



Science Asia Conference 2021

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2021 ZGC FORUM
中关村论坛

3AS
北京国际学术交流会
2021
BEIJING INTERNATIONAL ACADEMIC EXCHANGE

中关村生命科学园
Zhongguancun Life Science Park

TIE国际创新走廊
Talents Innovation Ecosystem

SEPT 9-10, 2021

3rd Floor, No.4 Building, Medical Science and Technology Center,
Zhongguancun Life Science Park, Beijing



Website



WeChat

Welcome to Science Asia Conference

In 2021, The Science Asia conference, **Genome Biology and Disease**, is a hybrid one, with speakers and participants attending both virtually and in person. The conference accepts in-person registration for sessions at ZhongGuanCun Life Science Park (Beijing), and provides live streaming for online registrants on www.scienceasia.cn. Registrants who are viewing from China can also watch the broadcast on Bilibili (<https://live.bilibili.com/23068072>).

Genome Biology and Disease will highlight recent progress in understanding the three-dimensional organization of gene expression in the context of the genome. Speakers will discuss how this progress informs basic biology and is being translated into approaches for understanding and managing human disease.

The conference includes 14 academic presentations from world famous as well as up-and-coming scientists, a panel discussion, and sponsored talks from excellent enterprises and R&D centers located in Zhongguancun Life Science Park. Registrants are encouraged to leave questions to the speakers via the conference Q&A board (www.scienceasia.cn/index/QuestionAndAnswer/show.html).

Organizer

Science/AAAS

Strategic Partner

Beijing Municipal Science & Technology Commission, Administrative Commission of Zhongguancun Science Park

Partners

Zhongguancun Life Science Park

Talents Innovation Ecosystem

Agenda

Beijing Time	Day 1 - September 9, 2021	Beijing Time	Day 2 - September 10, 2021
	Opening		
08:50	Holden Thorp (Editor-in-Chief of the Science family of journals)		
09:00-09:40	Rohit Pappu Molecular grammar of protein and RNA molecules that governs the phase behavior of nuclear bodies	09:00-09:40	Jennifer Doudna CRISPR: The Science and Opportunity of Genome Editing
09:40-10:20	Jay Shendure Systematic reconstruction of the cellular trajectories of mammalian embryogenesis	09:40-10:20	Steve Henikoff Genome-wide mapping of protein-DNA interaction dynamics
10:20-10:40	Tea Break	10:20-10:40	Tea Break
10:40-11:20	Xiaohua Shen (cochair) A glimpse of the noncoding genomes in chromatin and transcription regulation	10:40-11:20	David Gilbert Regulation of Replication Timing and Chromosome Architecture
11:20-12:00	Jing-Dong J Han The Heterogeneity of Human Aging	11:20-12:00	Mofang Liu The roles of PIWI/piRNAs in gene expression and diseases
12:00-13:30	Lunch	12:00-13:30	Lunch
	Afternoon session		Afternoon session
		13:30-14:40	Speeches of Young Scientists
		14:50-15:30	Ada Yonath From origin of life to exploiting genetic code translation principles and cellular connective tissues for the design of next generation therapeutics
13:30-16:30	2021 ZGC Life Science Park Development Forum	15:30-16:10	YanLi Wang DNA/RNA cleavage by class 2 CRISPR-Cas systems
		16:10-16:50	Ying Liu Epigenetic codes modulate mitochondrial stress response
	Evening session, view online		Evening session, view online
19:20-20:00	Richard Young Nuclear Condensates in Gene Regulation and Disease	19:00-20:10	Panel session: Frontiers of Science Communication Joy Ma (Eurekalert) moderating Wensheng Wei/Dapeng Wang /Dennis Normile/Emily Therese Cloyd A panel of experts will look at current challenges, differences between China and the West, and future trends. Learn how to communicate effectively in a changing world!
20:00-20:40	Jennifer Phillips-Cremins Genome Folding, Unfolding, and Refolding in Neurological Disease	20:10-20:50	Victor G. Corces CTCF regulates the transgenerational transmission of epiphenotypes in mice
		20:50-21:00	Closing Keynote Xiaohua Shen (cochair)

Organizing Committee



Xiaohua Shen

Professor, Tsinghua University

Di Jiang

Senior Editor, *Science* / AAAS



Barbara R. Jasny

Deputy Editor Emerita (Ret) /
Independent Contractor, AAAS



Speakers (In alphabetical order)



Victor G. Corces

Professor, Human Genetics at the Emory University School of Medicine



Jennifer Doudna

Professor, University of California, Berkeley



David Gilbert

Senior Scientist at the San Diego Biomedical Research Institute



Jing-Dong Jackie Han

Professor, Peking University, College of Interdisciplinary Studies



Steve Henikoff

Professor, Fred Hutchinson Cancer Research Center



Mofang Liu

Professor, Shanghai Institute of Biochemistry and Cell Biology, CAS



Ying Liu

Professor, Institute of Molecular Medicine, Peking University



Rohit Pappu

Professor, McKelvey School of Engineering at Washington University



Jennifer E. Phillips-Cremins

Associate Professor, Engineering and Medicine at the University of Pennsylvania

Speakers (In alphabetical order)



Jay Shendure

Professor, Genome Sciences at
the University of Washington



Yanli Wang

Professor, Institute of Biophysics,
Chinese Academy of Sciences



Ada Yonath

Professor, Biomolecular Structures
at Weizmann Institute



Richard A. Young

Whitehead Institute for Biomedical
Research and MIT

Science Asia

Panelists (In alphabetical order)



Emily Therese Cloyd

Director, Center for Public
Engagement, AAAS



Joy Ma

Editorial Content Manager
at EurekAlert!



Dennis Normile

Contributing Correspondent
for *Science*



Dapeng Wang

Researcher, China Research Institute
for Science Popularization



Wensheng Wei

Professor, School of Life
Sciences at Peking University

Science Asia

Organizing Committee



Xiaohua Shen

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Xiaohua Shen received her Ph.D. at the University of Michigan and did the postdoctoral training with Stuart Orkin at Harvard Medical School. Xiaohua Shen is a Professor and a Cheung Kong Scholar in the School of Medicine at Tsinghua University. Her major research is to understand how the non-coding portions of the genome influence chromatin structure, gene expression, and stem-cell fate in development. In the past years, the Shen lab has rigorously investigated novel aspects of ncRNAs, genomic repeats, and RNA-binding proteins in the regulation of transcription and chromatin. Her work facilitates the functional inference of ncRNA genes, and brings about a paradigm-shifted understanding of genomic repeats and their associated transcripts in organizing the genome and the higher-order chromatin structure.

A glimpse of the noncoding genomes in chromatin and transcription regulation

Much of the developmental complexity and biodiversity of higher eukaryotes is thought to arise from gene regulation. RNA represents a hidden layer of regulatory information in complex organisms. I will discuss our recent progress in exploring fundamental functions of genomic repeats, noncoding RNA, and RNA-binding protein in the regulation of transcription and genome organization.

Organizing Committee



Di Jiang

Senior Editor, *Science* / AAAS
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Di Jiang went to Beijing Medical University (now PKUHSC), and then St. Mary's College of Maryland, where he obtained a Bachelor of Arts degree. He has a PhD in Genetics from the George Washington University. He studied molecular biology and immune system development in NIAID, NIH for his PhD thesis. He studied developmental genetics in NICHD, NIH and UCSB as a post-doctoral researcher. Di was a principle investigator in the Sars Center at University of Bergen, Norway, where his group studied cell biology of morphogenesis. From 2015-16, he was an editor at Cell Research in Shanghai. From 2017-2020, he edited for PLOS Biology in San Francisco. Currently he is a senior editor at Science editing papers in molecular biology, synthetic biology, biotechnology development.



Barbara R. Jasny

Deputy Editor Emerita (Ret) /
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Barbara Jasny has a PhD in molecular biology from Rockefeller University; she has conducted research in virus-host cell interactions, DNA replication, and cellular senescence. She joined Science magazine, the weekly journal of the American Association for the Advancement of Science (AAAS), in 1985. Until 2018 she solicited papers and evaluated research reports for publication in genetics, medicine, and computational social science. She is an elected fellow of the AAAS and has been an advisor to the American Society for Gene Therapy, the Functional Genomics Data Society, and the Nvating science in books, articles, posters, virtual presentations, CDs, and podcasts. Although she retired as a Deputy Editor Emeritus in 2018, Dr. Jasny continues to evaluate manuscripts and edit on a pro bono basis for the Institute of International Education and the Journal of Science Fiction.

Day 1 - September 9, 2021

Morning Session



Rohit Pappu

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Rohit Pappu is the Edwin H. Murty Professor of Engineering in the Department of Biomedical Engineering in the McKelvey School of Engineering at Washington University in St. Louis (WashU), USA. Pappu is also the Director of the Center for Science & Engineering of Living Systems (CSELS) at WashU. Pappu is a biophysicist who uses a blend of novel computations, polymer physics theories, and experiments to understand the workings of intrinsically disordered proteins and the physical principles that underlie spatial and temporal organization of cellular matter. Work in the Pappu lab has focused on systems that drive phase separation and percolation transitions, and one of the major goals is to design novel biomolecular condensates as a route to understanding how cellular decisions and phenotypes are controlled by condensates.

Molecular grammar of protein and RNA molecules that governs the phase behavior of nuclear bodies

This talk will present an overview and some details of the physical principles that connect information written into protein and RNA sequences that govern the driving forces for phase separation that gives rise to nuclear bodies with distinct compositional biases and material properties.

