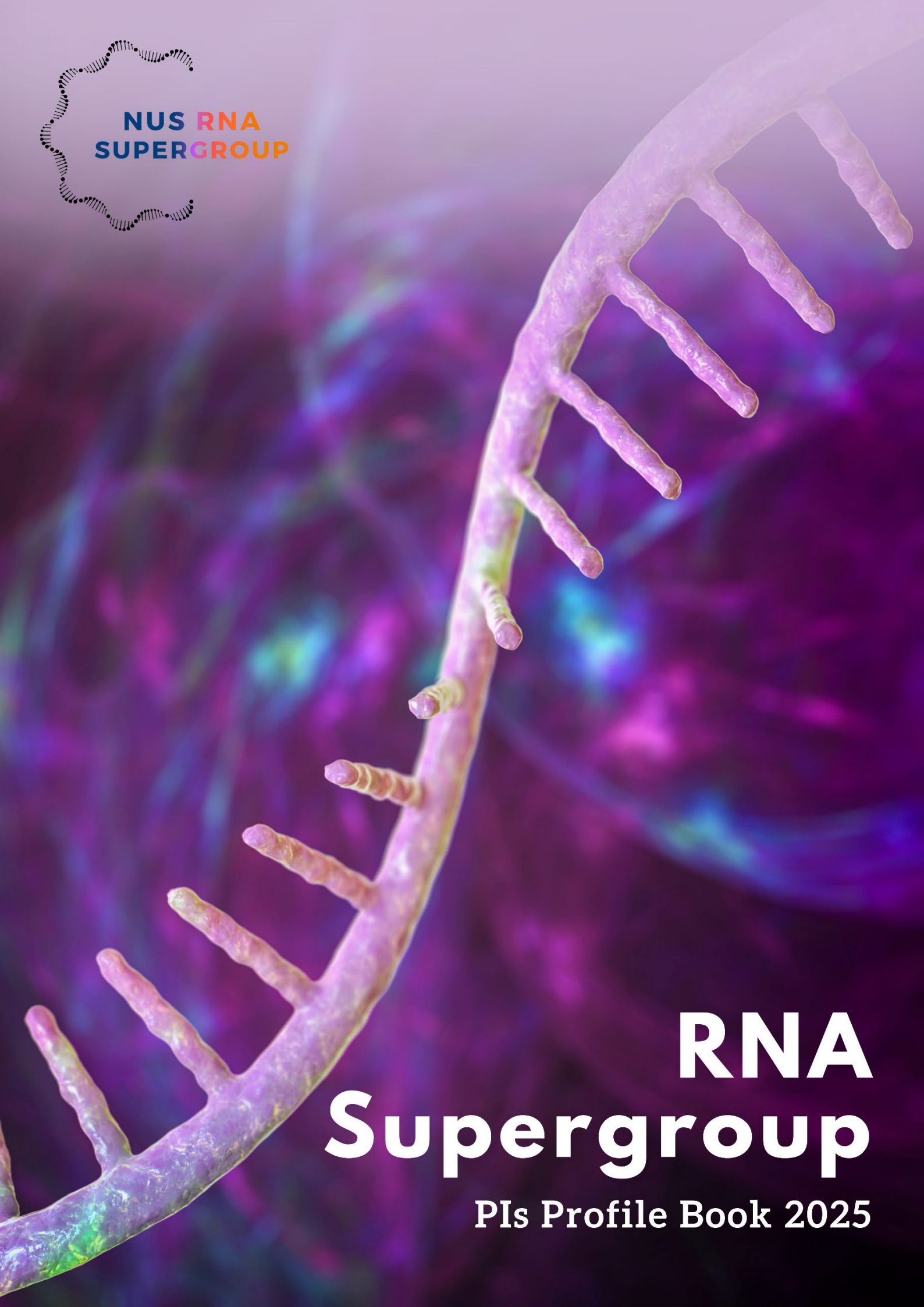
NUS RNA SUPERGROUP



RNA Supergroup

PIs Profile Book 2025

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CHAN Eric Chun Yong

Faculty of Science

Research Interests:

RNA Biomarkers & Therapeutics RNA Delivery

RNA Structure and Modelling

Chan's lab specializes in physiologically-based pharmacokinetic-pharmacodynamic (PBPK-PD) modeling to study pharmacology and toxicology. This approach integrates physiological, biochemical, and molecular data to predict the absorption, distribution, metabolism, and excretion of drugs including RNA therapeutics, as well as their pharmacological effects and potential toxicity. By using PBPK-PD models, the lab aims to enhance the understanding of drug behavior in the body, optimize dosing regimens, and improve the safety and efficacy of therapeutic interventions.

Areas for collaboration:

- PBPK-PD modeling of RNA therapeutics

Selected Publicationss:

Qian L, Wang Z, Paine MF, Chan ECY, Zhou Z. Application of physiologically-based pharmacokinetic modeling to inform dosing decisions for geriatric patients. CPT Pharmacometrics & Systems Pharmacology. (2024). doi:10.1002/psp4.13241

Ng TM, Wang Z, Chan ECY. Physiologically-based pharmacokinetic modelling guided dose evaluations of nirmatrelvir/ritonavir in renal impairment for the management of COVID-19. British Journal of Clinical Pharmacology. (2024). doi:10.1111/bcp.16074

Cheong EJY, Chin SY, Ng ZW, et al. Unraveling complexities in the absorption and disposition kinetics of abiraterone via iterative PBPK model development and refinement. Clinical Pharmacokinetics. (2023);62(9):1243-1261. doi:10.1007/s40262-023-01266-y

Leow JWH, Ang XJ, Chan ECY. Development and verification of a physiologically based pharmacokinetic model of dronedarone and its active metabolite N-desbutyldronedarone: Application to prospective simulation of complex drug–drug interaction with rivaroxaban. British Journal of Clinical Pharmacology. (2023);89(6):1873-1890. doi:10.1111/bcp.15670

Wang Z, Chan ECY. Role of Cytochrome P450 2C8 in Drug–Drug Interaction between Amiodarone and Nirmatrelvir/Ritonavir Via Physiologically-Based Pharmacokinetic Modeling. Clinical Pharmacology & Therapeutics. 2023;113(6):1183-1184. doi:10.1002/cpt.2885

CHAN Kuan Rong

Duke-NUS Medical School

Research Interests:
Innate Immunity RNA Biomarkers & Therapeutics
Transcriptomics and Bioinformatics

Chan's research employs systems biology approaches in virology and vaccinology. By examining host transcriptomic responses to viruses, the lab aims to elucidate virus-host interactions that cause human diseases. Furthermore, by characterizing the transcriptional atlas of vaccine responses, the lab seeks to identify early correlates of protection to advance vaccine development.

