China; Tianjin Institutes of Health Science, Tianjin, China. 36

cFOOT-seq—A high-resolution platform for TF occupancy profiling in single-molecule and single-cell
Heng Wang, Ang Wu, Mengchen Yang, Xiaoyu Liu, Jiejun Shi, Shaorong Gao, Jia-min Zhang
Presenter affiliation: Tongji Hospital, Shanghai, China; Shanghai First Maternity and Infant Hospital, Shanghai, China. 37

Engineering mesenchymal stem cells to activate macrophage STING and promote M1 polarization for enhanced cancer immunotherapy
Yanhui Zheng, Wei Chen, Qianxiang Wu
Presenter affiliation: Tongji University, Shanghai, China. 38

DART-seq uncovers a regulatory crosstalk network of N^6-methyladenosine, splicing, and gene expression underlying Alzheimer's disease pathogenesis
Zhiyuan Zhu, Huanchang Tu, Jenna Libera, Junming Hu, Benjamin Wolozin, Lei Hou
Presenter affiliation: Zhejiang University School of Medicine, Hangzhou, China. 39

TUESDAY, October 21—7:00 PM

SESSION 3 FUNCTIONAL GENOMICS

Chairperson: **Alexander Stark,** Research Institute of Molecular Pathology, Vienna, Austria

Reestablishing the epigenome in early mammalian development
Wei Xie [20’+10’]
Presenter affiliation: Tsinghua University, Beijing, China. 40

The role of facilitators in super-enhancers and gene regulation
Mira Kassouf [20’+10’]
Presenter affiliation: Weatherall Institute of Molecular Medicine, University of Oxford, Oxford, United Kingdom. 41

Mediator regulates transcriptional termination through crosstalk with pre-mRNA 3′ end processing factors
Gang Wang [10’+5’]
Presenter affiliation: Fudan University, Shanghai, China. 42

A computational genomics approach to characterize transcriptional condensates
Shengyuan Wang, Zhenjia Wang, Chongzhi Zang [10’+5’]
Presenter affiliation: University of Virginia, Charlottesville, Virginia. 43

De novo assembly and delivery of synthetic megabase-scale human DNA into mouse early embryos
Yue Liu, Yingjin Yuan [10’+5’]
Presenter affiliation: Tianjin University, Tianjin, China. 44

WEDNESDAY, October 22—9:00 AM

SESSION 4 EPIGENETIC MECHANISMS

Chairperson: **Mikko Taipale,** University of Toronto, Toronto, Canada

Macrophage remodeling links exercise to enhancer stability in the aging heart
Jack Clarke, Sam Bagot, Vaibhao Janbandu, David Zheng, Xueqian Zhuang, Yen Tran, Disha Anand, Alex Pinto, Lee Jones, Richard Harvey, Tuomas Tammela, Emily Wong [20’+10’]
Presenter affiliation: Victor Chang Cardiac Research Institute, Darlinghurst, Australia. 45

Decoding transcription, translation, and mRNA stability with massively parallel approaches
Srikar Gopinath, Haejeong Lee, Tami Gjorgjieva, Wilder Wohns, Ethan Strayer, Jonathan Pritchard, Antonio J. Giraldez [20’+10’]
Presenter affiliation: Yale University, New Haven, Connecticut. 46

Enhancer poising enables pathogenic gene activation by noncoding variants
Ethan W. Hollingsworth, Evgeny Z. Kvon [20’+10’]
Presenter affiliation: University of California, Irvine, Irvine, California. 47

Break

Epigenetic control of metabolic identity across cell types
Maria Pires Pacheco, Déborah Gerard, Riley J. Mangan, Alec R. Chapman, Dennis Hecker, Manolis Kellis, Marcel H. Schulz, Lasse Sinkkonen, Thomas Sauter [10’+5’]
Presenter affiliation: University of Luxembourg, Belvaux, Luxembourg. 48

Chromatin association and methylation sequencing
Falong Lu [10’+5’]
Presenter affiliation: Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China. 49

Human gene regulatory code encoded in nucleosome
Xin Zheng, Ying Tian, Jinyu Li, Xue Yue, Zhiyuan Xie, Ke Xu, Yimeng Yin [10’+5’]
Presenter affiliation: School of Medicine, Tongji University, Shanghai, China. 50

WEDNESDAY, October 22—1:30 PM

Visit to Old Suzhou

WEDNESDAY, October 22—7:00 PM

SESSION 5 GENE REGULATION IN DISEASE

Chairperson: **Evgeny Kvon,** University of California, Irvine, Irvine, California

Epigenomic rewiring of *Cis*-regulatory elements and retrotransposons in hepatocellular carcinoma
Danny Leung [20’+10’]
Presenter affiliation: Hong Kong University of Science and Technology, Hong Kong, China. 51

Plasma cf-EpiTracing reveals disease of origin and therapy response
Aibin He [20’+10’]
Presenter affiliation: Peking University Cancer Hospital & Institute, Peking University, Beijing, China; Peking-Tsinghua Center for Life Sciences, Peking University, Beijing, China; Peking University Chengdu Academy for Advanced Interdisciplinary Biotechnologies, Chengdu, China. 52

PKM2-mediated Histone lactylation alters three-dimensional genomic architecture in polycystic ovary syndrome
Hongbo Yang, Chuanjin Yu, Xinghui Guo, Xinmei Liu, Tingting Liu, Hefeng Huang [10’+5’]
Presenter affiliation: Fudan University, Shanghai, China. 53

pertTF models single-cell genetic perturbation responses during pancreatic development and type-2 diabetes
Yangqi Su, Vipin Menon, Dingyu Liu, Bicna Song, Danwei Huangfu, Wei Li [10’+5’]
Presenter affiliation: University of Maryland – Institute for Health Computing, North Bethesda, Maryland; University of Maryland School of Medicine, Baltmore, Maryland. 54