Day 1 - September 9, 2021

Morning Session



Jay Shendure

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Jay Shendure is an Investigator of the Howard Hughes Medical Institute, Professor of Genome Sciences at the University of Washington, Director of the Allen Discovery Center for Cell Lineage Tracing, and Scientific Director of the Brotman Baty Institute for Precision Medicine. His 2005 doctoral thesis with George Church included one of the first successful reductions to practice of next generation DNA sequencing. Dr. Shendure's research group in Seattle pioneered exome sequencing and its earliest applications to gene discovery for Mendelian disorders and autism; cell-free DNA diagnostics for cancer and reproductive medicine; massively parallel reporter assays, saturation genome editing; whole organism lineage tracing, and massively parallel molecular profiling of single cells. Dr. Shendure is the recipient of the 2012 Curt Stern Award from the American Society of Human Genetics, the 2013 FEDERAprijs, a 2013 NIH Director's Pioneer Award, the 2014 HudsonAlpha Life Sciences Prize, the 2018 Richard and Carol Hertzberg Prize for Technology Innovation, and the 2019 Richard Lounsbery Award from the National Academy of Sciences. He serves or has served as an advisor to the NIH Director, the US Precision Medicine Initiative, the National Human Genome Research Institute, the Chan-Zuckerberg Initiative and the Allen Institutes for Cell Science and Immunology. He received his MD and PhD degrees from Harvard Medical School in 2007.

Systematic reconstruction of the cellular trajectories of mammalian embryogenesis

Mammalian embryogenesis is characterized by rapid cellular proliferation and diversification. Within a few weeks, a single cell zygote gives rise to millions of cells expressing a panoply of molecular programs, including much of the diversity that will subsequently be present in adult tissues. Although intensively studied, a comprehensive delineation of the major cellular trajectories that comprise mammalian development in vivo remains elusive. Here we set out to integrate several single cell RNA-seq datasets (scRNA-seq) that collectively span mouse gastrulation and organogenesis. We define cell states at each of 19 successive stages spanning E3.5 to E13.5, heuristically connect them with their pseudo-ancestors and pseudo-descendants, and for a subset of stages, deconvolve their approximate spatial distributions. Despite being constructed through automated procedures, the resulting trajectories of mammalian embryogenesis (TOME) are largely consistent with our contemporary understanding of mammalian development. We leverage TOME to nominate transcription factors (TF) and TF motifs as key regulators of each branch point at which a new cell type emerges. Finally, to facilitate comparisons across vertebrates, we apply the same procedures to single cell datasets of zebrafish and frog embryogenesis, and nominate "cell type homologs" based on shared regulators and transcriptional states.

Day 1 - September 9, 2021

Morning Session



Jing-Dong Jackie Han

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of Interdisciplinary Studies**
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Prof. Jing-Dong Jackie Han obtained Ph.D. degree from Albert Einstein College of Medicine. She had her postdoctoral training at The Rockefeller University and Dana-Farber Cancer Institute. In 2004, she became an investigator/professor at the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences. In 2010-2019, she was a director of the CAS-Max Planck Partner Institute for Computational Biology. In 2019, she became a tenured professor at Peking University, and an adjunct professor at National University of Singapore. Her research focuses on the structure and dynamic inference of molecular networks, using a combination of large-scale experiments and computational analysis to explore the design principles of the networks and to find how the complex phenotypes, such as aging, cancer and stem cell development are regulated through molecular networks. She was awarded the NSFC Outstanding Young Scientist Award in 2006, and the Hundred Talent Plan Outstanding Achievement Award in 2009, selected as a Max Planck Follow in 2011 and a MaxNetAging Fellow in 2014, F1000 faculty in developmental biology in 2016.

The Heterogeneity of Human Aging

Aging is a systems level process and quantification requires systems level models. After searching for quantitative aging biomarkers and models at the epigenomic and transcriptomic levels, we have recently focused our attention on 3D facial images. Based on a small cohort, we generated the first comprehensive mapping of the aging human facial phenotype, and found quantitative facial features, such as eye slope and forehead size, highly associated with age. Even based on this small cohort, linear age predictors identified slow- and fast-agers that are significantly supported by health. By extending the study to a large Northern Chinese cohort of 5,000 people we can now use deep learning AI models trained on either chronological age or perceived age of the 3D facial images to more precisely estimate individuals' aging status. These models achieve an average difference between chronological or perceived age and predicted age of ± 2.8 years. We further profile blood transcriptomes from 280 individuals and infer the molecular regulators mediating the impact of lifestyles on facial aging speed through a causal inference model. Overall, we find that humans age with different rates both in the blood and in the face, but coherently, with heterogeneity peaking at middle age. Our study provides an example how artificial intelligence can be leveraged to determine perceived age of humans as marker of biological age, no longer relying on prediction errors to chronological age, and to estimate the heterogeneity of aging rates within a population. I will also share some of our newest results on the oral microbiota aging rate association and ethnic group differences on facial aging rate.

Day 1 - September 9, 2021

Evening Session



Richard A. Young

**Whitehead Institute for Biomedical
Research and MIT**
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Richard Young is a Professor at the Whitehead Institute and MIT. Dr. Young studies gene regulation in health and disease. He has served as an advisor to the World Health Organization, the National Institutes of Health and numerous scientific societies and journals. Dr. Young's honors include Membership in the National Academy of Sciences and Scientific American has recognized him as one of the top 50 leaders in science, technology and business. He has founded and advised companies in the biotechnology and pharmaceutical industry, and currently serves on the Board of Syros Pharmaceuticals, CAMP4 Therapeutics, Omega Therapeutics and Dewpoint Therapeutics. Dr. Young is also an aviator and holds a commercial pilot license. He received his PhD from Yale University.

Nuclear Condensates in Gene Regulation and Disease

Nuclear processes such as transcription, splicing and chromosome maintenance depend on the concerted action of many protein and RNA molecules. Recent studies have shown that many nuclear processes occur within biomolecular condensates, which compartmentalize the community of protein and RNA molecules involved in each process, typically at specific genomic loci. I will discuss the features of condensates that provide the cell with regulatory capabilities beyond canonical molecular regulatory mechanisms, note where these are dysregulated by pathological mutations, and explain how our new understanding of chemical partitioning is influencing the development of new therapeutic^s for cancer and other diseases.

Day 1 - September 9, 2021

Evening Session



Jennifer Phillips-Cremens

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Jennifer Phillips-Cremens, Ph.D. is an Associate Professor and Deans' Faculty Fellow in Engineering and Medicine at the University of Pennsylvania with primary appointments in the Departments of Bioengineering and Genetics. Dr. Cremens obtained her Ph.D. in Biomedical Engineering from the Georgia Institute of Technology in the laboratory of Andres Garcia. She then conducted a multi-disciplinary postdoc in the laboratories of Job Dekker and Victor Corces. Dr. Cremens now runs the 3-D Epigenomics and Systems Neurobiology laboratory at UPenn. Her primary research interests lie in understanding the long-range chromatin architecture mechanisms that govern neural specification and synaptic plasticity in healthy neurons and how these epigenetic mechanisms go awry in neurodevelopmental and neurodegenerative diseases. She has been selected as a 2014 New York Stem Cell Foundation Robertson Investigator, a 2015 Albert P. Sloan Foundation Fellow, a 2016 and 2018 Kavli Frontiers of Science Fellow, 2015 NIH Director's New Innovator Award, 2020 NSF CAREER award, and a 2020 CZI Neurodegenerative Disease pairs award.

Genome Folding, Unfolding, and Refolding in Neurological Disease

The Cremens Lab focuses on higher-order genome folding and how classic epigenetic modifications work through long-range, spatial mechanisms to govern synaptic plasticity in healthy and diseased neural circuits. Much is already known regarding how transcription factors work in the context of the linear genome to regulate brain development. Yet, severe limitations exist in our ability to engineer chromatin in neural circuits to correct synaptic defects in vivo. At the lab's inception, it remained unclear whether and how genome folding could functionally influence cell type-specific gene expression. We have developed and applied new molecular and computational technologies to discover that nested subTADs and long-range loops undergo marked reconfiguration during neural lineage commitment, somatic cell reprogramming, neuronal activity stimulation, and in repeat expansion disorders. We demonstrated that loops induced by neural circuit activation, engineered through synthetic architectural proteins, and miswired in fragile X syndrome were tightly connected to transcription, thus providing early insight into the genome's structure-function relationship. We are currently focused on understanding how, when, and why 3D genome folding patterns contribute to synaptic plasticity in neural circuits and synaptic dysfunction. Addressing this knowledge gap will provide an essential foundation for our long-term goal to engineer the 3D genome to reverse pathologic synaptic defects in debilitating neurological diseases.

Day 2 - September 10, 2021 Morning Session



Jennifer Doudna

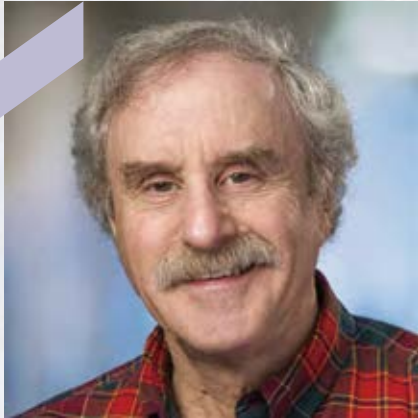
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Jennifer Doudna, PhD is a biochemist at the University of California, Berkeley. Her groundbreaking development of CRISPR-Cas9 — a genome engineering technology that allows researchers to edit DNA — with collaborator Emmanuelle Charpentier earned the two the 2020 Nobel Prize in Chemistry and forever changed the course of human and agricultural genomics research. She is also the founder and President of the Innovative Genomics Institute, the Li Ka Shing chancellor's chair in Biomedical and Health Sciences, and a member of the Howard Hughes Medical Institute, Lawrence Berkeley National Lab, Gladstone Institutes, the National Academy of Sciences, and the American Academy of Arts and Sciences. She is a leader in the global public debate on the responsible use of CRISPR and has co-founded and serves on the advisory panel of several companies that use the technology in unique ways. Doudna is the co-author of "A Crack in Creation," a personal account of her research and the societal and ethical implications of gene editing.

CRISPR: The Science and Opportunity of Genome Editing

Fundamental research to understand how bacteria fight viral infections uncovered the function of CRISPR-Cas programmable proteins that detect and cut specific DNA or RNA sequences. I will describe our research showing how CRISPR-Cas9, an RNA-guided protein, can be used for re-writing the DNA in cells and organisms to create a widely accessible technology for genome editing. Current research focuses on continuing to explore the biochemical basis for genome editing, and to develop effective applications in medicine and agriculture. I will also discuss the development of CRISPR-based diagnostics technology to address the current coronavirus pandemic and improve future preparedness.