Areas for collaboration:

- Various RNA sequencing technology including single-cell RNAseq and TCR single-cell sequencing
- Machine learning and artificial intelligence

Selected Publications:

Mok DZ, Tng DJ, Yee JX, et al. Electron transport chain capacity expands yellow fever vaccine immunogenicity. EMBO Molecular Medicine. (2024);16(6):1310-1323. doi:10.1038/s44321-024-00065-7

Zhong Y, Kang AYH, Tay CJX, et al. Correlates of protection against symptomatic SARS-CoV-2 in vaccinated children. Nature Medicine. (2024);30(5):1373-1383. doi:10.1038/s41591-024-02962-3

Ong EZ, Koh CWT, Tng DJH, et al. RNase2 is a possible trigger of acute-on-chronic inflammation leading to mRNA vaccine-associated cardiac complication. Med. (2023);4(6):353-360.e2. doi:10.1016/j.medj.2023.04.001

Koh CWT, Ooi JSG, Ong EZ, Chan KR. STAGEs: A web-based tool that integrates data visualization and pathway enrichment analysis for gene expression studies. Scientific Reports. (2023);13(1). doi:10.1038/s41598-023-34163-2

Chan KR, Koh CWT, Ng DHL, et al. Early peripheral blood MCEMP1 and HLA-DRA expression predicts COVID-19 prognosis. EBioMedicine. (2023);89:104472. doi:10.1016/j.ebiom.2023.104472

CHEN Leilei Polly

Cancer Science Institute of Singapore

Research Interests:
RNA Modification RNA Biomarkers & Therapeutics
Innate Immunity

Chen's lab was among the first to report that dysregulated adenosine-to-inosine (A-to-I) RNA editing contributes to human liver, stomach, and esophageal cancers. Their research has shown how adenosine deaminases acting on RNA (ADARs) regulate gene functions and RNA processing in cancer. Additionally, the lab identified numerous non-ADAR RNA editing regulators and their role in shaping the cancer editome. To translate these findings into clinical applications, they developed antisense oligonucleotide (ASO) and small molecule-based RNA editing inhibitors for cancer therapy.

The current and future research of Chen's lab focuses on the molecular mechanisms behind RNA-associated immune regulation. The lab is also investigating how pre-neoplastic and tumor cells evade immune detection and activation by interfering with RNA sensing pathways.

Areas for collaboration:

- Study of RNA editing/modifications using Cell Lines, Clinical Samples, Patient-Derived Xenografts, Organoids, Genetic Models, Mouse Xenograft Models, etc.
- Bulk and Single-Cell RNA Sequencing, Spatial Transcriptomics, CRISPR/Cas9 Screening, Loss/Gain of Function Analysis

Selected Publications:

Han J, Song Y, Xie J, et al. Modulation of m6A RNA modification by DAP3 in cancer cells. Proceedings of the National Academy of Sciences. (2024);121(40). doi:10.1073/pnas.2404509121

Gan WL, Ren X, Ng VHE, et al. Hepatocyte-macrophage crosstalk via the PGRN-EGFR axis modulates ADAR1-mediated immunity in the liver. Cell Reports. (2024);43(7):114400. doi:10.1016/j.celrep.2024.114400

Guo M, Chan HMT, Zhou QL, et al. Core binding factor fusion downregulation of ADAR2 RNA editing contributes to AML leukemogenesis. Blood. (2023). doi:10.1182/blood.2022015830

Chen L. A-to-I editing prevents self-RNA sensing. Nature Reviews Molecular Cell Biology. (2022);24(2):85. doi:10.1038/s41580-022-00540-4

Shen H, An O, Ren X, et al. ADARs act as potent regulators of circular transcriptome in cancer. Nature Communications. (2022);13(1). doi:10.1038/s41467-022-29138-2

CHEONG Jit Kong

Yong Loo Lin School of Medicine

Research Interests:

Non-Coding RNAs RNA Biomarkers & Therapeutics

RNA-Protein Interactions

The Cheong lab focuses on investigating the complex interplay between non-coding RNAs and untranslated regions (UTRs) of key effector mRNAs in cancer pathophysiology. As a proof of concept, they revealed Casein Kinase 1 alpha's role as an oncogenic RAS signaling effector in colon cancer, where its protein translation is mediated by mutant RAS-regulated RNA-binding proteins and its 5' UTR. Dr Cheong also established the NUSMed ncRNA Core to support miRNA/ncRNA biomarker discovery by collaborating with local and overseas institutions as well as biopharma companies (Mirxes Pte Ltd, etc). To date, the ncRNA Core has helped to identify various human disease-relevant miRNA biomarker panels for future development of in vitro diagnostics and therapeutics. Going forward, they are keen to work with the RNA community on discovering cell-free RNA modifications to inform tissue origin and serve as disease biomarkers.

Areas for collaboration:

- Discovery of cfRNA modifications that inform tissue of origin and serve as disease biomarkers.
- Promega Maxwell RSC automated nucleic acid isolation system
- Mirxes ID3EAL high-throughput miRNA expression screens custom miRNA assay development.
- Gateway to Mirxes Next-Gen-Seq services at preferential rate

Selected Publications:

Masroni MSB, Eng GWL, Jeon AJ, et al. MicroRNA expression signature as a biomarker in the diagnosis of nodal T-cell lymphomas. Cancer Cell International. (2024);24(1). doi:10.1186/s12935-024-03226-3

Blandino G, Dinami R, Marcia M, et al. The new world of RNA diagnostics and therapeutics. Journal of Experimental & Clinical Cancer Research. (2023);42(1). doi:10.1186/s13046-023-02752-8

Kok VJT, Tang JY, Eng GWL, et al. SFPQ promotes RAS-mutant cancer cell growth by modulating 5'-UTR mediated translational control of CK1α. NAR Cancer. (2022);4(3). doi:10.1093/narcan/zcac027

Cheong JK, Rajgor D, Lv Y, Chung KY, Tang YC, Cheng H. Noncoding RNome as enabling biomarkers for precision health. International Journal of Molecular Sciences. (2022);23(18):10390. doi:10.3390/ijms231810390

Cheong JK, Tang YC, Zhou L, Cheng H, Too HP. Advances in quantifying circulatory microRNA for early disease detection. Current Opinion in Biotechnology. (2022);74:256-262. doi:10.1016/j.copbio.2021.12.007

CHEOW Lih Feng

College of Design and Engineering

Research Interests:
New Technologies Non-coding RNAs
Transcriptomics and Bioinformatics

Cheow's lab focuses on developing innovative technologies for RNA detection, with a particular emphasis on single-cell analysis of RNA and other modalities. A key achievement of Cheow's lab is the development of the scComplete-seq platform, which enables simultaneous measurement of both coding and non-coding RNA (such as tRNA, miRNA, snRNA, and lncRNA) within single cells. In addition to this, Cheow's lab is working on creating new technology platforms for rapid RNA detection and high-throughput screening. Cheow's lab is actively seeking collaborations to explore and uncover new aspects of RNA biology using these advanced methodologies.

