

PROGRAM

MONDAY, September 3—7:00 PM

SESSION 1 INTRINSIC DISORDER

Chairperson: **Yunlong Liu**, Indiana University School of Medicine,
Indianapolis, Indiana, USA

Keith Dunker.

Presenter affiliation: Indiana University School of Medicine,
Indianapolis, Indiana.

Predicting functional long non-coding RNAs validated by low throughput experiments

Bailing Zhou, Yuedong Yang, Jian Zhan, Xianghua Dou, Jihua Wang,
Yaoqi Zhou.

Presenter affiliation: Griffith University, Southport, Australia 1

Ligand design targeting intrinsically disordered proteins

Luhua Lai.

Presenter affiliation: Peking University, Beijing, China. 2

GC content bias in nucleic acids encoding for intrinsically disordered proteins is reduced by codon selection

Christopher J. Oldfield, Zhenling Peng, Vladimir N. Uversky, Lukasz Kurgan.

Presenter affiliation: Virginia Commonwealth University, Richmond, Virginia. 3

TUESDAY, September 4—9:00 AM

SESSION 2 RNA I

Chairperson: **Steven Brenner**, University of California, Berkeley,
Berkeley, California, USA

Identification of functional variants impacting splicing regulation

Yunlong Liu.

Presenter affiliation: Indiana University School of Medicine,
Indianapolis, Indiana. 4

Harness unintended nucleic acid mutation to targeted base editing

Xiao Wang, Ying Wang, Liqun Lei, Lijie Wang, Wei Xue, Bei Yang, Xingxu Huang, Jia Chen, Li Yang.

Presenter affiliation: CAS-MPG Partner Institute for Computational Biology, Shanghai, China.

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Full-length transcripts associated with splicing factor mutations in cancer

Cameron M. Soulette, Alison Tang, Jeltje van Baren, Eva Robinson, Kevyn Hart, Catherine J. Wu, Angela N. Brooks.

Presenter affiliation: University of California, Santa Cruz, Santa Cruz, California.

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The multiple facets of post-transcriptional regulation by non-coding RNAs

Hanah Margalit.

Presenter affiliation: The Hebrew University of Jerusalem, Jerusalem, Israel.

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TUESDAY, September 4—2:00 PM

SESSION 3 POSTER SESSION

An integrative bioinformatic tool for gene ontology characterization and construction of functional networks from OMICs-derived data—Application to the phosphoproteomic-based study of a signal transduction pathway

Eduardo Zúñiga-León, Ulises Carrasco-Navarro, Francisco Fierro.

Presenter affiliation: Universidad Autónoma Metropolitana, Cd. de México, Mexico.

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Differential regulation analysis reveals dysfunctional regulatory mechanism of cancer

Quanxue Li, Wentao Dai, Jixiang Liu, Yi-Xue Li, Yuan-Yuan Li.

Presenter affiliation: East China University of Science and Technology, Shanghai, China; Shanghai Center for Bioinformation Technology, Shanghai, China.

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- A novel class of 20-nucleotide piRNA predominantly expressed in human oocytes**
 Qiyuan Yang, Ronghong Li, Qifeng Lyu, Li Hou, Zhen Liu, Qiang Sun, Miao Liu, Huijuan Shi, Beiying Xu, Mingru Yin, Mofang Liu, Yiping Li, Ligang Wu.
 Presenter affiliation: Shanghai Institute of Biochemistry and Cell Biology, Shanghai, China. 10
- A comprehensive differential regulation analysis in liver hepatocellular carcinoma**
Jixiang Liu, Wentao Dai, Quanxue Li, Yuan-Yuan Li.
 Presenter affiliation: Shanghai Academy of Science & Technology, Shanghai, China. 11
- NSAIDs, their targets, off-targets and adverse reactions**
Tianyun Liu, Russ B. Altman.
 Presenter affiliation: Stanford University, Stanford, California. 12
- Mutational signatures reveal widespread exposure to mutagenic and nephrotoxic aristolochic acids in East Asia**
Steven G. Rozen, Alvin Wei Tian Ng, Arnoud Boot, Song Ling Poon, Mi Ni Huang, Jing Quan Lim, Patrick Tan, Sen-Yung Hsieh, Alex Yuang-Chi Chang, Jacob See-Tong Pang, Bin Tean Teh.
 Presenter affiliation: Duke-NUS Medical School, Singapore. 13
- Computational and conceptual challenges in mutational signature analysis**
Steven G. Rozen, Alvin Wei Tian Ng, Mi Ni Huang, Arnoud Boot, Yang Wu, Mo Liu.
 Presenter affiliation: Duke-NUS Medical School, Singapore. 14
- NPInter v4.0—A comprehensive database of noncoding RNA interactions**
Xueyi Teng, Xiaomin Chen, Hua Xue, Shunmin He, Runsheng Chen.
 Presenter affiliation: Key Laboratory of RNA Biology, Beijing, China; Center of Big Data Research in Health, Beijing, China. 15
- Computational ranking of mutant DNA polymerase basing on catalyzed activation energy barriers**
Zi Wang, Lin Wang, Yuliang Dong, Yue Zheng, Chongjun Xu.
 Presenter affiliation: BGI Research Institute, Shenzhen, China. 16

