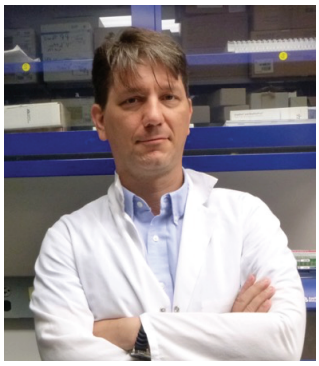
SingaRNA SYMPOSIUM – Speakers

Yue Wan
Junior Principal Investigator, GIS, A*STAR, Singapore
Title: *In vivo* mapping of eukaryotic RNA interactomes genome-wide using psoralen crosslinking

Yue Wan received her B.Sc. in Cell Biology and Biochemistry from the University of California, San Diego. She obtained her PhD in Cancer Biology from Stanford University, California, USA, under the mentorship of Howard Y. Chang. During her PhD, she developed the first high-throughput method for probing RNA structures genome-wide. Yue is a recipient of the NSS-PhD scholarship from Agency for Science, Technology and Research (A*STAR) in Singapore. She is currently a Junior Principal Investigator in the Genome Institute of Singapore and a Society in Science-Branco Weiss Fellow. Yue is a recipient of the Young Scientist Award and a TR35 Asia Finalist. She is interested in studying functional RNA structures and understanding their roles in regulating cellular biology.

Luca Cartegni
Assistant Professor, Rutgers University, USA
Title: Therapeutic manipulation of RNA processing in cancer by antisense compounds



The focus of our research is the understanding of the role of deregulated pre-mRNA splicing in cancer events, and the development of novel approaches to harness RNA processing to induce the expression of natural dominant-negative variants of active oncogenes in cancer, especially in the context of relapsing tumors which have become resistant to traditional therapies. In particular, we use antisense compounds to modulate alternative splicing and/or to activate intronic polyadenylation, in order to promote the expression of natural antagonists. Some of the targets we are focusing on include the induction of soluble decoy variants from VEGFR, EGFR, MET and other Receptor Tyrosine Kinases, as well as oncogenic transcription factors such as STAT3 and others.

Marlene Oeffinger
Assistant Professor, Institut de recherches cliniques de Montreal, Canada
Title: Investigating dynamic interactomes and variances along gene expression pathways using proteomic approaches

Dr. Oeffinger has been interested in RNA ever since her undergraduate days in Vienna. Her particular curiosity for ribosomes, however, developed during her PhD in the Tollervey lab, and to dissect ribosome and other RNA maturation pathways in more detail, she established novel affinity purification mass spectrometry approaches as part of her post-doctoral work in Mike Rout's group at Rockefeller University. In her own lab, she keeps pursuing RNP dynamics and biogenesis with the development of an ever-expanding repertoire of new proteomic tools. And if she's not chasing RNPs along different pathways, she teaches yoga or writes poetry and prose.

Huili Guo
Junior Investigator, Institute for Molecular and Cellular Biology, A*STAR, Singapore
Title: Ribosome heterogeneity and translational control

Huili Guo obtained her B.A. in Natural Sciences (2005) from Cambridge University and her PhD in Biology (2011) from MIT. At MIT, she trained at the Whitehead Institute for Biomedical Research, in the laboratory of Prof. David Bartel, where she was the first to perform ribosome profiling in mammalian cells to uncover the characteristics of microRNA-mediated repression. In 2012, she joined IMCB as an Independent Fellow. Huili continues to use genome-wide techniques to probe RNA biology, with particular focus on how the control of protein synthesis impacts human health. Outside of lab, she enjoys singing and mothering her two kids.

Leah Vardy
Assistant Professor, Institute for Molecular and Cellular Biology, A*STAR, Singapore
Title: Polyamine mediated gene expression control in the epidermis

Leah Vardy received her Ph.D. from the Imperial Cancer Research Fund in London and went on to do post-doctoral work with Terry Orr-Weaver at the Whitehead Institute in Cambridge, in the US. Leah moved to the IMB in Singapore in 2008 to head a group focused on understanding gene expression control in embryonic stem cells and in the epidermis. More recently her focus has been on understanding how the polyamines help to regulate cellular function in these systems.

Eric Van Nostrand
Merck Fellow, Damon Runyon Cancer Research Foundation, USA
Title: Integrated analysis of RNA binding protein binding sites identified by enhanced CLIP enables RNA-centric views of RNA binding and reveals splicing dynamics

Eric Van Nostrand received his S.B. in Biology from MIT in 2005, with research experience in Dr. Chris Burge's lab on computational and experimental analysis of alternative splicing regulation. After spending a year with Dr. Fred Gage & Dr. Gene Yeo at the Salk Institute for Biological Studies, Eric attended Stanford University for graduate school, joining Dr. Stuart Kim's lab. Eric's thesis work focused on genomic, genetic, and molecular analysis of aging in *C. elegans*, identifying novel regulators of transcriptional changes with age that revealed links between developmental regulators and aging. As a part of this work, Eric identified transcription factor complexity (defined as the number of factors that bind to the same genomic loci) as a significant feature for biological interpretation of ChIP-seq data. Low-complexity binding sites tended to correlate with factor-responsive target expression, whereas analysis of HOT (highly occupied target regions) bound by 65% or more of factors revealed a potential novel regulatory mechanism for highly expressed, essential, ubiquitous genes. In 2013, Eric joined the Yeo lab to perform postdoctoral research on general RNA binding protein regulatory networks as well as identification and characterization of critical RNA binding proteins in neuronal stem cell maintenance and differentiation.