Areas for collaboration:

- Single cell analysis (coding and non-coding RNA)
- High throughput RNA screening
- RNA detection

Selected Publications:

Liu Y, Cui X, Lu R, Yang D, Ai Y, Cheow LF. Digital Sort-Enabled counting allows absolute electrical quantification of target nucleic acid. ACS Sensors. (2024);9(5):2695-2702. doi:10.1021/acssensors.4c00750

Dinçaslan FB, Ngang SWY, Tan RZ, Cheow LF. Automated high-throughput profiling of single-cell total transcriptome with scComplete-seq. bioRxiv (Cold Spring Harbor Laboratory). (2024). doi:10.1101/2024.03.12.584729

Luah YH, Wu T, Cheow LF. Identification, sorting and profiling of functional killer cells via the capture of fluorescent target-cell lysate. Nature Biomedical Engineering. (2023);8(3):248-262. doi:10.1038/s41551-023-01089-z

Wu T, Womersley HJ, Wang JR, Scolnick J, Cheow LF. Time-resolved assessment of single-cell protein secretion by sequencing. Nature Methods. (2023);20(5):723-734. doi:10.1038/s41592-023-01841-y

CHIA Gloryn

Faculty of Science

Research Interests:
New Technologies RNA delivery
Transcriptomics and Bioinformatics

Chia's lab is at the forefront of cancer immunotherapy research, focusing on personalized neoantigen vaccines. These vaccines target neoantigens, unique proteins from cancer-specific mutations, allowing for precise immunotherapy with minimal off-target effects. The lab utilizes advanced genomic technologies to identify neoantigens tailored to each patient, addressing the challenge of limited tumor immunogenicity. Researchers explore using engineered induced pluripotent stem cells for scalable vaccine production and developing artificial antigen-presenting cells to enhance cytotoxic T-cell activation. By addressing regulatory and logistical challenges, the lab aims to translate its research into clinical practice, improving cancer treatment personalization.

Areas for collaboration:

- RNA delivery to T cells

Selected Publications:

Ren Y, Manoharan T, Liu B, et al. Circular RNA as a source of neoantigens for cancer vaccines. Journal for ImmunoTherapy of Cancer. (2024);12(3):e008402. doi:10.1136/jitc-2023-008402

CHNG Wee Joo

Cancer Science Institute of Singapore

Research Interests:
Non-Coding RNAs RNA Biomarkers & Therapeutics
RNA Modification

Chng's Laboratory conducts a comprehensive translational research program focusing on haematological malignancies like multiple myeloma (MM), acute myeloid leukemias (AML), and natural killer/T-cell lymphoma (NKTL). The program leverages advanced genomics and proteomics techniques in human tumor samples and model systems to identify clinically relevant discoveries, including novel biological insights, new diagnostic subtypes, prognostic factors, therapeutic targets, and aspects of molecular epidemiology and pharmacogenomics. These findings aim to enhance patient care. The lab follows a bench-to-bedside approach, ensuring discoveries are validated pre-clinically before clinical validation. Their efforts are supported by a robust tissue bank and a clinical database for integrated system biology analysis.

Areas for collaboration:

- RNA editing in blood cancers
- RNA Modification in blood cancers
- MiRNA and lncRNA in blood cancers

Selected Publications:

Koh MY, Chung TH, Tang NXN, et al. ADAR1-regulated cytoplasmic dsRNA-sensing pathway is a novel mechanism of lenalidomide resistance in multiple myeloma. Blood. (2024). doi:10.1182/blood.2024024429

Guo M, Chan HMT, Zhou QL, et al. Core binding factor fusion downregulation of ADAR2 RNA editing contributes to AML leukemogenesis. Blood. (2023). doi:10.1182/blood.2022015830

Ran XB, Ding LW, Sun QY, et al. Targeting RNA exonuclease XRN1 potentiates efficacy of cancer immunotherapy. Cancer Research. (2023);83(6):922-938. doi:10.1158/0008-5472.can-21-3052

Pratanwanich PN, Yao F, Chen Y, et al. Identification of differential RNA modifications from nanopore direct RNA sequencing with xPore. Nature Biotechnology. (2021);39(11):1394-1402. doi:10.1038/s41587-021-00949-w

Teoh PJ, Koh MY, Chng WJ. ADARs, RNA editing and more in hematological malignancies. Leukemia. (2020);35(2):346-359. doi:10.1038/s41375-020-01076-2

CHU Justin Jang Hann

Yong Loo Lin School of Medicine

Research Interests:

Bacterial and Viral RNAs RNA Biomarkers & Therapeutics

RNA-Protein Interactions

Chu's lab investigates the viral RNA-host interactome to uncover how viruses manipulate host cellular machinery, affecting virus replication, pathogenesis and persistence. They focus on identifying virus-derived sfRNA and miRNAs that influence replication. Their research targets therapeutic avenues to alter cellular functions to hinder viral replication. The lab has advanced small molecule inhibitors and RNA-based therapeutics that target virus replication and translation. They have developed virus RNA genome recoding technology for next-generation vaccine development. Chu's team is also creating mRNA-based vaccines, including subunit and self-replicating vaccines, to advance vaccine innovation.

Areas for collaboration:

- Identification of novel host and viral factors that play critical roles in viral infection through comprehensive human genome-wide screening platform
- Mechanistic investigations of molecular interactions that govern RNA virology
- Antiviral efficacy evaluation of therapeutics against positive-sense RNA viruses

Selected Publications:

Lim TYM, Jaladanki CK, Wong YH, Yogarajah T, Fan H, Chu JJH. Tanomastat exerts multi-targeted inhibitory effects on viral capsid dissociation and RNA replication in human enteroviruses. EBioMedicine. (2024);107:105277. doi:10.1016/j.ebiom.2024.105277

Chen H, Phuektes P, Yeo LS, et al. Attenuation of neurovirulence of chikungunya virus by a single amino acid mutation in viral E2 envelope protein. Journal of Biomedical Science. (2024);31(1). doi:10.1186/s12929-024-00995-x

Chin WX, Kong HY, Zhu IXY, et al. Flavivirus genome recoding by codon optimisation confers genetically stable in vivo attenuation in both mice and mosquitoes. PLoS Pathogens. (2023); 19(10): e1011753. doi:10.1371/journal.ppat.1011753

Keng CT, Yogarajah T, Lee RCH, et al. AAV-CRISPR-Cas13 eliminates human enterovirus and prevents death of infected mice. EBioMedicine. (2023);93:104682. doi:10.1016/j.ebiom.2023.104682

Wu KX, Yogarajah T, Loe MWC, et al. The host-targeting compound peruvoside has a broad-spectrum antiviral activity against positive-sense RNA viruses. Acta Pharmaceutica Sinica B. 2023;13(5):2039-2055. doi:10.1016/j.apsb.2023.03.015

CHUA John Jia En

Yong Loo Lin School of Medicine

Research Interests:
RNA-Protein Interactions
Transcriptomics and Bioinformatics Translation

Chua's lab is focused on exploring the intricate dynamics of neuronal synapses and the extensive networks they form within the brain. Understanding that synapses are essential conduits for information transfer, the lab investigates how these connections contribute to the systematic organization of approximately 100 billion neurons into functional networks. Synaptic malfunctions or failures, which can disrupt and destroy these networks, are central to the study of neurodevelopmental and neurodegenerative disorders. The lab's research aims to uncover the mechanisms that drive both the formation of neuronal networks and their dysfunction. By doing so, Chua's lab seeks to elucidate the biological principles that govern the development of brain function and its decline due to aging and neurodegeneration, ultimately providing deeper insights into these critical processes.