Day 2 - September 10, 2021 Morning Session



Steve Henikoff

Fred Hutchinson Cancer Research
Center

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Steve Henikoff studies chromosomes, chromatin dynamics and epigenetics and develops genomics and computational tools to facilitate this research. He received a BS from the University of Chicago and a PhD from Harvard University and did post-doctoral work at the University of Washington. He has been a faculty member of the Fred Hutchinson Cancer Research Center since 1981. He is also an investigator of the Howard Hughes Medical Institute, an affiliate professor of Genome Sciences at the University of Washington, a member of the National Academy of Sciences and co-Editor-in-Chief of the open access journal *Epigenetics & Chromatin*.

Genome-wide mapping of protein-DNA interaction dynamics

We recently introduced new tools for high-resolution genome-wide chromatin profiling and have applied them to study chromatin organization and dynamics in a variety of model systems, including yeast, flies and mammals. CUT&RUN uses antibody-tethered Micrococcal Nuclease for mapping transcription factors, histone modifications and chromatin proteins in situ, providing low-cost high-resolution genome-wide maps. CUT&Tag similarly tethers the Tn5 cut-and-paste transposase that we have applied to low cell numbers and single cells with high efficiency and low backgrounds. We use these methods to address questions in chromatin biology including: How do transcription factors find their binding sites in DNA packaged into nucleosomes? How are nucleosomes depleted from gene regulatory regions? What is the relationship between nucleosome deposition pathways and chromatin deregulation in disease? Our findings illustrate ways in which chromatin dynamics can play a central role in regulating gene expression and silencing.

Day 2 - September 10, 2021 Morning Session



David Gilbert

**San Diego Biomedical Research
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David M. Gilbert currently leads the Laboratory of Chromosome Replication and Epigenome Regulation as a Senior Scientist at the San Diego Biomedical Research Institute (2021-present). Dr. Gilbert's work focuses on the mechanisms regulating DNA replication during the cell cycle and the relationship between DNA replication and structural and functional organization of chromosomes, most recently during differentiation in human and mouse embryonic stem cells and in pediatric leukemia. Dr. Gilbert received his BA degrees in Biochemistry/Cell Biology and Philosophy from the University of California at San Diego and his PhD in Genetics from Stanford University. He did two post-doctoral training periods, first as an EMBO Fellow with Pierre Chambon in Strasbourg, France studying transcriptional control, and second as a Roche Fellow with Melvin DePamphilis studying replication origin recognition. He joined the faculty at State University of New York (SUNY) Upstate Medical University in 1994 and was appointed Full Professor in 2003. In 2006, he moved to Florida State University where he served as J. Herbert Taylor Distinguished Professor of Molecular Biology in the Department of Biological Science and Co-founder and Associate Director of the Center for Genomics and Personalized Medicine at Florida State University (2006-2020). He was elected as a Fellow of the American Association for the Advancement of Science (AAAS) in 2008 and then elected as a Council Delegate of the AAAS in 2010, as well as to the American Society of Hematology in 2013 and the International Society for Stem Cell Research in 2014. Dr. Gilbert's other awards include the American Cancer Society Junior Faculty Research Award (2000), the SUNY President's Young Investigator Award (2002), the NIH Career Enhancement Award for Stem Cell Research (2004), Florida State University Distinguished Research Professor Award (2015), Florida State University Graduate Faculty Mentor award (2016) and the Pfeiffer Endowed Professorship for Cancer Research (2015). He is a former Principle Investigator in the NIH Encyclopedia of DNA Elements (ENCODE) Consortium (2011-2017), is a member of the NIH 4D Nucleome consortium and the Southeast Stem Cell Consortium (SESCC). He has served on American Cancer Society (1996 - 2004) and NIH study sections (1997 - present), is an editorial member of the Epigenetics Society and is on the editorial board of the Journal of Cell Biology (2008 - present) and has authored over 160 publications.

Regulation of Replication Timing and Chromosome Architecture

The mammalian genome is replicated in a defined temporal order in domains of several hundred kilobases that each complete replication in 40-60 minutes. Since chromatin is assembled at the replication fork, this is a critical time to maintain or alter chromatin composition of chromosome domains. Indeed, developmentally-programmed changes in replication timing during cell fate transitions affect at least half the genome, coordinated with changes in transcription, sub-nuclear position, chromatin structure and 3D architecture. I will summarize our current understanding of the cis- and trans-regulation of this program, causal relationships between these closely correlated structural and functional features of chromosome domains, and the consequences of disrupting the replication timing program.

Day 2 - September 10, 2021 Morning Session



Mofang Liu

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and Cell Biology, Chinese Academy
of Sciences

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Dr. Mo-Fang Liu is the Professor and Principal Investigator in Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences (CAS). She received her Bachelor and Master's degree in Biochemistry from East China University of Sciences and Technologies, Shanghai, in 1991 and 1994, respectively. She obtained her Ph.D degree from Shanghai Institute of Biochemistry, CAS, in 2000. From 2000 to 2006, she was a postdoctoral fellow in National Cancer Institute, NIH, and then as a research assistant in Johns Hopkins University School of Medicine. She joined in Shanghai Institute of Biochemistry and Cell Biology in 2006. The major research interests in her group are the roles and mechanisms of small noncoding RNAs, including PIWI-interacting RNAs (piRNAs) and microRNAs (miRNAs). The goals of ongoing projects in the laboratory are to gain new insights into the physiological and pathological roles of small noncoding RNAs in mammal spermatogenesis, human male infertility, and cancers.

The roles of PIWI/piRNAs in gene expression and diseases

PIWI proteins and their interacting piRNAs are specifically expressed in animal germlines and play essential roles during gametogenesis in animals. The primary function of PIWI/piRNAs are to silence transposable elements to protect the genome integrity in animal germlines, whereas they are also involved in regulating protein-coding genes in animal germ cells. In particular, we show that mouse PIWI (MIWI) piRNA plays a dual role in regulating target mRNAs in mouse spermatids through interacting with different co-factors, including translationally activating a subset of ARE-containing mRNAs in round spermatids and inducing massive mRNA degradation in late spermatids. By sequencing human Piwi (Hiwi), we identified multiple Hiwi mutations in infertile patients and further demonstrated that such mutations play causative roles in male infertility, indicating Piwi as a factor in human infertility. Moreover, we reported that PIWI, which is aberrantly expressed in human tumors, functions as an oncoprotein in a piRNA-independent manner in cancer cells.

Day 2 - September 10, 2021 Afternoon Session



Ada Yonath

Weizmann Institute of Science
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Ada Yonath is focusing on the translation of the genetic code to proteins by ribosomes, on antibiotics hampering this process, on human diseases associated with ribosomal mutations and on origin of life. She initiated these studies despite persistent global skepticism, and introduced forefront key scientific developments, which became the common routine within a few months.

She is Directing the Kimmelman Center for Biomolecular Structures at Weizmann Institute (WIS), where she got her PhD and is currently a Professor. She postdoced in Carnegie Mellon, MIT and U. Chicago. In the seventies, she established at WIS the first structural-biology laboratory in Israel, which was the only one in the country for almost a decade. During 1986-2004 she headed Max-Planck-Research-Unit-for Ribosome-Structure in Hamburg, in parallel to her WIS activities.

Among others, she is a member of US-National Academy; British Royal Society; Israel Academy; German Leopoldina; Pontificia Accademia-delle-Scienze (Vatican); Japanese, Korean, Italian and European Academies, and holds honorary doctorates from over 45 Universities worldwide. Her awards include Louisa-Gross-Horwitz, Wolf, Harvey & Israel prizes; Linus-Pauling Gold Medal; UNESCO/L' Oreal Award; Albert-Einstein Award for Excellence; and 2009 Chemistry Nobel Prize.

From origin of life to exploiting genetic code translation principles and cellular connective tissues for the design of next generation therapeutics

Illuminating architectural principles of the dynamic genetic code translation process, alongside the plausible variability of cellular connective tissues led to the design of unique translatable mRNA-collagen constructs, designed for controllable protein synthesis.

Similarly, in principle, structural analyses of diseases associated with genetically mutated human ribosomes should shed light on specific translation properties and specific biological pathways. Thus hints for novel the therapeutical platforms can be provided.

Parallel studies identified the ribosomal internal active pocket that provides the stereochemistry for peptide bond formation, which seems to represent a prebiotic synthetic machinery.

Day 2 - September 10, 2021 Afternoon Session



Yanli Wang

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Yanli Wang is a professor in Institute of Biophysics, Chinese Academy of Sciences, and a HHMI International Research Scholar. Prof. Wang has completed her PhD from University of Science and Technology of China and postdoctoral studies from Memorial Sloan-Kettering Cancer Center. Prof. Wang's group interests in understanding how small regulatory RNA or DNA mediates prokaryotic defense against invasion by foreign nucleic acids. The main focus of her work is to systematically demonstrate the mechanisms of the CRISPR-Cas system, and Ago protein-mediated DNA interference.

DNA/RNA cleavage by class 2 CRISPR-Cas systems

Class 2 CRISPR-Cas systems are further divided into types II, V and VI. Type II CRISPR-Cas9 protects bacterial hosts against invasive nucleic acids and also provides a revolutionary RNA-guided genome-editing platform. We reported the structural analyses of Cas9 in multiple functional conformations, including pre-catalytic state, catalytically activated state, and post-cleavage state. In the catalytic state, the catalytic residues of HNH domain are poised close to the cleavage site of the target DNA, explaining why the HNH domain cleaves target strand between nucleotides 3 and 4. In type VI, Cas13a exhibits both target and "collateral" cleavage upon target RNA binding. We report a series of structures of Cas13 in complex with crRNA and its complementary target strand. Our studies revealed how Cas13 proteins defend against RNA phages, and the mechanistic insights of Cas13 likely expand the possible application of Cas proteins.

