

Abstracts of papers presented
at the 2026 Cold Spring Harbor Asia Conference

GENOME BIOLOGY: COMPUTATION, TECHNOLOGY & DISCOVERY

October 12–October 16, 2026

Arranged by

Christophe Dessimoz, *University of Lausanne*

Jing-Dong Jackie Han, *Peking University*

Jian Ma, *Carnegie Mellon University*

Chaolin Zhang, *Columbia University*



Cold Spring Harbor Conferences Asia
Cold Spring Harbor Laboratory



**GENOME BIOLOGY:
COMPUTATION, TECHNOLOGY & DISCOVERY**
Monday, October 12 – Friday, October 16, 2026

Monday	7:00 pm	1 Keynote Session
Tuesday	9:00 am	2 RNA and Post-Transcriptional Regulation
Tuesday	2:00 pm	Poster Session
Tuesday	7:00 pm	3 Single-cell and Spatial Multi-omics
Wednesday	9:00 am	4 Genome Biology and Disease
Wednesday	1:30 pm	<i>Visit to Old Suzhou</i>
Wednesday	7:00 pm	5 Genomic Variation, Function and Evolution
Thursday	9:00 am	6 Genome Organization, Epigenetics and Transcriptomics
Thursday	2:00 pm	7 AI and Machine Learning for Genome Biology
Thursday	5:00 pm	<i>Cocktails and Banquet</i>
Friday		<i>Departure</i>

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 12:00am - 1:30pm

Dinner: Main Cafeteria 6:00pm - 7:30pm

Banquet: Suz Garden 6:00 pm

More information will be available at CSHA office.

(Map at the end of this abstract book)

PROGRAM

MONDAY, October 12—7:00 PM

SESSION 1 KEYNOTE SESSION

Introduction by: Jian Ma, Carnegie Mellon University, Pittsburgh, Pennsylvania, USA

Human transcription factor footprint and discovery

Xiaoliang Sunney Xie [35'+10']
Changping Laboratory, Beijing, China

Introduction by: Jackie Han, Peking University, Beijing, China

AI and human immunology driven biotherapeutics

X. Shirley Liu [35'+10']
GV20 Therapeutics, Newton, Massachusetts.

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TUESDAY, October 13—9:00 AM

SESSION 2 RNA AND POST-TRANSCRIPTIONAL REGULATION

Chairperson: Zefeng Wang, Southern University of Science and Technology, Shenzhen, China

RNA secondary structure prediction—Language models, thermodynamics, and chemical probing

Mile Sikic [20'+10']
Presenter affiliation: ASTAR, Singapore; University of Zagreb, Zagreb, Croatia.

2

Regulation of gene expression through 3' end processing and transcriptional termination in the context of nuclear domain organization

Fengyi Ma, Heqiao Zhu, Qingbao Ding, Shan Yu, Bin Tian [20'+10']
Presenter affiliation: The Wistar Institute, Philadelphia, Pennsylvania.

3

LIFT enables single-cell T-cell clonal analysis and splice-derived neoantigen discovery by integrating long- and short-read sequencing

Mingxiang Li, Yichi Xu [10'+5']

Presenter affiliation: Fudan University, Shanghai, China.

4

Ku regulates Alu-mediated alternative splicing to safeguard primate transcriptome integrity with brain-specific adaptation

Jimin Yoon, Tianji Yu, Yimeng Zhu, Lin Huang, Shiqi Liu, Angelina Li, Brian J. Lee, Daniel F. Moakley, Mauro Modesti, Vincenzo A. Gennarino, Ke Zhang, Bing Yao, Liang Tong, Shan Zha, Chaolin Zhang [10'+5']

Presenter affiliation: Columbia University, New York, New York.

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Break

Foundation language model for RNA regulation

Hanwen Zhou, Zefeng Wang [20'+10']

Presenter affiliation: Southern University of Science and Technology, Shenzhen, China.

6

Reverse engineering and contextualizing neuronal splicing-regulatory networks

Chaolin Zhang [20'+10']

Presenter affiliation: Columbia University, New York, New York.

