

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

# AI AND BIOLOGY

April 20–April 24, 2026

Arranged by

Stein Aerts, *VIB – KULeuven*

Maria Chikina, *University of Pittsburgh*

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Jian Zhou, *The University of Chicago*



Cold Spring Harbor Conferences Asia  
Cold Spring Harbor Laboratory



## AI AND BIOLOGY

Monday, April 20 – Friday, April 24, 2026

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Monday	7:00 pm	<b>1</b> Opening Perspectives in AI and Biology
Tuesday	9:00 am	<b>2</b> Regulatory Genomics I: Causal Models, Sequence Logic and Perturbation
Tuesday	2:00 pm	<b>Poster Session</b>
Tuesday	7:00 pm	<b>3</b> Cells: Single Cell Genomics, Epigenomics, and Networks
Wednesday	9:00 am	<b>4</b> Regulatory Genomics II: Variants, Chromatin and Disease
Wednesday	1:30 pm	<i>Visit to Old Suzhou*</i>
Wednesday	7:00 pm	<b>5</b> Spatial, Imaging and Neural Systems
Thursday	9:00 am	<b>6</b> RNA, Immune and Therapeutic Platforms
Thursday	2:00 pm	<b>7</b> Protein, Cryo-EM and Molecular Design
Thursday	5:30 pm	<i>Cocktails and Banquet</i>
Friday		<i>Departure</i>

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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, April 20—7:00 PM

## Opening Remarks

*Organizers welcome, thanks and logistics*

### SESSION 1      OPENING PERSPECTIVES IN AI AND BIOLOGY

**Chairperson:**      **Maria Chikina**, University of Pittsburgh, Pittsburgh, Pennsylvania, USA

#### **From molecules to machines—Building AI co-scientists to accelerate biomedical innovation**

Le Cong [20'+10']

Presenter affiliation: Stanford University School of Medicine, Stanford, California.

1

#### **On routes toward AI virtual cells**

Xuegong Zhang [20'+10']

Presenter affiliation: Tsinghua University, Beijing, China.

2

TUESDAY, April 21—9:00 AM

### SESSION 2      REGULATORY GENOMICS I: CAUSAL MODELS, SEQUENCE LOGIC AND PERTURBATION

**Chairperson:**      **Julien Gagneur**, Technical University of Munich, Munich, Germany.

#### **Scaling sequence-to-function models for regulatory variant interpretation**

Sara Mostafavi [20'+10']

Presenter affiliation: University of Washington, Seattle, Washington.

3

#### **Where does it hurt (in your genome)?**

Julien Gagneur [20'+10']

Presenter affiliation: Technical University of Munich, Munich, Germany.

4

**Causal *in vivo* perturbation data for biological foundation models**

Reuben A. Saunders, Xiaowei Zhuang, Jonathan S. Weissman

[10'+5']

Presenter affiliation: Harvard University, Cambridge, Massachusetts;  
Whitehead Institute, Cambridge, Massachusetts.

5

**Dissecting cell-type-specific regulatory grammar via reinforcement learning-guided generative optimization**

Wanjuan Bu, Mingqian Ma, Guoqing Liu, Yuxuan Liu, Yu He, Sizhen

Liu, Mo Xu, Haiguang Liu, Tao Qin, Zeyu Chen [10'+5']

Presenter affiliation: Peking University, Beijing, China.

6

**Break**

**Improving genomic deep learning with perturbation data**

Peter Koo [20'+10']

Presenter affiliation: Cold Spring Harbor Laboratory, Cold Spring  
Harbor, New York.

7

**Sequence-conditioned generative modeling for enrichment sequencing**

Mengjie Chen [20'+10']

Presenter affiliation: University of Chicago, Chicago, Illinois.

8

**Multi-ISM enables efficient *in silico* saturation mutagenesis of long-context sequence models**

Han Yuan, Xingfan Huang, Benjamin Auerbach, Divyanshi Srivastava,  
David Kelley [10'+5']

Presenter affiliation: Calico Life Sciences, LLC, South San Francisco,  
California.

9

**Towards a causality-oriented regulatory foundation model based on large-scale perturbation-free data**

Cheng Li, Zhi-Jie Cao, Jia-Chen Wei, Yi-Han Chen, Zi-Yu Chen, Ge  
Gao [10'+5']

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

10

**POSTER SESSION**

**An automated detection and removal system for purple seedlings in maize using UAV aerial imagery and deep learning**

Jia Cao

Presenter affiliation: China Agricultural University, Beijing, China.