Areas for collaboration:

- Transcriptomics
- transcriptional and translational control of gene/protein expression

Selected Publications:

Qu Y, Lim JJY, An O, Yang H, Toh YC, Chua JJE. FEZ1 participates in human embryonic brain development by modulating neuronal progenitor subpopulation specification and migrations. iScience. (2023);26(12):108497. doi:10.1016/j.isci.2023.108497

Kok VJT, Tang JY, Eng GWL, et al. SFPQ promotes RAS-mutant cancer cell growth by modulating 5'-UTR mediated translational control of CK1α. NAR Cancer. (2022);4(3). doi:10.1093/narcan/zcac027

Chua JJE, Schob C, Rehbein M, Gkogkas CG, Richter D, Kindler S. Synthesis of two SAPAP3 isoforms from a single mRNA is mediated via alternative translational initiation. Scientific Reports. (2012);2(1). doi:10.1038/srep00484

DENG Lih Wen

Yong Loo Lin School of Medicine

Research Interests:
Non-Coding RNAs
RNA Biomarkers & Therapeutics

Deng's group is focused on leveraging RNA molecules, particularly microRNAs (miRNAs), as biomarkers for disease prediction and assessing therapeutic responses. The team employs miRNA profiling and functional validation, concentrating primarily on cancers such as cervical cancer, nasopharyngeal cancer, and hepatocellular carcinoma. The group's work involves developing miRNA-based biomarker panels that predict treatment outcomes, including stratification for radiotherapy response, and validating these panels across diverse patient cohorts to ensure their clinical applicability.

Additionally, the group investigates the role of miRNAs in therapeutic resistance, with a specific emphasis on radiation therapy. This research explores the potential of miRNAs as predictive tools for treatment response. By conducting multi-cohort, retrospective studies and integrating advanced bioinformatics with wet lab validation.

Areas for collaboration:

- biomarker discovery of miRNA
- functional studies of miRNA in disease mechanisms
- miRNA-based diagnostics

Selected Publications:

Nin DS, Wujanto C, Tan TZ, et al. GAGE mediates radio resistance in cervical cancers via the regulation of chromatin accessibility. Cell Reports. (2021);36(9):109621. doi:10.1016/j.celrep.2021.109621

DING Lingwen

Yong Loo Lin School of Medicine

Research Interests:
Innate Immunity RNA Biomarkers & Therapeutics
RNA Surveillance and Degradation

Ding's research group focuses on developing innovative therapeutic strategies to overcome resistance to cancer immunotherapy, including targeting abnormal RNA (e.g., dsRNA) degradation and detection pathways to trigger anti-cancer immunity, as well as advancing mRNA and dendritic cell-based cancer vaccines. Additionally, they are investigating genetic and epigenetic abnormalities in cancers and pre-cancerous conditions, with the aim of identifying new therapeutic targets and early screening or MRD detection biomarkers arising from cancer-specific abnormalities. They are also interested in utilizing large-scale screening technologies, such as CRISPR library screening, to identify key oncogenic drivers, functionally characterize them, and develop siRNA-LNP therapies targeting these drivers.

Areas for collaboration:

- Customized mRNA sequence design, IVT synthesis, LNP encapsulation, and evaluation of its effects in various murine cancer models (e.g., syngeneic mouse models and human cancer murine models)
- Customized lentivirus expression system and stable expression cell line generation

Selected Publications:

Lao Z, Ding LW, Sun QY, et al. A Pre-Leukemic DNA methylation signature in healthy individuals at higher risk for developing myeloid malignancy. Clinical Cancer Research. (2024);30(10):2170-2180. doi:10.1158/1078-0432.ccr-22-3804

Liu J, Zhang Y, Yang B, et al. Synergistic glutathione depletion and STING activation to potentiate dendritic cell maturation and cancer vaccine efficacy. Angewandte Chemie International Edition. (2024);63(10). doi:10.1002/anie.202318530

Liu J, Zhan J, Zhang Y, et al. Ultrathin Clay Nanoparticles-Mediated mutual reinforcement of ferroptosis and cancer immunotherapy. Advanced Materials. (2023);36(9). doi:10.1002/adma.202309562

Ran XB, Ding LW, Sun QY, et al. Targeting RNA exonuclease XRN1 potentiates efficacy of cancer immunotherapy. Cancer Research. (2023);83(6):922-938. doi:10.1158/0008-5472.can-21-3052

Loh XY, Sun QY, Ding LW, et al. RNA-Binding protein ZFP36L1 suppresses hypoxia and Cell-Cycle signaling. Cancer Research. (2020);80(2):219-233. doi:10.1158/0008-5472.can-18-2796

FOO Sik Yin Roger

Yong Loo Lin School of Medicine

Research Interests:
RNA Biomarkers & Therapeutics
RNA Modification RNA Processing

The Foo lab investigates cardiac biology and disease mechanisms through genomic, transcriptomic, and epigenomic analyses. Utilizing single-cell RNA-sequencing, they study heart failure cardiomyocyte subpopulations and genetic variations in Southeast Asia. The lab embraces new technologies like spatial RNA-sequencing and CRISPR, alongside stem cells and gene therapy. They have expanded into clinical and population health to prevent heart disease in Southeast Asia and explore RNA modification pathways for heart cell maturation and aging. Their goal is to rejuvenate the heart and reverse cardiac aging, while also training scientists and promoting heart health initiatives in Singapore.

Areas for collaboration:

- Pre-mRNA processing - capping, splicing, and polyadenylation.
- Biogenesis and functions of noncoding RNAs.
- Targeting of RNA - subcellular trafficking and localization.
- RNA folding, structure, modifications and editing.
- RNA-interactions; RNA-protein, RNA-RNA interactions including microRNAs.
- Therapeutic applications: in vitro and in vivo models

Selected Publications:

Yang Y, Dashi A, Soong PL, et al. Long noncoding RNA VENTHEART is required for ventricular cardiomyocyte specification and function. Journal of Molecular and Cellular Cardiology. (2024);197:90-102. doi:10.1016/j.yjmcc.2024.10.009

Neufeldt D, Schmidt A, Mohr E, et al. Circular RNA circZFPM2 regulates cardiomyocyte hypertrophy and survival. Basic Research in Cardiology. (2024);119(4):613-632. doi:10.1007/s00395-024-01048-y

Honardoost MA, Adinatha A, Schmidt F, et al. Systematic immune cell dysregulation and molecular subtypes revealed by single-cell RNA-seq of subjects with type 1 diabetes. Genome Medicine. (2024);16(1). doi:10.1186/s13073-024-01300-z

Lu D, Chatterjee S, Xiao K, et al. A circular RNA derived from the insulin receptor locus protects against doxorubicin-induced cardiotoxicity. European Heart Journal. (2022);43(42):4496-4511. doi:10.1093/eurheartj/ehac337

Zhai W, Lai H, Kaya NA, et al. Dynamic phenotypic heterogeneity and the evolution of multiple RNA subtypes in hepatocellular carcinoma: the PLANET study. National Science Review. (2021);9(3). doi:10.1093/nsr/nwab192

HO Cyrus Su Hui

Yong Loo Lin School of Medicine

Research Interests:
RNA Biomarkers & Therapeutics
Transcriptomics and Bioinformatics

Ho's team is focused on unraveling the complex pathomechanisms and neurobiology of mood disorders and their psychosocial impacts through a multifaceted approach that includes clinical studies, basic science investigations, animal models, and meta-analyses. The team aims to enhance the diagnosis, prediction, and treatment of mood disorders by identifying RNA biomarkers and utilizing therapeutics, transcriptomics, and bioinformatics. Additionally, they are leveraging neuroimaging and biological markers, along with artificial intelligence, to pioneer novel therapies for treatment-resistant cases.