7

Single-cell profiling and genetic regulation of alternative polyadenylation in the human brain

Jiuhong Nan, Carles Boix, Shaohui Shi, Xushen Xiong [10'+5']

Presenter affiliation: Zhejiang University School of Medicine, Hangzhou, China.

8

Transcriptome reconstruction at single-cell resolution

Mingfu Shao [10'+5']

Presenter affiliation: The Pennsylvania State University, University Park, Pennsylvania.

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POSTER SESSION

Gpro 2.0—Generative AI toolkit for automated sequence design

Qixiu Du, Han Yu, Yixuan Zhi, Lei Wei, Xiaowo Wang

Presenter affiliation: Tsinghua University, Beijing, China.

10

Integrated methylome and transcriptome mapping reveals distinct epigenetic landscapes and repeat-element regulation in serrated versus conventional colorectal polyp

Anastasiya Kazachenka, Eoghan Mulholland-Illyingworth, Enbo Lyu,

Andrew Blake, Sura Atatri, Hayley Belnoue-Davis, David Church,

Simon Leedham

Presenter affiliation: University of Oxford, Oxford, United Kingdom.

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CluVar—Clustering of variants using autoencoder for inferring the phylogeny of cancer subclones in single cell RNA sequencing data

Chaewon Kim, Heewon Kim, Dohyeon Kim, Yuchang Seong, Minhae

Kwon, Junil Kim

Presenter affiliation: Soongsil University, Seoul, South Korea.

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De novo design of functional 5'UTRs with a generative RNA foundation model

Daoqian Li, Hanwen Zhou, Zefeng Wang

Presenter affiliation: Southern University of Science and Technology, Shenzhen, China.

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DSR-FOODIE enables high-resolution mapping of chromatin organization and transcription factor co-binding

Dubai Li, Jun Ren, Zhen Zhang, Xiaoliang a.. Xie

Presenter affiliation: Changping Laboratory, Beijing, China; Biomedical Pioneering Innovation Center, Beijing, China; Academy for Advanced Interdisciplinary Studies, Beijing, China.

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MoRe-CRE—Modular reconstruction of compact cis-regulatory elements with DenseLSTM2-guided cross-length prediction

Zhijie Li, Pengcheng Zhang

Presenter affiliation: Xiaowo Wang, Beijing, China.

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Mutational processes in the normal colorectal epithelium of individuals with and without colorectal cancer

Jiali Pang, William Knight, Nicolas Wyvekens, Yvette Hooks, Nick Coleman, Michael R. Stratton

Presenter affiliation: Wellcome Sanger Institute, Cambridge, United Kingdom.

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FOODIE maps transcription factor occupancy during early mouse development

Fangnong Lai, Yuxuan Pang, Muhong Xu, Jingzhi Zhang, Runsheng He, Yuan Yuan, Shuang Liu, Xuechen Zhao, Yinghui Zheng, Chunxian Yang, Ke Shen, Gang Li, Chen Xie, Fuchou Tang, Xiaoliang Xie

Presenter affiliation: Peking University, Beijing, China; Changping Laboratory, Beijing, China.

17

TransAAI—A multi-protein language model fusion framework for predicting nanobody-antigen interactions

Qiao Zhenghao, Liu Weiwei, Wang Ming, Wang Sheng, Yu Yang

Presenter affiliation: Guangzhou Medical University, Guangzhou, China.

18

A toxin-loaded EV-based functional screening platform for EV uptake and intracellular trafficking

Chaeyeon Song, Hunsang Lee

Presenter affiliation: Korea University, Seoul, South Korea; National Research Laboratory for Convergence Degradation Biology, Seoul, South Korea.

19

Decoding sequence recognition code of nucleic acid-binding proteins of human-infecting DNA viruses

Meifang Tang, Shifei Yang, Haiqian Ma, Ruoying Guo, Jie Chen, Hui Zhang, Jinghan Zhang, Wei Sun, Yun Wei, Ligang Fang, Jian Yan
Presenter affiliation: Northwest University, Xi'an, China; City University of Hong Kong, Hong Kong, China.