11

**FastStack—An AI-guided strategy to develop future crops**

Chensong Chen, Dilani Jambuthenne, Dan Liu, Tara Garrard, Hari Dadu, Hugh Wallwork, Mark Maclean, Xuechen Zhang, Lisle Snyman, Lee Hickey, Kai P. Voss-Fels, Ben Hayes, Eric Dinglasan

Presenter affiliation: Queensland Alliance for Agriculture and Food Innovation (QAAFI), Brisbane, Australia.

12

**Cross-species Biomedical Cell Atlas**

Dongsheng Chen

Presenter affiliation: Suzhou Institute of Systems Medicine, Chinese Academy of Medical Sciences & Peking Union Medical College, Suzhou, China.

13

**Beyond the paradigm---When foundations aren't enough for spatial and single-cell omics**

Sally Chen, Roxana Zahedi, Lucy Chhuo, Ricky Nguyen, Marjan BaghGolshani, Amin Beheshti, Mark Grosser, Ahmadreza Argha, Youqiong Ye, Fatemeh Vafaei, Hamid Alinejad-Rokny

Presenter affiliation: BioMedical Machine Learning Laboratory, School of Biomedical Engineering, Randwick, Australia; School of Biotechnology and Biomolecular Sciences, Randwick, Australia.

14

**Decomposing multi-scale dynamic regulation from single-cell multiomics with scMagnify**

Xufeng Chen, Xi Yan, Bihan Shen, Heqi Wang, Zhixuan Tang, Yan Zang, Ping Lin, Haibing Zhang, Yu Li, Hong Li

Presenter affiliation: University of Chinese Academy of Sciences, Chinese Academy of Sciences, Shanghai, China.

15

**Rethinking diffusion models with symmetries through canonicalization with applications to molecular graph generation**

Cai Zhou, Zijie Chen, Zian Li, Jike Wang, Kaiyi Jiang, Pan Li, Rose Yu, Muhan Zhang, Stephen Bates, Tommi Jaakkola

Presenter affiliation: Zhejiang University, Hangzhou, China.

16

- Context-dependent single-cell and spatial multiomics reconstruction using SOARER**  
Xin Dong, Zijia Li, Chenfei Wang  
 Presenter affiliation: Tongji University, Shanghai, China; Sycamore Research Institute of Life Sciences, Shanghai, China. 17
- GAUGE—Geometry-aware unified grid embedding for standardized cross-sample spatial transcriptomics comparison**  
Tiannan Feng, Tao Zhou, Youzhe He, Lei Han, Zhenkun Zhuang, Shiping Liu  
 Presenter affiliation: University of Chinese Academy of Sciences, Beijing, China; BGI Research, Hangzhou, China. 18
- Spatiotemporal analyses of the pan-cancer single-cell landscape reveal widespread profibrotic ecotypes associated with tumor immunity**  
Ya Han, Qiu Wu, Chenfei Wang  
 Presenter affiliation: Tongji University, Shanghai, China. 19
- BindCraft-based design of functional binders targeting the KAT8**  
Junyang Huang, Shoudeng Chen  
 Presenter affiliation: Sun Yat-sen University, Zhuhai, China. 20
- 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. 21
- Multi-sample spatial transcriptomics analysis using deep learning-predicted spatial expression profiles in prostate cancer**  
Taewoo Jung, Marija Pizurica, Nele De Witte, Jo Van Dorpe, Piet Ost, Kathleen Marchal  
 Presenter affiliation: Ghent University, Ghent, Belgium. 22
- RVQ-Alpha—A unified understanding-generation framework for single-cell transcriptomics via discrete tokenization and chain-of-thought reinforcement learning**  
Guangpeng Li, Yue You, Luyi Tian  
 Presenter affiliation: Guangzhou National Laboratory, Guangzhou, China; South China University of Technology, Guangzhou, China. 23

**Genome-wide maps of transcription factor footprints identify noncoding variants rewiring gene regulatory networks with varTFBridge**

Jiecong Lin, Wenyang Dong, Jiaxiang Zhang, Chen Xie, Xiaoxi Jing, Junpeng Zhao, Kaiyan Ma, Hongen Kang, Yilin Jiang, Xiaoliang Sunney Xie, Yajie Zhao

Presenter affiliation: Changping Laboratory, Beijing, China.