Areas for collaboration:

- Mood disorder diagnostics, disease and treatment prediction, therapeutics
- Suicide and suicidality biomarker
- Artificial intelligence in psychiatric diagnostics and therapeutics

Selected Publications:

Chan YL, Ho CSH, Tay GWN, Tan TWK, Tang TB. MicroRNA classification and discovery for major depressive disorder diagnosis: Towards a robust and interpretable machine learning approach. Journal of Affective Disorders. (2024);360:326-335. doi:10.1016/j.jad.2024.05.066

Ho CSH, Soh MWT, Tay GWN. The diagnostic utility of miRNA and elucidation of pathological mechanisms in major depressive disorder. Comprehensive Psychiatry. (2022);121:152363. doi:10.1016/j.comppsych.2022.152363

HO Lena

Duke-NUS Medical School

Research Interests:
Innate Immunity Non-Coding RNAs
Translation

Ho's group is interested in small open reading frames (smORF) that are nestled in non-coding RNAs as well as untranslated regions of mRNAs. They perform ribosome profiling to uncover these smORF translation events. smORF-encoded peptides (SEPs) can either be functional proteins or by-products of cis-acting translational regulatory mechanisms (such as uORFs). They are interested in the mechanisms that regulate smORF translation. Ho's group are looking for collaborators who are interested in understanding what determines ORF selection (e.g. uORF versus downstream cis ORFs), such as RNA structure, modifications and ribosome composition.

Areas for collaboration:

- Small open reading frames (smORF) and smORF-encoded peptides (SEPs) prediction
- smORF-encoded peptides (SEPs) functionalization
- Ribosome profiling

Selected Publications:

Zhang S, Guo Y, Fidelito G, et al. LINC00116-encoded microprotein mitoregulin regulates fatty acid metabolism at the mitochondrial outer membrane. iScience. (2023);26(9):107558. doi:10.1016/j.isci.2023.107558

Chothani S, Ho L, Schafer S, Rackham O. Discovering microproteins: making the most of ribosome profiling data. RNA Biology. (2023);20(1):943-954. doi:10.1080/15476286.2023.2279845

Chothani SP, Adami E, Widjaja AA, et al. A high-resolution map of human RNA translation. Molecular Cell. (2022);82(15):2885-2899.e8. doi:10.1016/j.molcel.2022.06.023

Lee CQE, Kerouanton B, Chothani S, et al. Coding and non-coding roles of MOCCI (C15ORF48) coordinate to regulate host inflammation and immunity. Nature Communications. (2021);12(1). doi:10.1038/s41467-021-22397-5

Zhang S, Reljić B, Liang C, et al. Mitochondrial peptide BRAWNIN is essential for vertebrate respiratory complex III assembly. Nature Communications. (2020);11(1). doi:10.1038/s41467-020-14999-2

HO Sook Yuin Jessica

Duke-NUS Medical School

Research Interests:
Innate Immunity RNA Processing
RNA-Chromatin Interactions

Ho's lab focuses on understanding how epigenetic and transcriptional mechanisms affect the cellular response to Influenza A viral infections over both short and long terms. They employ biochemistry, next-generation sequencing, and in vivo animal models to explore several areas of interest. These areas include the regulation of host RNA splicing and transcription during influenza infection, chromatin control of the host response, and the role of RNA modifications in the innate immune response. Furthermore, the lab is working on developing RNA-based therapeutics against viral infections and studying transcriptional control of stress-inducible and inflammatory genes in cancer and other diseases.

Areas for collaboration:

- Study RNA-chromatin and RNA-protein interactions genome-wide by next generation sequencing techniques (eCLIP, ChIP-seq)
- Investigate splicing and transcript isoform expression by using combination of short and long read sequencing analysis

Selected Publications:

Torre D, Fstkchyan YS, Ho JSY, et al. Nuclear RNA catabolism controls endogenous retroviruses, gene expression asymmetry, and dedifferentiation. Molecular Cell. (2023); 83(23):4255-4271.e9. doi:10.1016/j.molcel.2023.10.036

Zhao N, Ho JSY, Meng F, et al. Generation of host-directed and virus-specific antivirals using targeted protein degradation promoted by small molecules and viral RNA mimics. Cell Host & Microbe. (2023);31(7):1154-1169.e10. doi:10.1016/j.chom.2023.05.030

Ho JSY, Di Tullio F, Schwarz M, et al. HNRNPM controls circRNA biogenesis and splicing fidelity to sustain cancer cell fitness. eLife. (2021);10. doi:10.7554/elife.59654

Ho JSY, Zhu Z, Marazzi I. Unconventional viral gene expression mechanisms as therapeutic targets. Nature. (2021);593(7859):362-371. doi:10.1038/s41586-021-03511-5

Ho JSY, Mok BWY, Campisi L, et al. TOP1 inhibition therapy protects against SARS-CoV-2-induced lethal inflammation. Cell. (2021);184(10):2618-2632.e17. doi:10.1016/j.cell.2021.03.051

HU Chunyi

Faculty of Science

Research Interests:

Bacterial and Viral RNAs RNA Structure and Modeling
RNA Surveillance and Degradation

Hu's lab explores RNA biology, focusing on the molecular mechanisms of macromolecules and their assemblies. A key area is the study of CRISPR-Cas systems, where RNA-guided proteins in prokaryotes defend against viral infections, showcasing RNA's role in molecular recognition and regulation. The lab examines the assembly, function, and evolution of these systems, aiming for therapeutic applications. Beyond CRISPR, they investigate RNA-protein interactions and gene expression regulation. By combining structural biology, biochemistry, and advanced technologies, the Hu lab seeks to enhance understanding of RNA's role in molecular machinery for transformative biomedical advances.

Areas for collaboration:

- RNA modification
- CryoEM Structure Biology
- RNA base editing

Selected Publications:

Guo R, Sun X, Wang F, et al. Engineered IscB-ωRNA system with improved base editing efficiency for disease correction via single AAV delivery in mice. Cell Reports. (2024);43(11):114973. doi:10.1016/j.celrep.2024.114973

Hu T, Ji Q, Ke X, et al. Repurposing Type I-A CRISPR-Cas3 for a robust diagnosis of human papillomavirus (HPV). Communications Biology. (2024);7(1). doi:10.1038/s42003-024-06537-3

Li Z, Guo R, Sun X, et al. Engineering a transposon-associated TnpB-ωRNA system for efficient gene editing and phenotypic correction of a tyrosinaemia mouse model. Nature Communications. (2024);15(1). doi:10.1038/s41467-024-45197-z

Hu C, Myers MT, Zhou X, et al. Exploiting activation and inactivation mechanisms in type I-C CRISPR-Cas3 for genome-editing applications. Molecular Cell. (2024);84(3):463-475.e5. doi:10.1016/j.molcel.2023.12.034

Hu C, Van Beljouw SPB, Nam KH, et al. Craspase is a CRISPR RNA-guided, RNA-activated protease. Science. (2022);377(6612):1278-1285. doi:10.1126/science.add5064

HUANG Hua

Yong Loo Lin School of Medicine

Research Interests:
RNA Biomarkers & Therapeutics
RNA Modification RNA Processing

Huang's expertise encompasses patch-clamp electrophysiology, ion channel regulation through alternative splicing and RNA editing, and targeting channelopathies with nucleic acid therapeutics. He has extensively published on ion channel physiology regulation by RNA processing in high-impact journals. His recent discovery of novel human TRPA1 variations offers potential for developing splice-switching antisense oligonucleotides (ASO) as a novel therapeutic strategy for chronic pain by inhibiting ROS-sensitive TRPA1 channels, featured in Pain journal. Dr. Huang is also exploring other channelopathies, including monogenic epilepsy, in his recent research ventures.