Evolution of an X-linked miRNA family predominately expressed in mammalian male germ cells

Fengjuan Zhang, Ying Zhang, Ligang Wu.

Presenter affiliation: Shanghai Institutes for Biological Sciences, Shanghai, China.

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NONCODEV5—A comprehensive annotation database for long non-coding RNAs

ShuangSang Fang, Lili Zhang.

Presenter affiliation: University of Chinese Academy of Sciences, Beijing, China; CAS Key Laboratory of RNA Biology, Beijing, China.

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A covalent link-based SpyCLIP platform for gel-free characterization of protein-RNA interactions

Ya Zhao, Yao Zhang, Yilan Teng, Kai Liu, Yanqing Liu, Weihua Li, Ligang Wu.

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

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TUESDAY, September 4—4:30 PM

Chinese Tea and Beer Tasting

TUESDAY, September 4—7:00 PM

SESSION 4 SYSTEMS

Chairperson: **Angela Brooks**, University of California, Santa Cruz, Santa Cruz, California, USA

Cell reprogramming

Owen Rackham, Jaber Firas, Yoshihide Hayashizaki, Jose Polo, Julian Gough.

Presenter affiliation: MRC, Cambridge, United Kingdom.

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Systemic analysis of the human gut microbiome and beyond

Peer Bork.

Presenter affiliation: EMBL, Heidelberg, Germany.

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Making intrinsic disorder prediction practical with quality assessment

Gang Hu, Zhonghua Wu, Christopher Oldfield, Chen Wang, Lukasz Kurgan.

Presenter affiliation: Virginia Commonwealth University, Richmond, Virginia.

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WEDNESDAY, September 5—9:00 AM

SESSION 5 PRECISION MEDICINE

Chairperson: **Hanah Margalit**, Hebrew University of Jerusalem, Jerusalem, Israel

From genomics To therapeutics—Uncovering and manipulating the genomic circuitry of human disease

Manolis Kellis.

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

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Informatics approaches to understand drug response

Russ B. Altman.

Presenter affiliation: Stanford University, Stanford, California.

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Interpreting newborn genomes

Steven Brenner.

Presenter affiliation: University of California-Berkeley, Berkeley, California.

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KEYNOTE SPEAKER

Using the phenome to build richer targets for gene discovery and translation

Nancy Cox.

Presenter affiliation: Vanderbilt University, Nashville, Tennessee.

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WEDNESDAY, September 5—1:30 PM

Visit to Old Suzhou

WEDNESDAY, September 5—7:00 PM

SESSION 6 RNA II

Chairperson: **Li Yang**, CAS-MPG Partner Institute for Computational Biology, Shanghai, China

Deciphering the function of single-nucleotide variants in the RNA

Esther Hsiao, Yiwei Sun, Jae Hoon Bahn, Boon Xin Tan, Xinshu Xiao.

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

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Towards a molecular anatomy of the human body

Roderic Guigó.

Presenter affiliation: Centre for Genomic Regulation (CRG), Barcelona, Catalonia, Spain.

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A-to-I RNA editing as a mechanism of gene regulation in *Drosophila* and humans

Jian Lu.

Presenter affiliation: Peking University, Beijing, China.

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CIRCpedia v2—An updated database for comprehensive CircRNA annotation and expression comparison

Rui Dong, Xu-Kai Ma, Guo-Wei Li, Li Yang.

