Tsinghua-*Science* Workshops
Spliceosome and RNA
Session 1: Spliceosome Structure and Function

20:00-20:45
Yigong Shi, Tsinghua University/Westlake University, China
How does the ATPase/helicase Prp2 remodel the spliceosome?
20:45-21:00 Q&A

21:00-21:45
Narry Kim, Seoul National University, Korea
Transcriptome and Proteome of SARS-CoV-2
21:45-22:00 Q&A

Host

Dr. Valda Vinson

Valda Vinson is Editor (Research) at Science. She came to the United States as a Fulbright scholar and after completing a Ph.D and post-doctoral studies, returned to her birth country, South Africa, and spent 2 years as a Senior Lecturer at the University of the Western Cape. She started her career in publishing when she once again moved to the US and joined the Science staff in 1999. Since then, she has handled research papers in the areas of structural biology, biochemistry, and biophysics as an Associate and Senior Editor. In 2013 Dr. Vinson became Deputy Editor, overseeing research content in the areas of cellular and molecular biology and biomedicine, and in 2018 was named Editor, Research. As Editor she works with Life Science editors to attract and select exciting research papers and reviews, while following standards that support transparency and reproducibility. She also works with others on the editorial management team on editorial policies at Science and is involved in initiatives that bring together stake-holders within the publishing industry to discuss policies.

Speakers

Prof. Yigong Shi

Born in Zhengzhou, Henan Province in 1967, professor Yigong Shi is an Academician of the Chinese Academy of Sciences, a Foreign Associate of the US National Academy of Sciences and an Honorary Foreign Member of the American Academy of Arts and Sciences. As a structural biologist, he is also a recipient of Cheung Kong Scholar, National Distinguished Scholar and Outstanding Youth Talent of National Science Foundation for China. In 1985, he was recommended for admission to Tsinghua University. In 1989, he graduated one year ahead of schedule with a bachelor's degree. In 1995, he received his Ph.D. in molecular biophysics from Johns Hopkins University School of Medicine, and later did postdoctoral research at Memorial Sloan-Kettering Cancer Center. From 1998 to 2008, he was Assistant Professor, Associate Professor, Professor and Warner-Lambert/Parke-Davis Professor in the Department of Molecular Biology, Princeton University, USA. In 2008, he declined the invitation of a researcher from Howard Hughes Medical Center (HHMI) and returned to Tsinghua University full-time. He served as the Dean of the School of Life Sciences of Tsinghua University until 2016 and is now the President of Westlake University. His research group is devoted to combining structural biology and biochemistry to elucidate the molecular mechanisms of fundamental cellular events, with a focus on apoptosis, regulated intramembrane proteolysis related to Alzheimer's disease, and pre-mRNA splicing.

How does the ATPase/helicase Prp2 remodel the spliceosome?

Pre-mRNA splicing is accomplished by the highly dynamic spliceosome, which undergoes multiple steps of remodeling during each splicing cycle. Spliceosome remodeling is carried out by eight conserved ATPase/helicases exemplified by Prp2. Together with its coactivator Spp2, Prp2 remodels the activated spliceosome in an ATP-dependent manner. To understand the action of Prp2, we have determined atomic structures of Prp2 in isolation, Prp2 complexed with Spp2, and Prp2-loaded activated spliceosome. This information, together with structure-guided biochemical analysis. reveal elaborate mechanisms and explain how spliceosome remodeling is coupled to pre-mRNA splicing.

Prof. Narry Kim

Narry Kim is a Professor in the School of Biological Sciences at Seoul National University and a founding director of RNA Research Center at Institute for Basic Science. She received her Ph.D. in 1998 from the University of Oxford where she studied lentiviruses and gene delivery. With keen interest in RNA biology, she joined the Gideon Dreyfuss lab at the University of Pennsylvania and researched the role of the exon junction complex in mRNA surveillance. Her current research group investigates how genes are regulated at the RNA level, with particular interests in microRNA, mRNA, and viral RNA. She is a recipient of the L'Oreal-UNESCO Women in Science Award, Hoam Prize, and Asan Prize, and a member of KAS, NAS and EMBO.

Transcriptome and Proteome of SARS-CoV-2

SARS-CoV-2 is a betacoronavirus responsible for the COVID-19 pandemic. To delineate the viral transcriptomic architecture and provide a high-resolution map of the SARS-CoV-2, we performed deep sequencing of infected cells. Our data define the canonical transcripts (a genomic RNA and nine subgenomic RNAs) while invalidating the predicted ORF10 transcript. We learned that the viral transcriptome is highly complex owing to numerous discontinuous transcription events, both canonical and noncanonical. SARS-CoV-2 produces noncanonical transcripts encoding unknown ORFs with fusion, deletion, and/or frameshift. More recently, we have also performed proteomic analyses of the SARS-CoV-2 ribonucleoprotein complex. We identify many proteins that directly interact with viral RNAs and modulate viral growth. Functional investigation of the viral transcripts and host proteins discovered in this study will open new directions to the research efforts to elucidate the life cycle and pathogenicity of SARS-CoV-2.