Science Asia

Day 2 - September 10, 2021

Afternoon Session



Ying Liu

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CURRICULUM VITAE

EDUCATION (In reverse chronological order from latest to earliest including postdoctoral training)

Degree	Year	Major	Institution	Mentor
Postdoc	2011-2013	Genetics	Massachusetts General Hospital & Harvard Medical School	Gary Ruvkun
Ph.D.	2006-2011	Biochemistry	UT Southwestern Medical Center	Qinghua Liu
B.S.	2002-2006	Biochemistry	Nanjing University, China	

PROFESSIONAL APPOINTMENTS

Year	Position	Institution
2021.2-present	Professor	Institute of Molecular Medicine, College of Future Technology, Peking University
2020.12-present	Associate Dean	College of Future Technology, Peking University
2020.1-present	Vice Director	Institute of Molecular Medicine, Peking University
2019.8-2021.1	Associate Professor	Institute of Molecular Medicine, Peking University
2017-2022	HHMI International/ Research Scholar	Howard Hughes Medical Institute
2013.12-2019.7	Assistant Professor	Institute of Molecular Medicine, Peking University

HONORS AND AWARDS

Year	Honors and Awards
2019	Xplorer Prize
2019	National Science Fund for Distinguished Young Scholars
2019	15th China Young Female Scientist Award
2019	Young Investigator Award, Chinese Society for Cell Biology
2018	"Innovators under 35, CHINA" , MIT Technology Review
2017	HHMI International Research Scholar
2012-2014	Helen Hay Whitney Research Fellowship
2011	Nominata Award, UT Southwestern Medical Center
2010	Stanford Biochemistry Founders' Award for Doctoral Excellence

Epigenetic codes modulate mitochondrial stress response

The ability to detect, respond and adapt to mitochondrial stress ensures the development and survival of organisms. *Caenorhabditis elegans* responds to mitochondrial stress with induction of the mitochondrial unfolded protein response (UPR^{mt}), a surveillance program that monitors mitochondrial function and buffers the mitochondrial folding environment. Activation of UPR^{mt} also rewires the metabolic state, promotes innate immunity and lifespan extension. Our recent work has revealed that histone and DNA modifications play critical roles in modulating UPR^{mt} and UPR^{mt}-mediated innate immunity and longevity. Future genetic or pharmacological treatments to target these pathways may provide therapeutic potential for the treatment of mitochondrial diseases.

Science Asia

Day 2 - September 10, 2021 Evening Session



Victor G. Corces

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of Medicine

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Dr. Corces is a professor of Human Genetics at the Emory University School of Medicine. Research in Dr. Corces' laboratory studies the mechanisms by which the three-dimensional organization of the chromatin is established and maintained. His current research focuses on understanding the mechanisms by which the environment alters the epigenome of germline cells and how these epigenetic alterations can be transmitted from the gametes to the embryo after fertilization to cause disease states that can be passed on to subsequent generations. He has published extensively in the area of epigenetics and genomics, with a recent focus on the 3D organization of the nucleus of egg and sperm and the mechanisms of transgenerational inheritance of epiphenotypes.

CTCF regulates the transgenerational transmission of epiphenotypes in mice

The mechanisms by which epiphenotypes are transmitted trans-generationally through the parental germlines in mammals are poorly understood. Exposure of pregnant mouse F0 females during E7.5-E13.5 to bisphenol A results in obesity in the F2 progeny in the absence of additional exposure. This epiphenotype can be transmitted through the male and female germlines up to the F5 generation, decreases in F6, and disappears in F7. Analyses of chromatin changes in the sperm of the F1 generation reveal a widespread increase in chromatin accessibility at binding sites for CTCF and other transcription factors accompanied by alterations in 3D organization. Comparison of the transmission of obesity between F2 and F5 and its disappearance in F7 with alterations in the binding of these transcription factors points to the recruitment of CTCF to a new site located in an intron of the *Fto* gene and activation of two different enhancers. Deletion of the CTCF site using CRISPR-Cas9 results in mice that fail to gain weight after ancestral BPA exposure. Based on observations from Hi-C data, we suggest that the two enhancers form an autoregulatory feedback loop that, in combination with a decrease of m6A in sperm enhancer RNAs, may cause alterations of gene expression in the embryo after fertilization. Given the established involvement of SNPs in *FTO* in human obesity, the results suggest that both genetic and epigenetic alterations of the same gene can lead to the same phenotypic outcomes on human health.

Panel Discussion



Emily Therese Cloyd

**Center for Public Engagement,
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Emily Therese Cloyd is the Director of the American Association for the Advancement of Science Center for Public Engagement with Science and Technology. Emily oversees all Center programming, including the AAAS How We Respond project, the AAAS Leshner Leadership Institute and the Communicating Science program. Prior to joining AAAS in 2016, Emily led engagement and outreach for the U.S. Global Change Research Program and the Third National Climate Assessment, served as a Knauss Marine Policy Fellow at the National Oceanic and Atmospheric Administration, and studied the use of ecological models in Great Lakes management. She holds an Executive Certificate in Nonprofit Leadership & Management (University of Notre Dame), a Master's in Conservation Biology (SUNY College of Environmental Science and Forestry) and a Bachelor's in Plant Biology (University of Michigan). Emily enjoys paddling on the Potomac and Anacostia Rivers, especially in a dragon boat, and is slowly section hiking her way along the Appalachian Trail. Follow her on Twitter @EngageClimate.



Joy Ma

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Joy Ma is Editorial Content Manager at EurekAlert!, the non-profit science news-release distribution service operated by the American Association for the Advancement of Science (AAAS). Joy's main area of focus is increasing the diversity of the content sources on EurekAlert!, especially from countries and regions with high-volume and high-quality scientific research output but relatively low levels of science communication. Since 2015, she has helped dramatically increase the number of news releases available to science journalists through EurekAlert! from top institutions in China, Japan, and Korea by training and coaching new press officers and through strategic outreach. Before joining AAAS, she worked for NPR and the Penguin Group. She is a recipient of the Alfred I. duPont-Columbia University Award for NPR's coverage of the Chengdu Earthquake and winner of a Foreign Press Association Scholarship Award. Ms. Ma earned an M.A. in journalism from the Columbia University Graduate School of Journalism.

Panel Discussion



Dennis Normile

Science/AAAS

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Dennis Normile has been a contributing correspondent for *Science* since 1995, reporting on government science policy, trends within the scientific community, and the latest experimental results throughout the Asia-Pacific region. Normile wrote extensively about the avian influenza crisis in the mid-2000s, reporting from Thailand, Vietnam and China. He has written numerous stories about the Tohoku, Japan, earthquake, tsunami and nuclear plant meltdown of March 2011, focusing on scientific aspects of the calamity. His coverage of China includes recent stories on the Five-hundred-meter Aperture Spherical radio Telescope (FAST) in Guizhou Province, China's missions to the Moon and Mars, and the COVID-19 pandemic. Normile's articles have also appeared in *The New York Times*, the *Far Eastern Economic Review*, the *Financial Times* (UK), and other publications.



Dapeng Wang

China Research Institute for
Science Popularization

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WANG Dapeng, who is a researcher in CRISP(China Research Institute for Science Popularization) dedicating to science communication in China for more than 10 years. His interest is very broad, and mainly focus on the relationship between scientists and media, communicating science through new media-such as microblog (weibo), blog, Wechat, etc., the theory and practice of science communication in China. During the past few years, he published some journal papers in the field of science communication, and also he wrote more than 100 comments on newspaper and translated nearly 10 books. He is a media-savvy science communicator.

Panel Discussion



Wensheng Wei

School of Life Sciences at Peking University

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Professor of Biomedical Pioneering Innovation Center, Peking-Tsinghua Center for Life Sciences, and School of Life Sciences at Peking University; and the director of Peking University Genome Editing Research Center. The research of Wei group is mainly focused on the development of eukaryotic gene editing tools, with the emphasis on the high-throughput functional genomics and gene therapy. The combination of forward and reverse genetic means are employed, often in a high-throughput fashion, for the understanding of the molecular mechanisms underlying human diseases, including cancer and infection.

Science Asia



Organizer

Science



The American Association for the Advancement of Science (AAAS) is the world's largest multidisciplinary scientific society and a leading publisher of cutting-edge research through its *Science* family of journals. AAAS seeks to "advance science, engineering, and innovation throughout the world for the benefit of all people", it serves individual members in more than 91 countries around the globe.

Science has long been one of the most credible and trusted sources of information for scientists around the world since its founding in 1880 with seed money from Thomas Edison. Published by the not-for-profit AAAS, *Science* and its growing family of journals continue to set the standard for original research and news content that scientists have come to depend on. *Science* is a weekly publication, with a worldwide print circulation of nearly 130,000 and over 14 million pageviews to *Science* online each month. *Science* readers are educated and engaged. The audience of *Science* is composed of some of the brightest thinkers, scholars, researchers, politicians, and students in the world.

Science Asia

Strategic Partner



ZGC FORUM
中关村论坛

Since 2007, ZGC Forum (hereinafter referred to as "the Forum"), with the permanent theme of "innovation and development", has been held for 11 sessions with the aim to be built as an international platform for scientific and technological innovation, exchange and cooperation, which integrates scientific and technological exchanges and the display, release and trading of innovative achievements.

ZGC Forum is positioned to serve the national innovation and development strategy and the construction of Beijing Science and Technology Innovation Center. Centered on scientific and technological innovation, the Forum is intended to promote comprehensive innovation and serve the whole chain of science, technology, products and market. With the commitment to establish the communication platform for innovative ideas and new concepts, the leading platform for new science and technology and industry, and the releasing and trading platform for the new technologies and products, and the sharing platform for innovation rules and innovation governance, the Forum aims to build a high-level and comprehensive international technology cooperation platform, and strives to become a state-level major event for integration into international innovation network on behalf of China, in-depth involvement into global innovation governance, and promotion of international right of speech.