24

**Exploiting spatially resolved virtual expression profiling for the development of spatially aware prognostic models**

Taewoo Jung, Marija Pizurica, Nele De Witte, Thomas Demeester, Olivier Gevaert, Jo Van Dorpe, Kim Van Der eecken, Piet Ost, Nicolaas Lumen, Sofie Verbeke, Jo Van Dorpe, Kathleen Marchal

Presenter affiliation: IDlab, Ghent, Belgium; CRIG, Ghent, Belgium.

25

**EasyLAMP—A machine learning-based platform for LAMP primer design**

Yicheng Qi, Yihuan Xu, Ruiguang Cai, Peixuan Li, Hugo Sámano-Sánchez

Presenter affiliation: Zhejiang University-University of Edinburgh Institute (ZJE), Haining, China; Edinburgh Medical School, Edinburgh, United Kingdom.

26

**Mapping enhancer-gene regulatory interactions from single-cell data**

Maya U. Sheth, Wei-Lin Qiu, X. Rosa Ma, Andreas R. Gschwind, Evelyn Jagoda, Anthony S. Tan, James Galante, Judhajeet Ray, Dulguun Amgalan, Hjörleifur Einarsson, Bram L. Gorissen, Danilo Dubocanin, Christopher S. McGinnis, Jacob Huang, Glen Munson, Kayla Brand, Jesse M. Engreitz, Robin Andersson

Presenter affiliation: The Novo Nordisk Foundation Center for Genomic Mechanisms of Disease, Cambridge, Massachusetts; Section for Computational and RNA Biology, University of Copenhagen, Denmark.

27

**High-resolution time-series ChIP-seq analysis of RNA polymerase II elongation rates using a hidden Markov model**

Junichi Sakatsume, Ryuichiro Nakato

Presenter affiliation: The University of Tokyo, Tokyo, Japan.

28

**PlasmidGPT—A generative framework for plasmid analysis and generation**

Bin Shao

Presenter affiliation: Beijing Institute of Technology, Beijing, China.

29

<b>Cellist—Accurate, scalable and cross-platform cell identification for high-resolution spatial transcriptomics</b>	
<u>Dongqing Sun</u> , Lele Zhang, Tong Han, Qiu Wu, Peng Zhang, Chenfei Wang	
Presenter affiliation: Tongji University, Shanghai, China.	30
<b>SPCoral—Diagonal integration of spatial multi-omics across diverse modalities and technologies</b>	
<u>Heqi Wang</u> , Jiao Yuan, Kunshi Li, Xufeng Chen, Xi Yan, Ping Lin, Zhixuan Tang, Baihua Wu, Haitao Nan, Yiwei Lai, Yuan Lv, Miguel A. Esteban, Lu Xie, Gangqi Wang, Lijian Hui, Hong Li	
Presenter affiliation: Shanghai Institute of Nutrition and Health, University of Chinese Academy of Sciences, Shanghai, China.	31
<b>Decoding human brain non-coding variants and gene regulation programs with single-cell genomics and deep learning</b>	
<u>Jinjing Wang</u> , Yuting Fu, Lina Zhou, Guoji Guo	
Presenter affiliation: Liangzhu Laboratory, Hangzhou, China.	32
<b>Semi-supervised deep learning on direct RNA sequencing drives comprehensive pan-epitranscriptomic discovery</b>	
Zhijun Ren, Wenbing Guo, <u>Jinkai Wang</u>	
Presenter affiliation: Sun Yat-sen University, Guangzhou, China.	33
<b>AI-guided molecular design for precision circuit gene therapy in Parkinson’s disease</b>	
<u>Ruiyu R. Wang</u> , Haiyue Zou, Jinquan Gao, Yu Zhou, Danwei Weng, Minmin Luo	
Presenter affiliation: Chinese Institute for Brain Research, Beijing, Beijing, China.	34
<b>Conventional self-supervised pretraining paradigm constrains the capacity of genomic language models on regulatory decoding</b>	
Ye-Xi Liang, <u>Yu Wang</u> , Wang-Yue Pan, Zi-Yu Chen, Jia-Chen Wei, Ge Gao	
Presenter affiliation: Changping Laboratory, Beijing, China.	35
<b>Quantifying the gene expression predictability of AI models from histological images</b>	
<u>Chen-Rui Xia</u> , Jia-Wen Yao, Ge Gao	
Presenter affiliation: Peking University, Beijing, China.	36