Areas for collaboration:

- Mechanism and regulation of alternative splicing
- Mechanism and regulation of A-to-I RNA editing
- Splice-switching antisense oligonucleotide
- Gapmer ASO therapeutic for genetic disorders

Selected Publications:

Huang H, Rui D MA, Chan DWS, et al. Targeting heterozygous dominant negative variant of KCNA2 using Gapmer antisense oligonucleotides (ASO) for the treatment of drug-resistant epilepsy. Molecular Therapy — Nucleic Acids. (2024);35(4):102316. doi:10.1016/j.omtn.2024.102316

Zhai J, Navakkode S, Yeow SQZ, et al. Loss of Ca V 1.3 RNA editing enhances mouse hippocampal plasticity, learning, and memory. Proceedings of the National Academy of Sciences. (2022);119(32). doi:10.1073/pnas.2203883119

Huang H, Tay SH, Ng W, Ng SY, Soong TW. Targeting novel human transient receptor potential ankyrin 1 splice variation with splice-switching antisense oligonucleotides. Pain. (2021);162(7):2097-2109. doi:10.1097/j.pain.0000000000002216

Bartels P, Yu D, Huang H, Hu Z, Herzig S, Soong TW. Alternative splicing at N terminus and domain I modulates CAV1.2 inactivation and surface expression. Biophysical Journal. (2018);114(9):2095-2106. doi:10.1016/j.bpj.2018.03.029

Huang H, Kapeli K, Jin W, et al. Tissue-selective restriction of RNA editing of CaV1.3 by splicing factor SRSF9. Nucleic Acids Research. (2018);46(14):7323-7338. doi:10.1093/nar/gky348

ITAHANA Koji

Duke-NUS Medical School

Research Interests:
Innate Immunity RNA Modification
RNA Surveillance and Degradation

Itahana's lab is primarily interested in p53-mediated tumor suppression and cellular senescence. Their recent research also explores p53's role in tissue homeostasis, focusing on its involvement in regulating iron metabolism, mRNA stability and degradation, innate immunity, and RNA methylation.

Areas for collaboration:

- RNA recognition by macrophages in the context of innate immunity
- Iron-regulated mRNA degradation and translation
- RNA methylation and its functional implications
- RNA sensing and cellular senescence

Selected Publications:

Jagannathan NS, Koh JYP, Lee Y, et al. Multi-omic analysis of bat versus human fibroblasts reveals altered central metabolism. eLife. (2024);13. doi:10.7554/elife.94007

Koh JYP, Itahana Y, Krah A, et al. Exploring bat-inspired cyclic tryptophan diketopiperazines as ABCB1 Inhibitors. Communications Chemistry. (2024);7(1). doi:10.1038/s42004-024-01225-z

Lee Y, Itahana Y, Ong CC, Itahana K. Redox-dependent AMPK inactivation disrupts metabolic adaptation to glucose starvation in xCT-overexpressing cancer cells. Journal of Cell Science. (2022);135(15). doi:10.1242/jcs.259090

Guo AK, Itahana Y, Seshachalam VP, Chow HY, Ghosh S, Itahana K. Mutant TP53 interacts with BCAR1 to contribute to cancer cell invasion. British Journal of Cancer. (2020);124(1):299-312. doi:10.1038/s41416-020-01124-9

Itahana K, Bhat KP, Jin A, et al. Tumor suppressor ARF degrades B23, a nucleolar protein involved in ribosome biogenesis and cell proliferation. Molecular Cell. (2003);12(5):1151-1164. doi:10.1016/s1097-2765(03)00431-3

KAN Jeroen Anton Van

Faculty of Science

Research Interests:
New Technologies RNA Processing
RNA-Protein Interactions

Kan's lab focuses on developing micro/nanofluidic devices for DNA/RNA analysis and biomedical applications, using techniques like proton beam writing and nanoimprint lithography. As Director at the Centre for Ion Beam Applications, he designs nanofluidic devices for single-molecule DNA/RNA detection and high-throughput mapping. His research also investigates RNA transport dynamics and enhances RNA sensing capabilities. Kan aims to create lab-on-a-chip devices for RNA-based diagnostics, therapeutics, and biomarker discovery, clarifying RNA biology complexities, uncovering new disease mechanisms, and advancing personalized medicine with innovative RNA-based technologies.

Areas for collaboration:

- Detection and mapping of single RNA molecules in nanochannels
- Dynamic study of RNA and protein interactions
- Developing new methods for RNA studies with LOC devices
- High-throughput detection of irregularities in RNA molecules

Selected Publications:

Tan CJ, Basak R, Yadav I, Van Kan J, Arluison V, Van Der Maarel J. Mobility of Bacterial protein HFQ on DSDNA: Role of C-Terminus-Mediated Transient Binding. The Journal of Physical Chemistry B. (2022);126(7):1477-1482. doi:10.1021/acs.jpcb.1c10234

Basak R, Rosencrans W, Yadav I, et al. Internal motion of chromatin fibers is governed by dynamics of uncompressed linker strands. Biophysical Journal. (2020);119(11):2326-2334. doi:10.1016/j.bpj.2020.10.018

Yadav I, Basak R, Yan P, Van Kan JA, Arluison V, Van Der Maarel JRC. Role of internal DNA motion on the mobility of a Nucleoid-Associated protein. The Journal of Physical Chemistry Letters. (2020);11(19):8424-8429. doi:10.1021/acs.jpclett.0c02251

Yadav I, Rosencrans W, Basak R, Van Kan JA, Van Der Maarel JRC. Intramolecular dynamics of dsDNA confined to a quasi-one-dimensional nanochannel. Physical Review Research. (2020);2(1). doi:10.1103/physrevresearch.2.013294

Basak R, Liu F, Qureshi S, et al. Linearization and labeling of Single-Stranded DNA for optical sequence analysis. The Journal of Physical Chemistry Letters. (2019);10(3):316-321. doi:10.1021/acs.jpclett.8b03465

KAPPEI Dennis

Cancer Science Institute of Singapore

Research Interests:
RNA Modification RNA-Protein Interactions
Transcriptomics and Bioinformatics

Dennis Kappei's research group is interested in how telomere-driven genomic instability contributes to cancer development. They use quantitative mass spectrometry to identify novel telomere-binding proteins and to study changes in telomeric chromatin composition upon genetic manipulation. For the latter they have developed workflows for label-free quantitative proteomics analysis combined with chromatin immunoprecipitation (qChIP-MS) including locus-specific purification. Since many telomeric proteins moonlight as transcription factors, the group further examines their gene regulatory roles including putative feedback loops with telomeres. Their research extends to the long non-coding RNA TERRA, R-loop formation, as well as co-transcriptional RNA modifications and their impact on RNA stability and translation.