Targeting the permanent theme of "innovation and development", the Forum is held to focus on the frontier and hotspot issues on international science and technology innovation, set up different topics each year, invite the world's top scientists, leading entrepreneurs and cutting-edge entrepreneurs to participate, who share in-depth ideas on innovation with each other, attract extensive attention in the field of scientific and technological innovation and main bodies of innovation and entrepreneurship, continuously spread new ideas, refine new models, and guide new development.



BAS 2021
北京国际学术交流季
BEIJING INTERNATIONAL ACADEMIC SEASON

Beijing International Academic Season is a series of high-end brand academic exchange activities organized by the Beijing Municipal Commission of Science and Technology with the support of the Beijing Government.

In accordance with the principle of focusing on academic research, gathering the world's top scientists and deep-level multi-angle discussion, Beijing International Academic Season will build a platform for the extensive exchange of international scientific and technological circles in the frontier areas of the foundation, and help Beijing build a globally influential science and technology innovation center.

The Beijing International Academic Season organizes high-level academic series exchange activities around the basic frontiers of quantum science, graphene, brain science, medical health, and nanotechnology.

Partner



Founded in 2000, ZGC Life Science Park located between G6 and G7 expressway, on the north of Beijing Road, Changping District, is an important part of ZGC National Independent Innovation Demonstration Zone, and is a hi-tech science park engaged in life sciences, biotechnology and biomedical research.

The park has over 500 enterprises in life science field, including Novo Nordisk, Yangtze River Pharmaceutical Group, Wantai BioPharm, Mindray, CapitalBio, BeiGene, Shenogen, Berry Genomics, etc. and has attracted topnotch scientists such as Wang Xiaodong, He Fuchu, Shi Yigong, Shao Feng, etc. Innovation elements such as projects, talents and enterprises are now highly concentrated. The average R&D ratio of the park is 7.19% which is higher than the national average. In fields like biopharmaceuticals, gene testing and diagnostic reagents, a batch of breakthrough technologies and achievements have been produced, which make ZGC Life Science Park the R&D center with global influence, and welcome scientists, entrepreneurs and investors across the world.



 Partner**TIE国际创新走廊**
Talents Innovation Ecosystem

TIE, abbreviation of Talents Innovation Ecosystem, founded by Tsinghua Holdings in 2017, is an international platform which aims to gather global scientific technologies, projects and innovation talents. Since its foundation, TIE has made extensive communication and cooperation with Future Science City, Huairou Science City, Zhongguancun (ZGC) Development Group and Zhongguancun (ZGC) Life Science Park in the area of life science and biomedicine, information technology of new generation, energy and materials, and others.

TIE organizes and plans the top-level international conferences, and carries out the customized professional training both online and offline. Besides, TIE also provides the service of publishing special issues for companies, universities, industrial parks and local governments in order to introduce the achievements and policies of scientific researches to the global scientific researchers.

TIE sincerely welcome partners from all over the world to join us in promoting greater collaboration, cooperation, and development in the progression from technological to industrial innovation.

We are committed to:

Connecting domestic enterprises with overseas innovative technology projects for technological innovation integration and industrial upgrading;

Matchmaking overseas investment opportunities and looking for potential Unicorn companies from all over the world;

Enabling governments and organizations to have extensive contacts with technologies, governments and business leaders worldwide;

Providing supports and services for both domestic and international companies by linking capital, market and industries.

Science Asia



2021科学亚洲会议

指导单位：北京市科学技术委员会、中关村科技园区管理委员会

学术主办：Science | MAAS

联合主办方： 中关村生命科学园
Zhongguancun Life Science Park  TIE国际创新走廊
Talents Innovation Ecosystem

战略合作伙伴： 2021 ZGC FORUM
中关村论坛  BAS
北京国际学术交流季

2021-9-9 (周四) 至 9-10 (周五)

北京中关村生命科学园医药科技中心四号楼裙楼3层

欢迎来到“科学亚洲”会议

2021年“科学亚洲”会议，主题为“**基因组生物学与疾病**”，本届会议采用线下和线上结合的方式同步举办。北京中关村生命科学园医药科技中心会场可容纳200人到场参会，线上注册可以通过大会网站 (www.scienceasia.cn)、哔哩哔哩视频平台 (<https://live.bilibili.com/h5/23068072>) 以及微信公众号“TIE 国际创新走廊”-“科学直播台”实时观看会议直播。

2021“**基因组生物学与疾病**”会议将突出展示基因组环境中基因表达的三维组织在近期取得的重要进展。演讲专家将探讨这些进展是如何对基础生物学产生影响，以及如何转化为了解和应对人类疾病的途径。

大会包括14场学术演讲、1场圆桌讨论以及中关村生命科学园园区企业及青年科学家的现场演讲等活动。注册参会人员可以通过大会网站的“提问与回答”板块向参会嘉宾留言提问，或在直播讨论区提问。

指导单位

北京市科学技术委员会、中关村科技园区管理委员会

学术主办单位

Science
AAAS

联合主办单位



会议日程

北京时间	第一天 (2021年9月9日)	北京时间	第二天 (2021年9月10日)
	开幕式		
08:50	Holden Thorp (Science family of journals主编) /市科委领导		
09:00-09:40	Rohit Pappu 支配核质体相位行为的蛋白质和RNA分子的分子规则	09:00-09:40	Jennifer Doudna CRISPR: 基因组编辑的科学机遇
09:40-10:20	Jay Shendure 哺乳动物胚胎细胞轨迹的系统化重构	09:40-10:20	Steve Henikoff 全基因组蛋白质-DNA相互作用的动态描述
10:20-10:40	茶歇	10:20-10:40	茶歇
10:40-11:20	沈晓骅 (联合主席) 非编码基因组在染色质与转录调节中的作用	10:40-11:20	David Gilbert DNA复制时机与染色体结构调控
11:20-12:00	韩敬东 人口老龄化的异质性	11:20-12:00	刘默芳 PIWI/piRNAs在基因表达与疾病中的作用
12:00-13:30	午休	12:00-13:30	午休
	中关村生命科学园发展论坛2021	13:30-14:40	青年科学家演讲
13:30-13:40	开场 主持人		
13:40-13:50	嘉宾致辞 领导致辞		
13:50-14:10	蛋白质药物国家工程研究中心 学术领袖主旨演讲	14:50-15:30	Ada Yonath 从生命起源到利用基因密码翻译原则和细胞组织来设计 下一代疗法
14:10-14:30	北京脑科学与类脑研究中心		
14:30-14:45	北京合生基因科技有限公司	15:30-16:10	王艳丽 第二类CRISPR-Cas酶切DNA/RNA的分子机制
14:45-15:00	水木未来(北京)科技有限公司		
15:00-15:15	角井(北京)生物技术有限公司		
15:15-15:30	科研与产业协同发展 华夏奕泰(北京)生物技术有限公司	16:10-16:50	刘颖 表观遗传代码调节线粒体应激反应
15:30-15:45	北京荷塘生华医疗科技有限公司		
15:45-16:00	北京健为医学检验实验室有限公司		
16:00-16:15	北京生命科学园生物科技研究院有限公司		
16:15-16:30	茶歇 中场休息		
16:30-17:00	对话 主题: 发展生命科学, 造福人类健康		
	晚上: 线上观看		
19:20-20:00	Richard A. Young 基因调控与疾病中的核冷凝物	19:00-20:10	圆桌讨论: 科学传播与交流 Joy Ma (主持人) 魏文胜/王大鹏/Dennis Normile/ Emily Therese Cloyd 就中西方在科学传播上面临的挑战、差异、未来的趋势, 专家们将展开小组讨论, 学习如何在不断变化的世界中有效沟通
20:00-20:40	Jennifer Phillips-Cremens 神经系统疾病中的基因组的折叠, 展开以及重折叠	20:10-20:50	Victor G. Corces 调节小鼠表观遗传特性的跨代传递
		20:50-21:00	闭幕式 沈晓骅 (联合主席)

学术组委会



沈晓骅

清华大学医学院教授



江涛

《科学》高级编辑



Barbara R. Jasny

AAAS独立承揽人

演讲嘉宾（按姓氏的首字母排序）



Victor G. Corces

埃默里大学医学院教授



Jennifer Doudna

加州大学伯克利分校教授/诺奖获得者



David Gilbert

圣地亚哥生物医学研究所高级研究员



韩敬东

北京大学前沿交叉学科研究院教授



Steve Henikoff

霍华德休斯医学研究所研究员



刘默芳

中国科学院上海生命科学研究院
生物化学与细胞生物学研究所研究员



刘颖

北京大学分子医学研究所教授



Rohit Pappu

华盛顿大学麦凯尔维学院
生物医学工程系教授



Jennifer E. Phillips-Cremens

宾夕法尼亚大学生物工程系副教授

演讲嘉宾（按姓氏的首字母排序）



Jay Shendure

华盛顿大学基因组科学系教授



王艳丽

中国科学院生物物理研究所研究员



Ada Yonath

魏茨曼科学研究所结构生物系教授/
诺奖获得者



Richard A. Young

美国麻省理工学院及怀特海德研究所教授

Science Asia

圆桌嘉宾（按姓氏的首字母排序）



Emily Therese Cloyd

美国科学促进会
科学技术公共参与中心主任



Joy Ma

EurekAlert! 新闻网内容
编辑经理



Dennis Normile

《科学》特约记者



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沈晓骅，美国密歇根大学医学院博士、哈佛大学医学院博士后和讲师。现为清华大学医学院长聘教授、长江学者特聘教授。她的主要研究是关于基因组的非编码部分如何影响染色质结构、基因表达和干细胞命运。在过去的几年里，沈晓骅实验室细致地研究了ncRNAs、基因组重复序列和RNA结合蛋白在调节转录和染色质方面的新内容。她的研究促进了ncRNA基因的功能推断，并在组织基因组和高阶染色质结构方面，产生了对基因组重复序列及其相关转录本的范式转移的理解。