Gut microbiota-dependent gene regulation for liver disease
Chadmirah Zaratiana, Yiamunaa M, Yong-An Lee, Kazuyuki Kasahara, Torsten Wuestefeld, Poshen B. Chen [10’+5’]
Presenter affiliation: ASTAR, Singapore; National University of Singapore, Singapore. 55

THURSDAY, October 23—9:00 AM

SESSION 6 EMERGING TECHNOLOGIES

Chairperson: **Ting Wang,** Washington University School of Medicine, Saint Louis, Missouri, USA

Perturbing host cell pathways with pathogen effectors
Mikko Taipale [20’+10’]
Presenter affiliation: University of Toronto, Toronto, Canada. 56

A cross-biosample atlas of transcription factor binding sites from open chromatin and sequence-learned contribution scores
Zhiping Weng [20’+10’]
Presenter affiliation: University of Massachusetts Chan Medical School, Worcester, Massachusetts. 57

Coordinating histone traffic at the replication fork
Qing Li [20’+10’]
Presenter affiliation: Peking University, Beijing, China. 58

Break

Systematic real-time imaging of nascent RNA kinetics elucidates transcription bursting principles for dynamic genetic information flow
Danlin Xie, Xiangyu Wu, Lingling Li, Rui Sun, Hongjian Qi, Jiaqi Fan, Xibo Ma, Yanxiao Zhang, Yihan Wan [10’+5’]
Presenter affiliation: Westlake University, Hangzhou, China. 59

Single-cell multimodal chromatin profiling using S3Nano-CUT&Tag reveals regulatory dynamics during embryogenesis
Baekgyu Kim, Simone Procaccia, Eileen E. Furlong [10’+5’]
Presenter affiliation: European Molecular Biology Laboratory, Heidelberg, Germany. 60

Scalable profiling of native RNA-chromatin contacts by oligonucleotide-directed tagmentation
Guiping Wang, Howard Y. Chang, William J. Greenleaf [10’+5’]
Presenter affiliation: Stanford University School of Medicine, Stanford, California. 61

SPONSOR TALK

print("Hello, Discovery")—Twist Bioscience transforms code into biology
Julian Jude [15’+5’]
Presenter affiliation: Twist Bioscience, San Francisco , California. 62

THURSDAY, October 23—2:00 PM

SESSION 7 TRANSCRIPTION FACTORS AND COMPLEXES

Chairperson: **Emily Wong,** Victor Chang Cardiac Research Institute, Sydney, Australia

Overcoming confounders in high-content CRISPR screens on mosaic organoids
Silvia Domcke [20’+10’]
Presenter affiliation: University of Zurich, Zurich, Switzerland. 63

Building to understand—Enhancer-promoter communication in the context of regulatory landscapes
Christa Buecker [20’+10’]
Presenter affiliation: University of Vienna, Vienna, Austria. 64

Decoding transcriptional regulation
Alexander Stark [20’+10’]
Presenter affiliation: Research Institute of Molecular Pathology (IMP), Vienna, Austria. 65

Break

Distinct and compensatory roles for Stag1 and Stag2 in post-mitotic genome refolding
Manzhu Wang, Haoyue Zhang [10'+5']
Presenter affiliation: Shenzhen Bay Laboratory, Shenzhen, China. 66

Principles of synergistic gene regulation by transcription factors
Yuning Zhang, Michael Wilkinson, Jie Li, Jiayu Huang, Nina Tekkey, Mike A. White, Barak A. Cohen [10'+5']
Presenter affiliation: Washington University School of Medicine in St. Louis, St. Louis, Missouri. 67

KAS-CUT&Tag reveals RNA polymerase II oscillation regulates gene transcription and splicing
Weifang Wu, Kami Ahmad, Steven Henikoff [10'+5']
Presenter affiliation: Fred Hutchinson Cancer Center, Seattle, Washington. 68

THURSDAY, October 23—5:00 PM

COCKTAILS and BANQUET

FRIDAY, October 24—9:00 AM

SESSION 8 AI AND GENOMIC PREDICTIONS

Chairperson: **Wei Xie,** Tsinghua University, Beijing, China

Interpreting and designing regulatory DNA with deep learning
Peter Koo [20'+10']
Presenter affiliation: Cold Spring Harbor Laboratory, Cold Spring Harbor, New York. 69

NTv3—Joint sequence-function multi-species modeling at scale for long range genomic prediction
Thomas Pierrot [20'+10']
Presenter affiliation: InstaDeep, London, United Kingdom. 70

Beyond redundancy—Why does enhancer perturbation so often fail?
Jialiang Huang [10'+5']
Presenter affiliation: Xiamen University, Xiamen, China. 71

Break

Comprehensive functional assessment of NF1 and NF2 variants with high-resolution base editing screens
Jiayu Wu, Guangyu Li, Liheng Luo, Chenyu Ma, Shangqi Zhao, Xiaoyue Wang [10’+5’]
Presenter affiliation: Peking Union Medical College Hospital, Beijing, China. 72

Decoding gene regulation during zebrafish development using single-cell multiomics and deep learning
Jialin Liu, Sebastian Castillo-Hair, Lucia Du, Georg Seelig, Alexander Schier [10’+5’]
Presenter affiliation: Biozentrum, Basel, Switzerland; Allen Discovery Center for Cell Lineage Tracing, Seattle, Washington. 73

scHi-C enhancement via Graph Transformer unlocks high-resolutional 3D genomics and enhancer-driven GRN
Yuanyuan He, Kun Qian, Ruoqi Cheng, Ruibin Xi, Cheng Li [10’+5’]
Presenter affiliation: Peking University, Beijing, China. 74

Closing Remarks