Areas for collaboration:

- Analysis of RNA-protein interactions via quantitative mass spectrometry
  - In vitro reconstitution RNA pull-downs
  - In vivo RNA-protein interactions by e.g. dCas13 fusions to proximity labeling enzymes
- General expertise in quantitative mass spectrometry analysis via the CSI Quantitative Proteomics Core

Selected Publications:

Rane G, Kuan VLS, Wang S, et al. ZBTB48 is a priming factor regulating B-cell-specific CIITA expression. The EMBO Journal. (2024). doi:10.1038/s44318-024-00306-y

Chua BH, Anuar NZ, Ferry L, et al. E4F1 and ZNF148 are transcriptional activators of the −57A > C and wild-typeTERTpromoter. Genome Research. (2023);33(11):1893-1905. doi:10.1101/gr.277724.123

Yong WK, Rane G, Anuar NZ, et al. ChIP-MS reveals the local chromatin composition by label-free quantitative proteomics. bioRxiv (Cold Spring Harbor Laboratory). (2023). doi:10.1101/2023.01.27.525999

Roelofs PA, Goh CY, Chua BH, et al. Characterization of the mechanism by which the RB/E2F pathway controls expression of the cancer genomic DNA deaminase APOBEC3B. eLife. (2020);9. doi:10.7554/elife.61287

Jahn A, Rane G, Paszkowski-Rogacz M, et al. ZBTB48 is both a vertebrate telomere-binding protein and a transcriptional activator. EMBO Reports. (2017);18(6):929-946. doi:10.15252/embr.201744095

KHONG Anthony

Cancer Science Institute of Singapore

Research Interests:
RNA-Protein Interactions
RNP Condensates Translation

Khong's lab is dedicated to uncovering and understanding RNA-mediated biological principles that enable cells to adapt to cancer-related stresses. These stresses include oxidative stress, hypoxia, ER stress, oncogenic induction, and chemotherapy-induced stress. The lab focuses on RNA-dependent processes such as translation, RNA decay, RNA transport, and the formation of cytosolic RNA condensates like P-bodies and stress granules. By investigating these mechanisms, the lab aims to identify cancer-specific vulnerabilities in RNA-mediated processes, ultimately contributing to the development of novel therapeutic strategies for cancer treatment.

Areas for collaboration:

- Genetically edited or depleted cancer cell lines targeting stress granule assembly and other RNA processes.
- Long-term imaging to monitor biomolecular condensate dynamics with fluorescently tagged proteins.
- Impact of cancer-related mutations in RNA-binding proteins.
- RNA-mediated processes in cancer stress adaptation.
- Targeting RNA-dependent processes linked to cancer mutations or stress adaptations

Selected Publications:

Khong A, Matheny T, Huynh TN, Babl V, Parker R. Limited effects of m6A modification on mRNA partitioning into stress granules. Nature Communications. (2022);13(1). doi:10.1038/s41467-022-31358-5

Cirillo L, Cieren A, Barbieri S, et al. UBAP2L Forms Distinct Cores that Act in Nucleating Stress Granules Upstream of G3BP1. Current Biology. (2020);30(4):698-707.e6. doi:10.1016/j.cub.2019.12.020

Tauber D, Tauber G, Khong A, Van Treeck B, Pelletier J, Parker R. Modulation of RNA condensation by the DEAD-Box protein EIF4A. Cell. (2020);180(3):411-426.e16. doi:10.1016/j.cell.2019.12.031

Khong A, Parker R. The landscape of eukaryotic mRNPs. RNA. (2019);26(3):229-239. doi:10.1261/rna.073601.119

Moon SL, Morisaki T, Khong A, Lyon K, Parker R, Stasevich TJ. Multicolour single-molecule tracking of mRNA interactions with RNP granules. Nature Cell Biology. (2019);21(2):162-168. doi:10.1038/s41556-018-0263-4

LE Thi Nguyet Minh

Yong Loo Lin School of Medicine

Research Interests:
New Technologies RNA Biomarkers & Therapeutics
RNA Delivery

Le's lab is at the forefront of utilizing extracellular vesicles (EVs), which serve as natural nanoparticles derived from cells, for the delivery of RNA therapeutics. By incorporating various RNA types, such as antisense oligonucleotides (ASOs), small interfering RNAs (siRNAs), immunomodulatory RNA (immRNA), and messenger RNAs (mRNAs), the lab aims to modulate gene expression and achieve immunotherapeutic effects in diseased cells. The lab has successfully demonstrated that EVs sourced from red blood cells are robust carriers capable of being loaded with RNAs and functionalized with antibodies, allowing for targeted RNA delivery to cancer and virus-infected cells. This innovative approach holds promise for treating cancer and infectious diseases.

Areas for collaboration:

- Targeted anti-cancer therapy
- Immunotherapy

Selected Publications:

Tran TTT, Phung CD, Yeo BZJ, et al. Customised design of antisense oligonucleotides targeting EGFR driver mutants for personalised treatment of non-small cell lung cancer. EBioMedicine. (2024);108:105356. doi:10.1016/j.ebiom.2024.105356

Jayasinghe MK, Gao C, Yap G, et al. Red blood Cell-Derived extracellular vesicles display endogenous antiviral effects and enhance the efficacy of antiviral oligonucleotide therapy. ACS Nano. (2023);17(21):21639-21661. doi:10.1021/acsnano.3c06803

Peng B, Yang Y, Wu Z, et al. Red blood cell extracellular vesicles deliver therapeutic siRNAs to skeletal muscles for treatment of cancer cachexia. Molecular Therapy. (2023);31(5):1418-1436. doi:10.1016/j.ymthe.2023.03.036

Peng B, Nguyen TM, Jayasinghe MK, et al. Robust delivery of RIG-I agonists using extracellular vesicles for anti-cancer immunotherapy. Journal of Extracellular Vesicles. (2022);11(4). doi:10.1002/jev2.12187

Jayasinghe MK, Pirisinu M, Yang Y, et al. Surface-engineered extracellular vesicles for targeted delivery of therapeutic RNAs and peptides for cancer therapy. Theranostics. (2022);12(7):3288-3315. doi:10.7150/thno.68667

LING Shuo-Chien

Yong Loo Lin School of Medicine

Research Interests:
RNA Localization and Transport RNA Processing
RNA-Protein Interactions

Ling's lab focuses on the pathological aggregation of TDP-43, a DNA/RNA-binding protein involved in RNA metabolism, prevalent in neurodegenerative diseases like Alzheimer's (AD) and amyotrophic lateral sclerosis (ALS). The research aims to understand how TDP-43-mediated RNA metabolism is essential for normal function and how its dysregulation contributes to disease. The lab has developed the SpliCeAT computational pipeline to catalog and accurately quantify splicing events using short-read RNA-seq data. They are systematically examining cell-type-specific splicing changes due to TDP-43 loss in distinct CNS cell types.

