THE GIS
SPEAKER SERIES



Genome Institute of Singapore
A*STAR GIS

Non-B DNA: a blessing and a curse of the genome

Dr Kateryna MAKOVA
Professor, Penn State University

Host: NG Shi Yan

Wednesday 11 November 2026
10.00am – 11.00am

GIS L2 – Seminar Room
60 Biopolis Street, Genome, Singapore 138672

About The Speaker

A native of Ukraine, Kateryna Makova received her PhD degree from Texas Tech University, where she studied the genetic consequences of the Chornobyl Nuclear Power Plant accident. She then completed her postdoctoral studies at the University of Chicago, where she investigated differences in mutation rates between males and females, among other topics. She has been a Professor in the Department of Biology at Penn State University since 2003. Her laboratory conducts research in medical and evolutionary genomics. Current topics of interest include sex chromosomes, non-canonical DNA, mitochondrial genome, and childhood obesity. She has recently co-founded and co-led the International Primates Telomere-to-Telomere Consortium. The research in Kateryna's laboratory is highly interdisciplinary and collaborative. The group collaborates with statisticians, computer scientists, and biochemists. During her career, Kateryna has mentored 16 PhD students and 14 postdoctoral fellows, and has authored over 100 scientific manuscripts. Kateryna's research has been continuously funded by the NIH since 2004. She currently directs the Center for Medical Genomics, which brings together researchers from Penn State's University Park and Hershey campuses. She serves as an Editor of Genome Research and has recently served as the President of the International Society for Molecular Biology and Evolution.

About The Seminar

Telomere-to-telomere (T2T) genome assemblies now provide a complete representation of genomic sequences, enabling unprecedented exploration of non-B DNA structures—secondary conformations distinct from canonical B-DNA. These fully resolved genomes reveal the true abundance and chromosomal distribution of motifs capable of forming G-quadruplexes, Z-DNA, triplexes, and other non-canonical structures, including within previously inaccessible satellite and repetitive regions. T2T assemblies also illuminate how non-B DNA influences key biological processes such as replication, recombination, chromatin organization, and transcription. Moreover, emerging evidence links non-B DNA structures to genomic instability, mutation hotspots, and disease etiology. Comparative T2T analyses across species are beginning to uncover evolutionary patterns and selection pressures acting on these motifs. Integrating advanced prediction tools, AI-based analyses, and experimental validation promises to clarify the multifaceted roles of non-B DNA in genome function, regulation, and evolution.