Presenter affiliation: Shanghai Institute of Nutrition and Health, Shanghai Institutes for Biological Sciences, Shanghai, China.

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Virtual screening for nucleic acid aptamer

Qingtong Zhou, Liping Yang, Zhaofeng Luo, Suwen Zhao.

Presenter affiliation: iHuman Institute, Shanghai, China.

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THURSDAY, September 6—9:00 AM

SESSION 7 GENETIC VARIATION AND OMICS

Chairperson: **Julian Gough**, MRC Laboratory of Molecular Biology, Cambridge, United Kingdom

Founder events and burden of recessive diseases in South Asia

Kumarasamy Thangaraj.

Presenter affiliation: CSIR-Centre for Cellular and Molecular Biology, Hyderabad, India.

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Fine mapping and allelic heterogeneity

Eleazar Eskin.

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

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SVint, a light-weight tool for annotating structure variants located outside the coding genome

Jingqi Chen, Steven Brenner.

Presenter affiliation: University of California-Berkeley, Berkeley, California.

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KEYNOTE SPEAKER

Recent progress in omics science by The International FANTOM Consortium

Yoshihide Hayashizaki.

Presenter affiliation: RIKEN, Wako, Saitama, Japan.

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THURSDAY, September 6—2:00 PM

SESSION 8 STRUCTURE AND COMPUTATION

Chairperson: **Luhua Lai**, Peking University, Beijing, China

CATH functional families (FunFams)—Insights into impacts of genetic variations

Christine Orengo.

Presenter affiliation: University College London, London, United Kingdom.

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Detecting the tipping points of biological processes by dynamic network biomarkers

Luonan Chen.

Presenter affiliation: Key Laboratory of Systems Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, China.

The repertoire of mutational signatures in human tumours from the ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Network

Steven G. Rozen, Ludmil B. Alexandrov, Jaegil Kim, Nicholas Hardhvala, Mi Ni Huang, Avin Wei Tian Ng, Arnoud Boot, Kyle R. Covington, Dmitry A. Gordenin, Erik Bergstrom, Nuria Lopez-Bigas, Leszek J. Klimczak, Sandro Morganello, Radhakrishnan Sabarinahan, David A. Wheeler, Ville Mustonen, Gad Getz, Michael R. Stratton.
Presenter affiliation: Duke-NUS Medical School, Singapore.

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Novel algorithms for spatial modeling of cellular interactions in the tumor microenvironment

Yiyi Yan, Svetomir S. Markovic, Alexey Leontovich.

Presenter affiliation: Mayo Clinic, Rochester, Minnesota.

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Predictive modeling of primary resistance to androgen-deprivation in prostate cancer

Sukanya Panja, Sheida Hayati, Nusrat Epsi, James S. Parrott, Antonina Mitrofanova.

Presenter affiliation: Rutgers University, Newark, New Jersey; Rutgers University, New Brunswick, New Jersey.

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THURSDAY, September 6—6:00 PM

COCKTAILS and BANQUET

FRIDAY, September 7—9:00 AM

SESSION 9 STRUCTURE AND SYSTEMS

Chairperson: **Keith Dunker**, Indiana University School of Medicine, Indianapolis, Indiana, USA

Self-association primes proteins for new function—The role of altered dynamic properties

Shoshana J. Wodak, Michael Garton, karolina A. Mikulska-Ruminska, Ivet Bahar.

Presenter affiliation: VIB-VUB, Brussels, Belgium.

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Michal Linial.

Presenter affiliation: Hebrew University of Jerusalem, Jerusalem, Israel.

Harmonious diversity in GPCR activation mechanism

Qingtong Zhou, Suwen Zhao.

Presenter affiliation: ShanghaiTech University, Shanghai, China.

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Applying machine learning and optimization algorithms to the tyrosine and serine/threonine kinomes

Tomer M. Yaron, Jared L. Johnson, Charles J. Murphy, Olivier Elemento, Lewis C. Cantley.

Presenter affiliation: Meyer Cancer Center, New York, New York; Institute for Computational Biomedicine, New York, New York; Weill Cornell Medical College and Memorial Sloan Kettering Cancer Center, New York, New York.

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Membrane proteins with high N-glycosylation, high expression, and multiple interaction partners were preferred by mammalian viruses as receptors

Zheng Zhang, Zhaozhong Zhu, Yousong Peng.

Presenter affiliation: Hunan University, Changsha, China.

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