江涛

《科学》高级编辑

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江涛曾就读于北京医科大学药学院（现为北京大学医学部），而后就读于马里兰圣玛丽学院，并在此获得其文学学士学位。他在乔治·华盛顿大学获得博士学位。江涛在美国国立卫生研究院（NIH）过敏和传染病研究所（NIAID）对分子生物学与免疫系统的发展进行其博士论文的研究。他曾作为博士后研究员在NICHD、NIH 以及加利福尼亚大学圣塔芭芭拉分校（UCSB）研究发育遗传学。江涛曾在挪威卑尔根大学的萨斯中心担任项目负责人，其项目团队主要研究形态建成的细胞生物学。2015年至2016年，他在上海的《Cell Research》担任编辑。2017年至2020年，他在美国旧金山的《PLOS Biology》杂志从事编辑工作。目前江涛在《Science》杂志担任高级编辑，负责在分子生物学、合成生物学，以及生物技术发展方面的论文编辑工作。

学术组委会



Barbara R. Jasny

名誉副主编（已退休） /

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Barbara Jasny拥有美国洛克菲勒大学分子生物学博士学位。她致力于研究病毒宿主细胞的相互作用、DNA复制以及细胞衰老。她于1985年加入美国科学促进会（AAAS）旗下的周刊杂志《科学》。直到2018年，她一直在基因学、医药和计算社会学领域的研究论文的发布进行征集和评估。Barbara Jasny 是AAAS的当选会员，也是美国基因治疗学会、功能基因组数据学会以及美国国家科学院 Keck Futures 倡议的会务顾问。自2013年至2018年，她还担任《科学》杂志和 SciLife Lab颁发的青年科学家奖（Science & SciLifeLab Prize for Young Scientists）的年度竞赛的协调员。Jasny博士撰写过60多篇研究论文、述评以及概论，并且参与了在书籍、文章、海报、虚拟简报、光盘以及播客中的科学交流。虽然Jasny博士已经于2018年以名誉副主编的身份退休了，但是她仍然继续无偿服务于国际教育协会和《科幻》杂志，审阅以及编辑稿件。

Science Asia

第一天 (2021年9月9日)

上午部分



Rohit Pappu

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Rohit Pappu, 美国华盛顿大学麦凯尔维学院生物医学工程系教授, 同时也担任生命系统科学和工程中心 (CSELS) 院长。作为一名生物物理学家, Pappu教授使用新型计算方式、高分子物理理论以及实验研究结合的方式来理解内在混乱的蛋白质的运作原理, 以及构成细胞物质的空间和时间组织基础的物理学原理。Pappu实验室致力于驱动相位分离和渗透过渡的系统, 该实验室的主要目标之一就是设计出新型生物分子冷凝物, 来作为一种了解细胞表现型是如何被冷凝物控制的途径。



Jay Shendure

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Jay Shendure是霍华德·休斯医学研究所的研究员, 华盛顿大学基因组科学系教授, 艾伦细胞世系追踪发现中心主任, 以及布罗特曼·巴蒂精密医学研究所的科学主任。在2005年他与 George Church 的博士论文中, 包含了第一个成功的下一代DNA测序的实践。位于西雅图的Shendure博士的研究小组开创了外显体测序及其在孟德尔障碍和自闭症基因发现方面的最早应用; 针对癌症和生殖医学的无细胞区DNA诊断; 大规模平行报告分析、饱和基因组编辑; 全生物体谱系追踪, 以及单个细胞的大规模平行分子分析。Shendure博士获得了美国人类遗传学协会的2012年柯特斯特恩奖, 2013年费德拉普里斯奖, 2013年美国国立卫生研究院 (NIH) 先驱奖, 2014年哈森阿尔法生命科学奖, 2018年理查德和卡罗尔·赫茨伯格技术创新奖, 以及美国国家科学院颁发的2019年理查德·朗斯伯里奖。他还曾为美国国立卫生研究院、美国精密医学倡议、国家人类基因组研究所、陈·扎克伯格倡议和艾伦细胞科学和免疫学研究所担任过顾问。他于2007年获得哈佛医学院的医学博士以及博士学位。

第一天 (2021年9月9日)

上午部分



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韩敬东教授获得艾伯特爱因斯坦医学院的博士学位。她曾在美国洛克菲勒大学和丹娜·法伯癌症研究所接受过博士后培训。在2004年，她成为了中国科学院遗传学与发育生物学研究所的研究员/教授。2010-2019年，她担任中国科学院--马克斯·普朗克合作伙伴计算生物学研究所所长。2019年，她成为北京大学的终身教授，以及新加坡国立大学的兼职教授。她的研究重点是分子网络的结构和动态推断，利用大规模的实验和计算分析来探索网络的设计原理，并探索诸如老化、癌症和干细胞在内的复杂表现型是如何通过分子网络进行调节的。她被授予2006年国家自然科学基金 (NSFC) 杰出青年科学家奖，以及2009年百人计划杰出成就奖，2011年被选为马克斯·普朗克研究员，2014年被选为MaxNetAging研究员，2016年被选为F1000发育生物学研究员。

Science Asia

第一天 (2021年9月9日) 晚上部分



Richard A. Young

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Richard A. Young是美国麻省理工学院及怀特海德研究所的教授。Young博士研究健康和疾病中的基因调控。他曾担任世界卫生组织、国家卫生研究院和多种科学协会和期刊的顾问。Young博士的荣誉包括美国国家科学院院士及医学院院士，还被《科学美国人》评为科学、技术和商业领域的前50名领导者之一。他创立了生物技术和制药行业的公司并为业内公司提供咨询，目前任职于Syros Pharmaceuticals、Camp4 Therapeutics、Omega Therapeutics和Dewpoint Therapeutics的董事会。Young博士也是一名飞行员，持有商业飞行员执照。他在耶鲁大学取得博士学位。



Jennifer Phillips-Cremens

美国宾夕法尼亚大学
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Jennifer Phillips-Cremens博士，是宾夕法尼亚大学工程和医学系的副教授和教员，基础职位在生物工程和遗传学系。Cremens博士在乔治亚理工学院Andres Garcia实验室的生物医学工程专业获得其博士学位。然后，她在Job Dekker和Victor Corces的实验室里进行了多学科的博士后的学习。Cremens博士现在在宾夕法尼亚大学经营着3-D表观组学和系统神经生物学实验室。她的主要研究领域在于理解用控制健康神经元的远程染色质结构机制来控制神经规范和突触可塑性，以及这些表观遗传机制如何在神经发育和神经发育疾病中出现错误。她被选为2014年纽约干细胞基金会罗伯逊研究员，2015年艾伯特·斯隆基金会研究员，2016年和2018年Kavli Frontiers of Science Fellow奖项，2015年美国国立卫生研究院主任新创新者奖，2020年美国国家科学基金会职业成就奖，以及2020年CZI神经退行性疾病双奖。

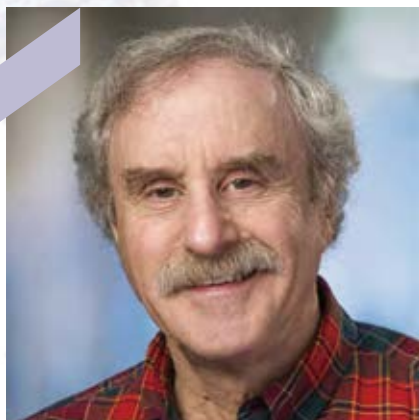
第二天（2021年9月10日） 上午部分



Jennifer Doudna

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Jennifer Doudna博士是加州大学伯克利分校的一名生物化学家。她与她的合作者Emmanuelle Charpentier开创性地开发了CRISPR-Cas9——一种允许研究人员编辑DNA的基因组工程技术，两人因此获得了2020年诺贝尔化学奖，并就此改变了人类和农业基因组学研究的进程。她也是创新基因组研究所的创始人和主席，李嘉诚生物医学与健康科学学院院长，以及霍华德·休斯医学研究所、劳伦斯伯克利国家实验室、格莱斯顿研究所、美国国家科学院和美国艺术与科学院的研究员。她是关于负责任地使用CRISPR的全球公开讨论的领导者，共同创立并且服务于几家以独特方式使用这项技术的公司的专家组顾问。Doudna是《创造中的裂缝》的合著者，这本书描述了她的个人研究、以及基因编辑的社会性和伦理性。



Steve Henikoff

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Steve Henikoff教授主要研究染色体、染色质动力学和表观遗传学，并致力于开发用于促进研究的基因组学和计算学工具。他获得了芝加哥大学学士学位，哈佛大学博士学位，并在华盛顿大学从事过博士后工作。自1981年以来，他一直是美国西雅图弗雷德·哈钦森癌症研究中心的教员。他还是霍华德·休斯医学研究所的研究员，华盛顿大学基因组科学客座教授，美国国家科学院的成员，以及开放式取用期刊《表观遗传学和染色质研究》（Epigenetics & Chromatin）的联合主编。

第二天 (2021年9月10日) 上午部分



David Gilbert

圣地亚哥生物医学研究所
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David M. Gilbert 目前在圣地亚哥生物医学研究所担任高级科学家，领导染色体复制和表观基因组调控实验室（2021年至今）。Gilbert博士的工作主要关注在细胞周期中调节DNA复制的机制，以及DNA复制与染色体的结构和功能组织之间的关系，在人类和小鼠胚胎干细胞和儿童白血病中的分化。Gilbert博士在美国加利福尼亚大学获得了生物化学/细胞生物学和哲学的学士学位，他在斯坦福大学获得遗传学的博士学位。他参加了两次博士后培训期，第一次是作为欧洲分子生物学组织（EMBO）的成员，跟 Pierre Chambon一起在法国斯特拉斯堡研究基因的转录控制，第二次作为知名制药企业罗氏公司（Roche）的成员，与Melvin DePamphilis一起研究基因的复制起源识别。他于1994年加入纽约州立大学（SUNY）上州医科大学任教，2003年被任命为正教授。2006年，他担任佛罗里达州立大学生物科学系的J. Herbert Taylor的分子生物学特聘教授，并且担任佛罗里达州立大学基因组学和个性化医疗中心的联合创始人及副主任（2006-2020年）。Gilbert博士于2008年当选为美国科学促进会（AAAS）的成员，2010年当选为AAAS的理事会代表，2013年当选为美国血液学学会的理事会代表，2014年当选为国际干细胞研究学会的理事会代表。Gilbert博士还获得了美国癌症协会初级教师研究奖（2000年）、纽约州立大学（SUNY）总统青年研究者奖（2002年）、美国国立卫生研究院干细胞研究职业生涯奖（2004年）、佛罗里达州立大学杰出研究教授奖（2015年）、佛罗里达州立大学研究生院导师奖（2016年）和菲弗捐赠基金癌症研究教授奖（2015年）。他曾是美国国立卫生研究院DNA因子百科全书（ENCODE）联合会（2011-2017年）的首席研究员，也是美国国立卫生研究院4D核聚体联合会和东南干细胞联合会（SESCC）的成员。他曾在美国癌症学会（1996-2004年）和美国国立卫生研究院的研究部门（1997年至今）任职，是表观遗传学学会和《细胞生物学杂志》的编委（2008年至今），并发表了160多篇出版物。