Dan Zenklusen
Assistant Professor, Université de Montréal, Canada
Title: Dissecting RNA metabolism using single molecule resolution microscopy

Dr. Zenklusen has a longstanding interest in RNA biology. He did his PhD at the University of Lausanne in Switzerland studying mRNA export in yeast, before carrying out a postdoc in laboratory of Robert H Singer at the Einstein College of Medicine, where he developed single RNA resolution microscopy techniques to study transcription at the single cell level. In this laboratory at the Université de Montréal, he continues to use single molecule and super-resolution microscopy tools to study different aspects of mRNA metabolism, including the role of noncoding RNAs in transcription regulation, mRNP organization and localization.

Eric Lecuyer
Associate Professor, Institut de recherches cliniques de Montreal, Canada
Title: Studying the highways and byways of subcellular RNA regulation

Our laboratory seeks to understand the biological functions and regulatory mechanisms of RNA intracellular localization. Our projects aim to elucidate the normal functions of RNA trafficking in the maintenance of genome stability and cell polarity, and how disruption of these pathways can contribute to the aetiology of diseases such as cancer and neuromuscular disorders. For this work, we combine the versatility of Drosophila genetics with high-throughput molecular imaging and functional genomics approaches in fly and human cellular models.

Meng How Tan
Assistant Professor, Nanyang Technological University, Singapore
Title: Sculpting the A-to-I RNA editing landscape in mammals by non-ADAR regulators

Meng How Tan is an Assistant Professor at the School of Chemical and Biomedical Engineering in the Nanyang Technological University, with a joint appointment at the Genome Institute of Singapore. He obtained his Ph.D. in developmental biology from Stanford University and undertook his post-doctoral training with Jin Billy Li, Wing Hung Wong, and Mylene Yao, also at Stanford University before returning to Singapore to start his own laboratory. His research interests are in DNA and RNA editing, particularly in the context of cell identity. His laboratory studies the functions and regulation of A-to-I RNA editing in human development and diseases.

Gabriel Pratt
NSF Graduate Fellow, University of California San Diego, USA
Title: Systematic discovery of RNA binding proteins that regulate alternative splicing in response to cellular stress

Gabriel Pratt received his B.S in Computer Science from the University of Washington in 2011. He is now in the Bioinformatics and Systems Biology graduate program at the University of California San Diego studying with Gene Yeo. Gabriel's work in the Yeo lab focuses on the characterization of RNA binding protein function and the design of large scale computational tools and pipelines to integrate many disparate types of data to achieve that goal.

Yoseph Barash
Assistant Professor, University of Pennsylvania, USA
Title: Predictive models for RNA splicing regulation – the next generation

Yoseph has a B.Sc. in Physics and Computer Science, and a PhD in Machine learning and computational biology from the Hebrew University. Yoseph's work involves solving problems from the biomedical field using machine learning. His lab focuses on understanding RNA biogensis, its regulation, and its role in human disease and in phenotipic diversity. The lab combines computational modeling, experimental validations, and software development.

Kristen Lynch
Professor, University of Pennsylvania, USA
Title: Environmental induced splicing regulation in the human immune system

My research focuses on pre-mRNA splicing in the human immune system. As a biochemist I am particularly interested in the mechanisms by which RNA binding proteins direct the activity of the spliceosome and how signaling pathways alter the expression and/or function of these RNA binding proteins. My lab also studies the genome-wide activity of RNA binding proteins in lymphocytes and the physiologic impact of splicing on the function of the immune system. When not in the lab I can be found in the yoga studio or enjoying outside activities with my kids.

David Nelles
CTO, Locana, USA
Title: Programmable RNA recognition and tracking with CRISPR/Cas9 in live cells

David Nelles received his B.S. in Engineering Physics from the University of Pittsburgh in 2009 and now studies at the University of California, San Diego in the Materials Science and Engineering Ph.D. program. David is an NSF Graduate Research Fellow, ARCS Fellow, and Powell-Focht graduate fellow. David's graduate work in the Yeo lab focuses on applying principles in synthetic biology and polymer chemistry to persistent problems in RNA biology and neurodegeneration.

John Conboy
Principal Investigator, Lawrence Berkeley National Laboratory, USA
Title: Dynamic intron retention in differentiating human erythroblasts

With assistance from many wonderful collaborators, my lab has studied regulatory motifs and splicing factors that control splicing programs in several systems. Currently we focus on the robust and dynamic alternative splicing program that is executed during terminal erythropoiesis. Another recurring interests is control of splicing by distant regulatory elements, such as the two-step intrasplicing mechanism that couples promoter choice with alternative 3'ss choice in the protein 4.1R and 4.1B genes, and the distal RBFOX2 splicing enhancer ~1.9kb downstream of ENAH alternative exon 11a that is recruited close to the regulated via an 'RNA bridge'.

Xavier Roca
Assistant Professor, Nanyang Technological University Singapore
Title: Splicing mechanisms and regulation: the problem of too many choices

We are using single-gene and transcriptome-wide approaches to study mechanisms of pre-messenger RNA splicing in human cells and their implications in genetic diseases. We are following up my post-doctoral work by demonstrating new mechanisms for 5' splice-site recognition by diverse base-pairing registers with U1 small nuclear RNA. We are also studying two alternative-splicing events in CD46 and BIM, with consequences in immunity and drug resistance in tyrosine kinase-driven cancers, respectively. Finally, we are characterizing the global alternative-splicing changes during differentiation and activation of human monocytes to macrophages. At the symposium I will present our data on some of these projects.