<b>DeepD—A biologically informed and efficient genome foundation model for interpretable prediction and controllable sequence design</b>	
<u>Beibei Xin</u> , An Yu, Ziyang Chen, Zijian Wang, Mingpei Zhang, Xiangde Hong, Fanghui Ge, Hainan Zhao, Jinsheng Lai	
Presenter affiliation: China Agricultural University, Beijing, China.	37
<b>Hi-READ—Integrating regional attention and conditional diffusion for regulator-directed genome architecture prediction and interpretation</b>	
Haonan Feng, Jing Wan, Shaohui Shi, <u>Xushen Xiong</u>	
Presenter affiliation: Zhejiang University, Hangzhou, China.	38
<b>Contrastive panel embedding with transformers enables cross-platform single-cell and spatial transcriptomics annotation</b>	
<u>Tian Xu</u> , Zexian Zeng	
Presenter affiliation: Peking-Tsinghua Center for Life Sciences, Beijing, China.	39
<b>Transcriptome regulation by NEIL2-dependent DNA G4-unfolding and methylation maintenance</b>	
<u>Mingyi Yang</u> , Adeel Manaf, Christine G. Neurauter, Junbai Wang, Magnar Bjoras	
Presenter affiliation: Oslo University Hospital, Oslo, Norway.	40
<b>A discrete token language of prokaryotic genomes learned by MicroVQVAE</b>	
<u>Haohong Zhang</u> , Kang Ning	
Presenter affiliation: Huazhong University of Science and Technology, Wuhan, China.	41
<b>A multimodal foundation model linking histology to spatial molecular programs for cancer biology</b>	
<u>Zongxu Zhang</u> , Zexian Zeng	
Presenter affiliation: Center for Quantitative Biology, Peking, China.	42
<b>Integrating spatial BCR repertoire and transcriptomics to predict therapeutically relevant antibodies via AI</b>	
<u>Yanping Zhao</u> , Zexian Zeng	
Presenter affiliation: Tsinghua University, Beijing, China.	43

**Cytoarchitectural profiling of white adipose tissue depots links serum amyloid a expressing adipocytes to immune cell activation**

Jutta Jalkanen, [Jiawei Zhong](#), Lucas Massier, Mikael Rydén, Niklas Mejhert

Presenter affiliation: Karolinska Institutet Huddinge, Stockholm, Sweden.

44

**stTransfer enables transfer single-cell annotation to spatial transcriptomics with single-cell resolution**

[Tao Zhou](#), TianNan Feng, ZhenKun Zhuang, ShiPing Liu

Presenter affiliation: University of Chinese Academy of Sciences, Beijing, China; BGI Research, HangZhou, China.

45

**Dissecting biological signals in protein language models through attention sub-component fine-tuning**

[Ziyan Zhuang](#), Qianyu Zhao, Shengfei Wang, Zifan Zhao

Presenter affiliation: Xinjiang University, Urumqi, China.

46

TUESDAY, April 21—7:00 PM

**SESSION 3** CELLS: SINGLE CELL GENOMICS, EPIGENOMICS AND NETWORKS

**Chairperson:** [Guoji Guo](#), Zhejiang University School of Medicine, Hangzhou, China

**Towards a regulatory language model for cells in silico**

[Ge Gao](#) [20'+10']

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

47

**Deciphering single-cell epigenomic language with EpiAgent**

[Rui Jiang](#) [20'+10']

Presenter affiliation: Tsinghua University, Beijing, China.

48

**Systematic discovery of protein-knowledge informed single-cell gene networks with Shusi**

Tianyun Zhang, Jiajun Yu, Shang Lou, Haishuai Wang, Shanshan Pei,

[Ning Shen](#) [10'+5']

Presenter affiliation: Zhejiang University, Hangzhou, China.

49

**Mapping and modeling cell landscapes using deep learning**

Guoji Guo [20'+10']

Presenter affiliation: Zhejiang University, Hangzhou, China.

50

**GFETM—Genome foundation-based embedded topic model for scATAC-seq modeling**

Yimin Fan, Yu Li, Jun Ding, Yue Li [10'+5']

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

51

**Cell2net—Mapping multi-scale and genotype-specific gene regulation using interpretable deep learning**

Zhijian Li, Jiecong Lin, Eugenio Mattei, Bradley Bernstein, Jason Buenrostro, Noam Shores, Luca Pinello [10'+5']

Presenter affiliation: Broad Institute of MIT and Harvard, Cambridge, Massachusetts; Massachusetts General Hospital, Cambridge, Massachusetts.