20

HDAC complex mediated epigenetic remodeling regulates human T helper cell differentiation

Longjun Yan, Xia Ran, Hongshan Guo, Yu Hou

Presenter affiliation: Zhejiang University School of Medicine, Hangzhou, China.

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Data-driven identification of cell subtypes for single-cell transcriptomic data with subtypist

Yue Yao, Xin Shao, Renjie Chen, Jingyang Qian, Han Gao, Yiyang Peng, Jie Gao, Xiaohui Fan
Presenter affiliation: Pharmaceutical Informatics Institute, College of Pharmaceutical Sciences, Zhejiang University, Hangzhou, China; State Key Laboratory of Chinese Medicine Modernization, Innovation Center of Yangtze River Delta, Zhejiang University, Jiaxing, China. 22

Iresearch—An RNA language model to predict IRES activity

Hanwen Zhou, Jiang Hu, Xiaonan Chen, Yun Yang, Zefeng Wang
Presenter affiliation: Southern University of Science and Technology, Shenzhen, China. 23

TUESDAY, October 13—7:00 PM

SESSION 3 SINGLE-CELL AND SPATIAL MULTI-OMICS

Chairperson: **Xiao Wang**, Broad Institute of MIT and Harvard, Cambridge, Massachusetts, USA

Seq2image—Concept and applications in genomic analysis

Kai Ye [20'+10']
Presenter affiliation: Xi'an Jiaotong University, Xi'an, China; Leiden University, Leiden, the Netherlands. 24

Translating spatial molecular atlas to brain function and dysfunction

Xiao Wang [20'+10']
Presenter affiliation: The Broad Institute, Cambridge, Massachusetts; MIT, Cambridge, Massachusetts. 25

Single-cell somatic mutation analyses reveal a source of missing heritability in Alzheimer's disease

Chengyu Li, Xiaoyu Shuai, Zexiang Zhou, Yanmei Dou, Xushen Xiong [10'+5']
Presenter affiliation: The Second Affiliated Hospital & Liangzhu Laboratory, Hangzhou, China. 26

Multi-omic dissection of human meningeal immunity in Alzheimer's disease and cognitive resilience

Yanling Wang [10'+5']
Presenter affiliation: Rush University Medical Center, Chicago , Illinois. 27

Scalable single-cell joint profiling of the DNA methylome, transcriptome and lineage histories in humans

Shou-Wen Wang [10'+5']

Presenter affiliation: Westlake University, Hangzhou, China.

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Biological heteropolymers, from physics and from data

Kyogo Kawaguchi [20'+10']

Presenter affiliation: RIKEN, Kobe, Japan; RIKEN, Kobe, Japan; The University of Tokyo, Tokyo, Japan.

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WEDNESDAY, October 14—9:00 AM

SESSION 4 GENOME BIOLOGY AND DISEASE

Chairperson: **Yin Shen**, University of California, San Francisco, USA

Linking disease-associated variants to function in neurons

Yin Shen [20'+10']

Presenter affiliation: University of California, San Francisco, San Francisco, California.

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Plasma proteomics reveal menopause as a systemic non-linear transition in female aging

Natàlia Pujol-Gualdo, Pau Clavell-Revelles, Tecla Duran-Fort, Oleksandra Soldatkina, Maria Sopena-Rios, Fairlie Reese, Kader Saribulak, Miguel Ángel Pérez-Elena, David Torrents, Marta Melé [10'+5']

Presenter affiliation: Barcelona Supercomputing Center (BCN-CNS), Barcelona, Spain.

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Multi-tissue genetic dissection of intronic polyadenylation reveals a distinct layer of cancer susceptibility

Le Wang, Xiaochuan Liu, Yang Yang [10'+5']

Presenter affiliation: Tianjin Medical University, Tianjin, China.

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CDK11 transcriptionally regulates DNA repair genes in liver cancer cells

Zhijian Kuang, Jack Wong [10'+5']

Presenter affiliation: The University of Hong Kong, Hong Kong, China.