第二天 (2021年9月10日) 上午部分



刘默芳

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细胞生物学研究所
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刘默芳博士，中国科学院（CAS）上海生物化学与细胞生物学研究所教授、首席研究员。于1991年和1994年分别取得了上海华东理工大学生物化学专业学士和硕士学位。于2000年取得了中国科学院上海生物化学研究所分子生物学专业博士学位。从2000年到2006年，她在美国国立卫生研究院国家癌症研究所从事博士后研究，然后在约翰霍普金斯大学医学院担任研究助理。2006年加入上海生物化学与细胞生物学研究所。刘默芳博士的主要研究领域是非编码小RNA的作用和机制，包括PIWI相互作用RNA (piRNA) 和microRNA，旨在了解非编码小RNA在哺乳动物精子生成、男性不育及癌症中的生理病理功能机制。

Science Asia

第二天 (2021年9月10日) 下午部分



Ada Yonath

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Ada Yonath专注于核糖体将遗传密码翻译为蛋白质、阻碍这一过程的抗生素、与核糖体突变相关的人类疾病和生命起源。尽管全球对这些领域仍持怀疑的态度，但她还是发起了对这些领域的研究，并且带来了前沿的关键性科学进展，而这些进展在几个月内就成为了规范。

她负责以色列魏茨曼研究所 (WIS) 的金梅尔曼生物分子结构中心，并在那里取得博士学位，目前是一名教授。她在卡耐基梅隆大学、麻省理工学院和芝加哥大学担任博士后。20世纪70年代，她在WIS建立了以色列的第一个结构生物学实验室，这是以色列近十年来唯一的一个实验室。在1986-2004年期间，她领导了汉堡核糖体结构的马克斯-普朗克研究单位，与她的WIS活动平行。

同时，她是美国国家学院；英国皇家学会；以色列学会；德国利奥波尔迪纳；印度科学学院（梵蒂冈）；日本、韩国、意大利和欧洲学院的成员，被全球45所大学授予荣誉博士。Ada Yonath还获得了路易撒奖 (Louisa-Gross-Horwitz Prize)、沃尔夫奖 (Wolf Prize)、哈维奖 (Harvey Prize)、以色列奖 (Israel Prize)、莱纳斯-鲍林金奖；联合国教科文组织/欧莱雅奖；艾尔伯特-爱因斯坦卓越奖；以及2009年诺贝尔化学奖。



王艳丽

中国科学院生物物理研究所

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王艳丽，中国科学院生物物理研究所研究员，HHMI国际研究学者。王教授在中国科技大学获得博士学位，并在美国斯隆-凯特琳癌症中心完成博士后研究。她主要研究具有调控功能的非编码小RNA或DNA的作用机理，揭示它们是如何介导原核生物的免疫防御系统；系统地阐释了CRISPR-Cas系统的机制，以及Ago蛋白介导的DNA干扰。

第二天 (2021年9月10日)

下午部分



刘颖

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个人履历

教育

学位	年份	专业	机构	导师
博士后	2011-2013	遗传学	马萨诸塞州总医院和哈佛医学院	Gary Ruvkun
博士	2006-2011	生物化学	美国德州大学西南医疗中心	Qinghua Liu
学士	2002-2006	生物化学	中国南京大学	

专业任命

年份	职位	机构
2021.2至今	教授	北京大学未来技术学院分子医学研究所
2020.12至今	副院长	北京大学未来技术学院
2020.1至今	副所长	北京大学分子医学研究所
2019.8-2021.1	助理教授	北京大学分子医学研究所
2017-2022	HHMI国际/研究学者	霍华德·休斯医学研究所
2013.12-2019.7	助理教授	北京大学分子医学研究所

荣誉和奖项

年度	荣誉和奖项
2019	Xplorer奖
2019	国家杰出青年科学基金
2019	第15届中国青年女科学家奖
2019	中国细胞生物学学会青年研究员奖
2018	“中国35岁以下的创新者”，麻省理工学院技术评论
2017	HHMI国际研究学者
2012-2014	海伦海·惠特尼研究奖学金
2011	德州大学西南医疗中心提名奖
2010	斯坦福生物化学创始人杰出博士奖

第二天 (2021年9月10日) 晚上部分



Victor G. Corces

埃默里大学医学院

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Corces博士是埃默里大学医学院的人类遗传学教授。在Corces博士的实验室中，主要研究了染色质三维组织的建立和维持的机制。他目前的研究重点是了解环境改变生殖系细胞表观基因组的机制，以及这些表观遗传改变如何在受精后从配子传递到胚胎，从而导致疾病状态并传递给后代。Corces博士在表观遗传学和基因组学领域发表了大量的文章，近期重点关注卵子和精子核的三维组织以及表型的跨代遗传机制。

圆桌嘉宾



Emily Therese Cloyd

美国科学促进会科学技术
公共参与中心
ecloyd@aaas.org

Emily Therese Cloyd是美国科学促进会（AAAS）科学技术公共参与中心的主任。Emily 监督科学中心所有的项目，包括AAAS How We Respond项目，AAAS莱什纳领导研究所和交流科学项目。在2016年加入AAAS之前，Emily在美国国家海洋和大气管理局担任克诺斯海洋政策研究员，她领导并拓展了美国全球变化研究计划和第三次国家气候评估，并在五大湖的管理工作中研究了生态模型的使用。她取得了非营利性领导与管理执行证书（美国圣母大学），保护生物学硕士学位（纽约州立大学环境科学与森林学院），以及植物生物学学士学位（密歇根大学）。Emily 喜欢在波托马克河和阿纳科斯蒂亚河上划桨，尤其是在龙舟上，她也很喜欢缓慢地沿着阿帕拉契亚山脉的小径进行徒步旅行。可以在推特上关注她@EngageClimate。



Joy Ma

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Joy Ma是EurekAlert! 新闻网的内容编辑经理，EurekAlert!是由美国科学促进会（AAAS）运营的非营利性科学新闻发布分发服务商。Joy的主要领域集中在增加EurekAlert!上面内容来源的多样性，特别是来自高容量、高质量科研产出但科学交流水平相对较低的国家和地区。自2015年以来，通过培训和指导新的新闻报道人员，以及战略拓展，她大幅增加了来自中国、日本和韩国的顶级机构的科学记者在EurekAlert!的新闻发布数量。在加入AAAS之前，她曾在美国国家公共广播电台（NPR）和企鹅集团工作。她曾因为在NPR时对成都地震的新闻报道而获得Alfred I. duPont哥伦比亚大学奖，也是外国记者协会奖学金的获得者。Joy Ma在哥伦比亚大学新闻学研究生院取得了新闻学专业的文学硕士学位。

圆桌嘉宾



Dennis Normile

《科学》杂志
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自1995年以来，Dennis Normile 一直是《科学》的特约记者，报道政府科学政策、科学界的趋势以及亚太地区的最新的实验结果。Normile在泰国、越南和中国报道了大量关于21世纪中期禽流感危机的报道。他写了很多关于日本东北地区的的故事，包括地震、海啸和2011年3月核电站崩溃，重点关注灾难的科学方面。他对中国的报道包括最近关于贵州省500米口径球面射电望远镜（FAST）的故事，中国的月球和火星任务，以及新型冠状病毒疫情。

Normile的文章也曾发布在《纽约时报》、《远东经济评论》、《金融时报》（英国）和其他出版物上。



王大鹏

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王大鹏，中国科普研究所（CRISP）研究员，致力于中国科学交流10多年。他的兴趣非常广泛，重点关注科学家与媒体之间的关系，通过微博、博客、微信等新媒体方式传播科学，以及在中国科学交流的理论与实践。在过去的几年里，他发表了一些科学传播领域的旅行论文，还在报纸上写了100多篇评论，翻译了近10本书。他是一位精通媒体的科学传播者。

圆桌嘉宾



魏文胜

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魏文胜，担任生物医学前沿创新中心（BIOPIC）、北大-清华生命科学联合中心、以及北京大学生命科学学院的教授；北京大学基因组编辑研究中心的主任。魏文胜团队的研究主要集中在真核基因编辑工具的开发上，重点是高通量功能基因组学和基因治疗。采用正向和反向遗传手段的结合，通常以一种高通量的方式，以理解人类疾病背后的分子机制，包括癌症和感染。

Science Asia

学术合作伙伴

Science



美国科学促进会（The American Association for the Advancement of Science，简称AAAS）是世界上最大的综合性科学社团和国际性非营利组织，近13万名个人会员分布在全球91个国家。AAAS的宗旨是推动科学、工程及创新领域的发展，为人类造福。AAAS也是世界顶级的科学出版机构，通过旗下的《科学》系列期刊出版最前沿的科研成果。

《科学》杂志每周发行，全年51期，在科学领域一直保持着权威的学术地位。其印刷版订阅量每期保持在13万册，官网的月浏览量高达1400万，在同类学术网站中高居第一。65%以上的读者群体拥有博士学位，他们是来自世界各地的高校、研究所、医疗行业、政府机构等单位的科研工作者及科学爱好者。