52

WEDNESDAY, April 22—9:00 AM

**SESSION 4** REGULATORY GENOMICS II: VARIANTS, CHROMATIN AND DISEASE

**Chairperson:** **Stein Aerts**, VIB-KULeuven, Leuven, Belgium

**Mechanism over scale—Building interpretable sequence-to-function models**

Maria Chikina [20'+10']

Presenter affiliation: University of Pittsburgh, Pittsburgh, Pennsylvania.

53

**Sequence-based regulatory code for heterogeneous and dynamic chromatin**

Jian Zhou [20'+10']

Presenter affiliation: University of Chicago, Chicago, Illinois.

54

**Simple yet effective—Basic population and evolutionary statistics contain richest information to infer systematic variant effects**

Zhengyuan Xue, Eleftheria Zeggini, Francesco Paolo Casale, Daniel Kotlarz [10'+5']

Presenter affiliation: Helmholtz Zentrum München, Neuherberg, Germany; Helmholtz Association, Munich School for Data Science, Germany.

55

**From foundation model to agentic workflow for context specific transcriptional regulation**

Yong Zhang [10'+5']

Presenter affiliation: Tongji University, Shanghai, China.

56

**Break**

**Modeling genome regulation using single-cell atlases**

Stein Aerts [20'+10']

Presenter affiliation: VIB, Leuven, Belgium.

57

**Linking cell identities to disease phenotypes using single-cell spatial multi-omics and AI**

Chenfei Wang [10'+5']

Presenter affiliation: Tongji University, Shanghai, China; Sycamore Research Institute of Life Sciences, Shanghai, China.

58

**Comprehensive IRES identification, directed mutation, and de novo generation using AI-driven methods**

Yanyi Chu, Di Yin, Dan Yu, Guangxue Xu, Junze Zhang, Xiaotong Wang, Ning Zhao, Yi Zhu, Yue Shen, Yupeng Li, Jason Zhang, Hani Goodarzi, Mengdi Wang, Le Cong [10'+5']

Presenter affiliation: Arc Institute, Palo Alto, California; Chinese Academy of Sciences, Shanghai, China.

59

**Development of a platform for high-throughput transcription factor characterization**

William Cheney, Omar Tariq, Carl de Boer [10'+5']

Presenter affiliation: University of British Columbia, Vancouver, Canada.

60

**Scooby—Modeling multimodal genomic profiles from DNA sequence at single-cell resolution**

Johannes C. Hingerl, Laura D. Martens, Alexander Karollus, Trevor Manz, Jason D. Buenrostro, Fabian J. Theis, Julien Gagneur [10'+5']

Presenter affiliation: Technical University of Munich, Munich, Germany.

61

WEDNESDAY, April 22—1:30 PM

**Visit to Old Suzhou**

**SESSION 5** SPATIAL, IMAGING AND NEURAL SYSTEMS

**Chairperson:** **Anna Kreshuk**, European Molecular Biology Laboratory, Heidelberg, Germany

**Context aware frameworks for multimodal integration and tissue dynamics**

Jovan Tanevski [20'+10']

Presenter affiliation: Heidelberg University, Heidelberg, Germany. 62

**Learning visual phenotypes**

Anna Kreshuk [20'+10']

Presenter affiliation: European Molecular Biology Laboratory, Heidelberg, Germany. 63

**Understanding tissue adaptability through spatial omics and graph learning**

Carlos Talavera-López [10'+5']

Presenter affiliation: GSK, Heidelberg, Germany. 64

**The neuroscience of prosocial behavior—From helping and cooperation to social AI**

Weizhe Hong [20'+10']

Presenter affiliation: University of California, Los Angeles, Los Angeles, California. 65

**Decoding organ morphology and disease mechanisms via AI-driven pan-organ imaging and multi-omics integration**

Fengyuan Hu, Boxing Liu, Chao Li, Quanli Wang, Slavé Petrovski [10'+5']

Presenter affiliation: AstraZeneca, Cambridge, United Kingdom. 66

**Transferable pixel embeddings for robust cross-modality cell instance segmentation and profiling**

Jingcheng Liu, Jing Zhang [10'+5']

Presenter affiliation: Beihang University, Beijing, China. 67

**SESSION 6** RNA, IMMUNE AND THERAPEUTIC PLATFORMS

**Chairperson:** **Qiangfeng Cliff Zhang**, Tsinghua University, Beijing, China

**AI-powered RNA-guided diagnostics for rare diseases**

Yi Xing [20'+10']

Presenter affiliation: The Children's Hospital of Philadelphia, Philadelphia, Pennsylvania; University of Pennsylvania, Philadelphia, Pennsylvania.