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Break

May the force be with TCR

Wanlu Liu [20'+10']

Presenter affiliation: Zhejiang University School of Medicine, Hangzhou, China; Stanford University School of Medicine, Stanford, California. 34

Histone crotonylation is a novel epigenetic regulation and a therapeutic vulnerability for liver cancer treatment

Qidong Li, Xiaodan Zhang, Zhijian Kuang, For-Fan Chan, Chun-Ming Wong [10'+5']

Presenter affiliation: HKUMed, Hong Kong, China. 35

The paradoxical association of ERCC6L/PICH-related proliferation with favorable colorectal cancer outcomes

Dingyan Hu, Ying Wai Chan [10'+5']

Presenter affiliation: The University of Hong Kong, Hong Kong, China. 36

SynLethHub—An agentic AI platform for mechanism-resolved prioritization of synthetic lethal drug targets

Yimiao Feng, Jie Zheng [10'+5']

Presenter affiliation: ShanghaiTech University, Shanghai, China. 37

WEDNESDAY, October 14—1:30 PM

Visit to Old Suzhou

WEDNESDAY, October 14—7:00 PM

SESSION 5 GENOMIC VARIATION, FUNCTION AND EVOLUTION

Chairperson: **Maria Anisimova**, Zürich University of Applied Sciences, Zürich, Switzerland

Short tandem repeats (STRs) as drivers of diversity—Insights on evolution, populations and disease

Maria Anisimova [20'+10']

Presenter affiliation: Zürich University of Applied Sciences, Wädenswil, Switzerland; Swiss Institute of Bioinformatics, Lausanne, Switzerland. 38

**A scalable framework for ancestral genome reconstruction—
Gene content, order, and function**

Christophe Dessimoz [20'+10']

Presenter affiliation: University of Lausanne, Lausanne, Switzerland;
SIB Swiss Institute of Bioinformatics, Lausanne, Switzerland.

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**Long-read transcriptomics of a diverse human cohort reveals
widespread ancestry bias in gene annotations**

Fairlie Reese, Pau Clavell-Revelles, Sílvia Carbonell-Sala, Fabien Degalez, Carme Aman, Winona Oliveros, Emilio Palumbo, Tamara Perteghella, Roderic Guigó, Marta Melé [10'+5']

Presenter affiliation: Barcelona Supercomputing Center, Barcelona, Spain.

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Widespread structural variation at human chromosome ends

Kar-Tong Tan, Ryan Jun Xiang Ong, Brandon Bing Rui Kee, Russell Ker Han Yap, Alicia Jun Ting Ng, Gihan Kaushalya Rajapaksha, Max Garrity-Janger, Qiyu Lin, Jerome Chong Rui, Cin Thet Kyi, Matthew Meyerson, Heng Li [10'+5']

Presenter affiliation: National University of Singapore, Singapore;
Dana-Farber Cancer Institute, Boston, Massachusetts.

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Break

**From sequence likelihood to selection coefficients—Grounding
protein language models in human population genetics**

Yufeng Shen [20'+10']

Presenter affiliation: Columbia University, New York, New York.

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**Leveraging AI to decode the emergence of novel zoonotic viral
pathogens**

Tommy Lam [20'+10']

Presenter affiliation: The University of Hong Kong, Hong Kong SAR,
China; The Hong Kong Jockey Club Global Health Institute, Hong
Kong SAR, China.

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Perturb-Env—Towards a GxE map for virtual cells

Nuo Liu, Lishi Li, Ayush Midha, Brandon Chew, Airol A.. Ubas, Jesse Zhang, Nicole Thomas, Johnny Yu, Isha Jain, Hani Goodarzi [10'+5']

Presenter affiliation: Arc Institute, Palo Alto, California.

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SESSION 6 GENOME ORGANIZATION, EPIGENETICS AND
TRANSCRIPTOMICS

Chairperson: **Melissa Jane Fullwood**, Nanyang Technological
University, Singapore

(How) can we quantify transcripts accurately with long reads?

Kin Fai Au [20'+10']

Presenter affiliation: University of Michigan, Ann Arbor, Michigan.

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**Dynami-C identifies overlooked chromatin extrusion dynamics
associated with transcription and cancer progression**

Benjamin Lebeau, Crystal Chia Yin Ling, Fuying Dao, Udhaya

Vijayakumar, Melissa Jane Fullwood [20'+10']

Presenter affiliation: Nanyang Technological University, Singapore.