Science Asia

战略合作伙伴



ZGC FORUM
中关村论坛

自2007年起，中关村论坛（以下简称“论坛”）以“创新与发展”为永久主题，已经举办十余届，努力打造成为集科技交流和创新成果展示、发布、交易于一体的国际化科技创新交流合作平台。

中关村论坛定位服务国家创新发展战略和北京科创中心建设，以科技创新为核心推动全面创新，服务于科学、技术、产品、市场全链条。论坛致力于搭建创新思想新理念的交流传播平台、新科技新产业的前沿引领平台、新技术新产品的发布交易平台、创新规则和创新治理的共商共享平台，着力打造高层次、综合性、高水平的国际科技合作平台，努力成为代表国家融入国际创新网络、深度参与全球创新治理，推动提升国际话语权的国家级国际化重大活动。

中关村论坛围绕“创新与发展”这一永久主题，聚焦国际科技创新前沿和热点问题，每年设置不同议题，邀请全球顶尖科学家、领军企业家、新锐创业者等共同参与，纵论创新，交流分享，产生思想碰撞和深度思考，引发科技创新领域和创新创业主体广泛关注，不断传播新思想、提炼新模式、引领新发展。



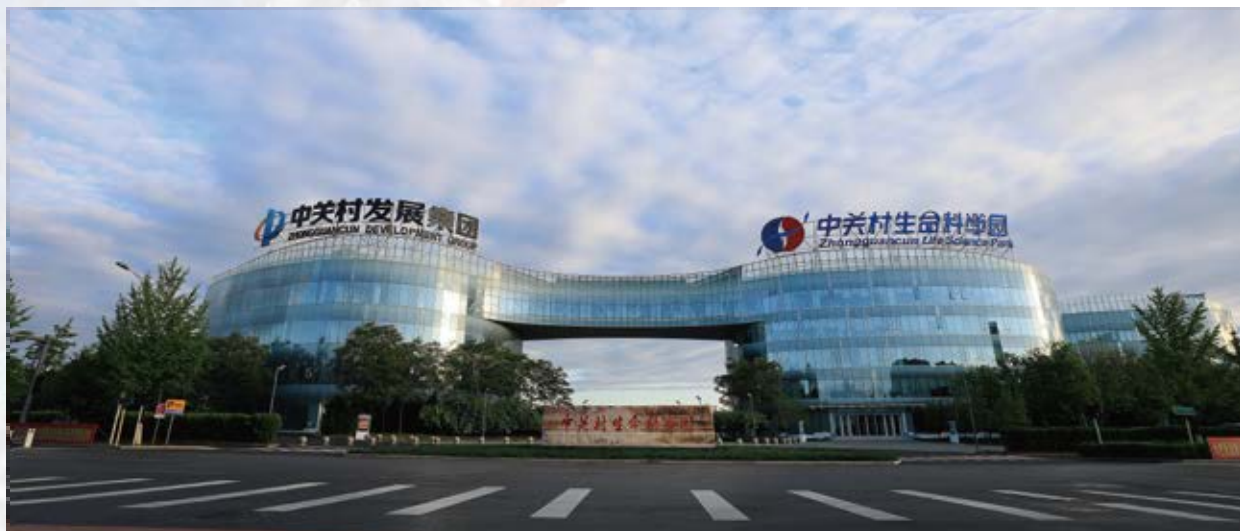
BAS

2021
北京国际学术交流季

BEIJING INTERNATIONAL ACADEMIC SEASON

“北京国际学术交流季”是在北京市政府支持下，由北京市科委策划组织的高端品牌系列学术交流活动，按照“聚焦学术研究”“聚集全球顶尖科学家”，以及“深层次多角度研讨”的原则，在基础前沿领域为国际科技界的广泛交流搭建平台，助力北京建设具有全球影响力的科技创新中心。北京国际学术交流季围绕量子科学、石墨烯、脑科学、医药健康、纳米技术等基础前沿领域，组织开展高水平学术系列交流活动。

合作伙伴



中关村生命科学园成立于2000年，占地面积2.49平方公里，位于北京市昌平区北清路北侧，G6和G7高速公路之间，是中关村国家自主创新示范区的重要组成部分，是以生命科学研究、生物技术和生物医药相关领域研发创新为主的高科技产业园区。园区现有从事生物医药领域研发企业500多家，包括诺和诺德、扬子江药业集团、养生堂万泰、迈瑞医疗、博奥生物、百济神州、坤奥基、贝瑞和康等领军企业，聚集了王晓东、贺福初、施一公、邵峰、程京等顶尖人才和专家团队，科研资源、顶尖人才、高科技企业高度集中。园区企业平均研发投入强度达7.19%，高于全国平均水平，在生物制药、基因检测、诊断试剂等领域产生了一批具有国际影响的、突破性重大科研技术和转化成果，为建设代表世界先进水平的生命科学研究与创新高地打下了坚实基础。诚挚欢迎世界各地的科学家、企业家、创业者和投资人来园投资兴业，共谋发展。



合作伙伴



TIE国际创新走廊 Talents Innovation Ecosystem

TIE国际创新走廊，简称“TIE”，是清华控股发起的全球性科学技术、项目与创新人才的交流平台。成立以来已经与未来科学城、怀柔科学城、中关村发展集团和中关村生命科学园等单位在生命科学与生物医药、新一代信息技术、能源与材料等领域开展了广泛交流与合作。

TIE所提供的服务包括组织筹划顶级国际会议，开展定制化的线上和线下专业培训，以及为企业、高校院所、产业园区和地方政府定制专题页面，出版专刊向全球科研群体推广，介绍科研成果和政策。其旨在成为为创新孵化机构提供国际化、数字化解决方案的领先者和区域产业创新生态塑造者。

TIE致力于：

链接国内企业与海外创新技术项目，促进技术创新整合和产业升级；
牵线搭桥国内外投资机会，并在世界各地寻找潜在的独角兽公司；
使政府和组织能够与全球的技术、政府和商业领袖建立广泛的联系；
通过将资本、市场和产业联系起来，为国内外公司提供支持和服务。

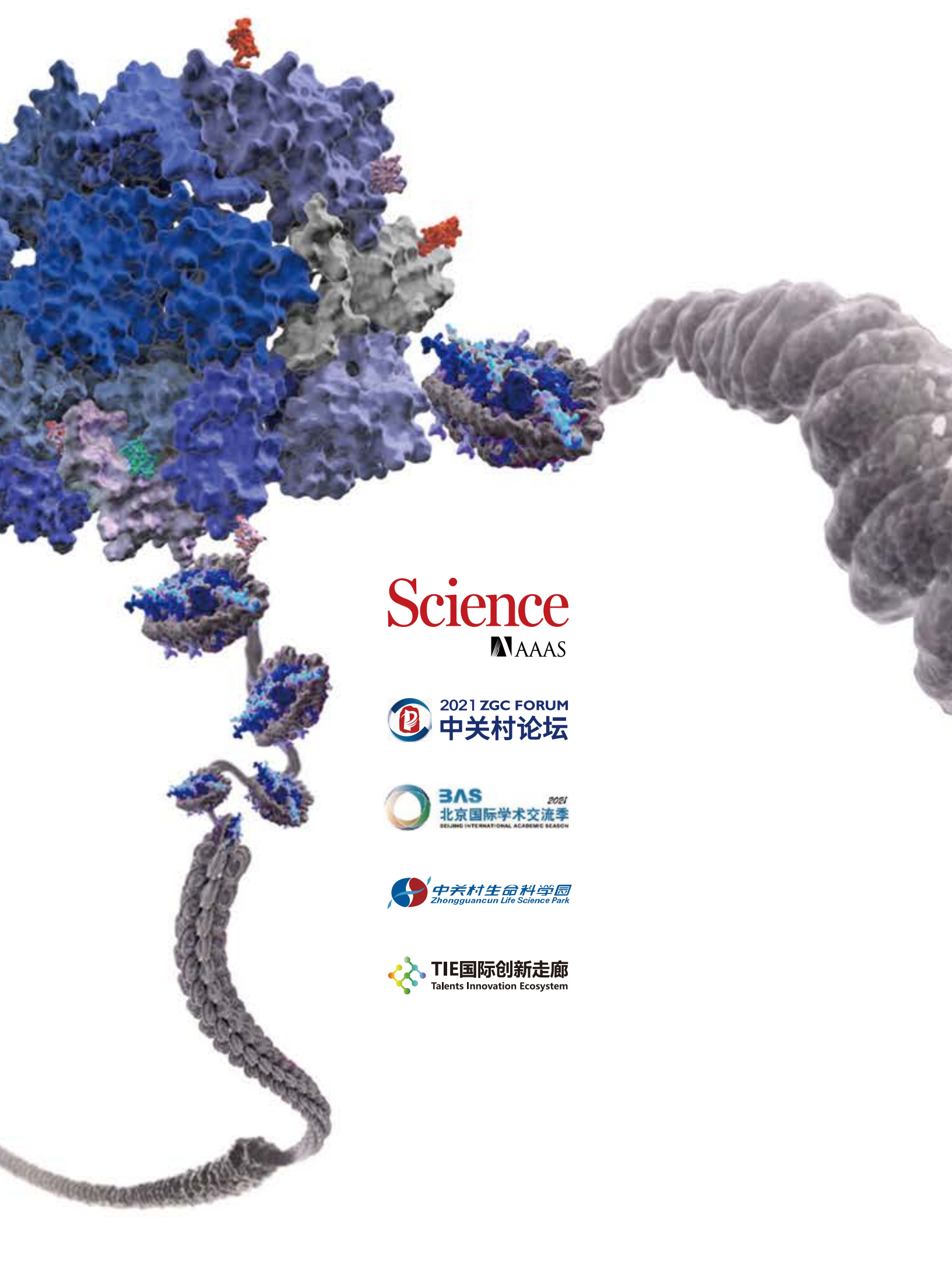
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