68

**Decoding RNA's functional logic for therapeutic discovery using a structure-informed AI approach**

Qiangfeng Cliff Zhang [20'+10']

Presenter affiliation: Tsinghua University, Beijing, China.

69

**Designing functional RNA sequences with conditional diffusion models**

Young-suk Lee [10'+5']

Presenter affiliation: KAIST, Daejeon, South Korea.

70

**Domain-informed vocabulary expansion in low-data settings enables epitranscriptome language modelling**

Alexandra Sneddon, Agin Ravindran, Aditya Sethi, Perlita Poh, Eduardo Eyra [10'+5']

Presenter affiliation: The Australian Research Council Centre of Excellence for the Mathematical Analysis of Cellular Systems, Canberra, Australia; EMBL Australia Partner Laboratory Network, Canberra, Australia.

71

**Break**

**Faster, better and antigen-informed TCR embedding for TCR repertoire analysis**

Bo Li [20'+10']

Presenter affiliation: Children's Hospital of Philadelphia, Philadelphia, Pennsylvania; University of Pennsylvania, Philadelphia, Pennsylvania.

72

Feng Yue [20'+10']

Presenter affiliation: Northwestern University, Chicago, Illinois.

**DigitalBrain—An AI framework for mapping functional gene dynamics in human brain aging and disease**

Meng Lu [10'+5']

Presenter affiliation: Peking University, Beijing, China.

73

**Agentic discovery of immune rejuvenators via deeply compressed multi-cellular foundation models**

Yue You, Guangpeng Li, Yunlin Fu, Xueying Fan, Luyi Tian [20'+10']

Presenter affiliation: Guangzhou Laboratory, Guangzhou, China.

74

THURSDAY, April 23—2:00 PM

**SESSION 7**      PROTEIN, CRYO-EM AND MOLECULAR DESIGN

**Chairperson:**    **Sergey Ovchinnikov**, Massachusetts Institute of Technology, Cambridge, Massachusetts, USA

**AI-empowered multi-objective optimization for human health**

Xiaoqing Gao [20'+10']

Presenter affiliation: Stanford University, Stanford, California.

75

**Cryo-IEF, a Cryo-EM foundation model enables fully automated structure determination**

Huaizong Shen [20'+10']

Presenter affiliation: Westlake University, Hangzhou, China.

76

**The genetic architecture of protein interaction domain families**

Guillaume Diss [10'+5']

Presenter affiliation: Friedrich Miescher Institute for Biomedical Research, Basel, Switzerland.

77

**Structure-guided landscape learning for sample-efficient de novo biomolecule optimization**

Yi Chai, Yang Li [10'+5']

Presenter affiliation: National University of Singapore, Singapore.

78

**Break**

**Geometric deep learning for protein design**

Jian Tang [20'+10']

Presenter affiliation: Mila-Quebec AI Institute, HEC Montréal, Canada.

79

**Using AI for protein structure prediction and design**

Sergey Ovchinnikov [20'+10']

Presenter affiliation: Massachusetts Institute of Technology,  
Cambridge, Massachusetts.

80

**FrustrAI-Seq—Scaling local energetic frustration to the protein sequence space**

Jan-Philipp Leusch, Miriam Poley-Gil, Miguel Fernandez-Martin, Nicola Bordin, Burkhard Rost, R. Gonzalo Parra, Michael Heinzinger [10'+5']

Presenter affiliation: Helmholtz Munich, Munich, Germany; Technical University of Munich, Munich, Germany.

81

**UNAAGI—Atom-level diffusion for generating non-canonical amino acid substitutions**

Han Tang, Andreas Bjerregaard, Nikolaj H. Hinnerskov, Wouter Boomsma [10'+5']

Presenter affiliation: University of Copenhagen, Copenhagen, Denmark.

82

THURSDAY, April 23—5:30 PM

**COCKTAILS and BANQUET**

FRIDAY, April 24

***Departure***