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**Physical properties of reconstituted gene-scale chromatin with
defined modification patterns**

Yohsuke T. Fukai, Tomoya Kujirai, Masatoshi Wakamori, Setsuko
Kanamura, Lisa Yamauchi, Somayeh Zeraati, Satoshi Morita, Chiharu
Tanegashima, Mitsutaka Kadota, Mikako Shirouzu, Hitoshi
Kurumizaka, Takashi Umehara, Kyogo Kawaguchi [10'+5']

Presenter affiliation: RIKEN, Kobe, Japan.

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**SQANTI-EPI—Quality control, benchmarking and regulatory-
element calling for single-molecule chromatin**

Tianyuan Liu, Virtudes Calabuig, Ana Conesa [10'+5']

Presenter affiliation: Institute for Integrative Systems Biology
(I2SysBio), CSIC-University of Valencia, Paterna, Spain; University of
Valencia, Burjassot, Spain.

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Break

**Digital tissue twins—Turning histology into spatial omics at
population scale**

Mingyao Li [20'+10']

Presenter affiliation: University of Pennsylvania, Philadelphia,
Pennsylvania.

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Decoding molecular programs across the human lifespan

Marta Melé [20'+10']

Presenter affiliation: Barcelona Supercomputing Center, Barcelona, Spain. 50

Strong cis-regulatory elements are systematically pleiotropic and evade current sequence-to-function models

Jingjing Chen, Minzhang Zheng, Yong Cheng [10'+5']

Presenter affiliation: St. Jude Children's Research Hospital, Memphis, Tennessee. 51

A paired short- and long-read single-cell atlas delineates isoform diversity in early human organogenesis

Fei Gao, Yichi Xu [10'+5']

Presenter affiliation: Fudan University, Shanghai, China. 52

THURSDAY, October 15—2:00 PM

SESSION 7 AI AND MACHINE LEARNING FOR GENOME BIOLOGY

Chairperson: **Martin Steinegger**, Seoul National University, Seoul, Korea

A generative AI framework unifies human multi-omics to model aging, metabolic health, and intervention response

Jingdong J. Han [20'+10']

Presenter affiliation: Peking University, Beijing, China. 53

Learning cellular organization and function across scales

Jian Ma [20'+10']

Presenter affiliation: Carnegie Mellon University, Pittsburgh, Pennsylvania. 54

Decoding the microbial iron-net from genome sequences

Zhiyuan Li [10'+5']

Presenter affiliation: Peking University, Beijing, China. 55

eScreen—A deep learning framework for functionally decoding the regulatory genome at single-nucleotide resolution

Jialiang Huang [10'+5']

Presenter affiliation: Xiamen University, Xiamen, China. 56

Break

Exploring the protein universe via multimers and motifs

Martin Steinegger [20'+10']

Presenter affiliation: Seoul National University, Seoul, South Korea. 57

DeepDETAILS, a deep-learning-based cross-modality deconvolution framework to reconstruct cell-type-specific multi-omic signals with base-pair precision

Li Yao, Sagar Shah, Abdullah Ozer, Yutong Zhu, Tianyu Xia, Xiuqi Pan, John Lis, Haiyuan Yu [20'+10']

Presenter affiliation: Cornell University, Ithaca, New York. 58

Flexible multimodal attention enables multiscale in silico perturbation of 3D genome organization

Yilin Jiang, Jiecong Lin, Weihang Chen, Peiran Jin, Yajie Zhao, Zeyu Chen [10'+5']

Presenter affiliation: Peking University Health Science Center, Beijing, China. 59

DeepD enables efficient genome modeling and controllable long-context sequence generation across domains of life

Beibei Xin, Zijian Wang, An Yu, Ziyang Chen, Yucheng Guo, Hainan Zhao, Jinsheng Lai [10'+5']

Presenter affiliation: China Agricultural University, Beijing, China. 60

THURSDAY, October 15—5:00 PM

COCKTAILS and BANQUET

FRIDAY, October 16

Departure