Areas for collaboration:

- SpliCeAT computational pipeline to catalogue splicing events
- Quantification using short-read RNA-sequencing

Selected Publications:

Tu H, Yeo XY, Zhang ZW, et al. NOTCH2NLC GGC intermediate repeat with serine induces hypermyelination and early Parkinson's disease-like phenotypes in mice. Molecular Neurodegeneration. (2024);19(1). doi:10.1186/s13024-024-00780-2

Winanto N, Tan LY, Chooi WH, et al. Polystyrene nanoplastics promote neurodegeneration by catalyzing TDP43 hyperphosphorylation. bioRxiv (Cold Spring Harbor Laboratory). (2024). doi:10.1101/2024.11.11.622894

Feng J, Chuah YH, Liang Y, et al. PHF2 regulates genome topology and DNA replication in neural stem cells via cohesin. Nucleic Acids Research. (2024);52(12):7063-7080. doi:10.1093/nar/gkae457

Ho WY, Chak LL, Hor JH, et al. FUS-dependent microRNA deregulations identify TRIB2 as a druggable target for ALS motor neurons. iScience. (2023);26(11):108152. doi:10.1016/j.isci.2023.108152

Hartmann H, Ho WY, Chang J, Ling S. Cholesterol dyshomeostasis in amyotrophic lateral sclerosis: cause, consequence, or epiphenomenon? FEBS Journal. (2021);289(24):7688-7709. doi:10.1111/febs.16175

LIU Haiyan

Yong Loo Lin School of Medicine

Research Interests:
Innate Immunity RNA Biomarkers & Therapeutics
RNA Delivery

Liu's Lab is engaged in developing mRNA vaccines for the treatment of hematopoietic malignancies and solid tumors. The lab's research encompasses several critical areas, including the identification and validation of neoantigens, design and synthesis of mRNA vaccines, and the optimization of delivery methods. Additionally, the lab conducts in vivo efficacy studies to evaluate the therapeutic potential of these vaccines.

Areas for collaboration:

- RNA vaccine design, production and delivery.
- Animal models and immune phenotyping and function studies

Selected Publications:

Mei Y, Zhu Y, Yong KSM, et al. IL-37 dampens immunosuppressive functions of MDSCs via metabolic reprogramming in the tumor microenvironment. Cell Reports. (2024);43(3):113835. doi:10.1016/j.celrep.2024.113835

Teo HY, Song Y, Yong KSM, et al. IL12/18/21 preactivation enhances the antitumor efficacy of expanded ΓΔT cells and overcomes resistance to Anti–PD-L1 treatment. Cancer Immunology Research. (2023);11(7):978-999. doi:10.1158/2326-6066.cir-21-0952

Gong H, Ma S, Chen J, et al. Dendritic cell-derived IL-27 p28 regulates T cell program in pathogenicity and alleviates acute graft-versus-host disease. Signal Transduction and Targeted Therapy. (2022);7(1). doi:10.1038/s41392-022-01147-z

Lin D, Mei Y, Lei L, et al. Immune suppressive function of IL-1α release in the tumor microenvironment regulated by calpain 1. OncoImmunology. (2022);11(1). doi:10.1080/2162402x.2022.2088467

Chang H, Chew SWT, Zheng M, et al. Cryomicroneedles for transdermal cell delivery. Nature Biomedical Engineering. (2021);5(9):1008-1018. doi:10.1038/s41551-021-00720-1

MATTAR Citra Nurfarah Zaini

Yong Loo Lin School of Medicine

Research Interests:
Innate Immunity RNA Biomarkers & Therapeutics
Transcriptomics and Bioinformatics

Mattar's Research Group focuses on fetal medicine for genetic diseases through intrauterine and perinatal stem cell and gene therapy. Their work includes addressing fetal cardiac malformations, cell-free molecular therapeutics, and using Artificial Intelligence for fetal surveillance and labor management. They aim to treat major hemoglobinopathies starting in the fetal stage, exploring the interaction between the maternal immune system and transplanted cells to enhance engraftment in thalassemic bone marrow. Additionally, they investigate intrauterine in vivo gene therapy for conditions like hemophilia and thalassemia, using animal models to replace abnormal genes with normal ones during fetal development.

Areas for collaboration:

- Gene therapy
- In vivo gene delivery

Selected Publications:

Mahyuddin AP, Swa HLF, Weng R, et al. COVID-19 vaccination before or during pregnancy results in high, sustained maternal neutralizing activity to SARS-CoV2 wild-type and Delta/Omicron variants of concern, particularly following a booster dose or infection. International Journal of Infectious Diseases. (2024);146:107121. doi:10.1016/j.ijid.2024.107121

Kandasamy K, Johana NB, Tan LG, et al. Maternal dendritic cells influence fetal allograft response following murine in-utero hematopoietic stem cell transplantation. Stem Cell Research & Therapy. (2023);14(1). doi:10.1186/s13287-023-03366-9

Kandasamy K, Tan LG, Johana N, et al. Maternal microchimerism and cell-mediated immune-modulation enhance engraftment following semi-allogenic intrauterine transplantation. The FASEB Journal. (2021);35(3). doi:10.1096/fj.202002185rr

Chan JKY, Gil-Farina I, Johana N, et al. Therapeutic expression of human clotting factors IX and × following adeno-associated viral vector-mediated intrauterine gene transfer in early-gestation fetal macaques. The FASEB Journal. (2018);33(3):3954-3967. doi:10.1096/fj.201801391r

Massaro G, Mattar CNZ, Wong AMS, et al. Fetal gene therapy for neurodegenerative disease of infants. Nature Medicine. (2018);24(9):1317-1323. doi:10.1038/s41591-018-0106-7

NI Qianqian

Yong Loo Lin School of Medicine

Research Interests:

RNA Biomarkers & Therapeutics RNA Delivery

RNA Modification

Ni's research has focused on using nanotechnologies for RNA delivery in cancer theranostics and immunotherapy. The work emphasizes developing nucleic acid nanomedicines to enhance cancer immunomodulation and theranostics, and innovating lipid nanoparticle (LNP) technologies. Their novel LNPs, with two patents filed, overcome physiological barriers for RNA delivery, improving mucosal vaccination and targeting extrahepatic organs, and enabling in vivo RNA delivery to primary immune cells. The team has also developed RNA modification techniques to improve RNA delivery and protein production using in-situ rolling circle transcription and programmable self-assembly. These efforts aim to deliver therapeutic nucleic acids precisely and effectively for cancer treatment, by developing vaccines and methods to modulate immune cell function.

Areas for collaboration:

- mRNA delivery via improved LNP technologies and mRNA modification technologies
- RNA modification techniques to enhance mRNA stability and protein production yield

Selected Publications:

Li B, Zhao M, Lai W, et al. Activatable NIR-II photothermal lipid nanoparticles for improved messenger RNA delivery. Angewandte Chemie International Edition. (2023);62(25). doi:10.1002/anie.202302676

Wang K, Zhang X, Ye H, et al. Biomimetic nanovaccine-mediated multivalent IL-15 self-transpresentation (MIST) for potent and safe cancer immunotherapy. Nature Communications. (2023);14(1). doi:10.1038/s41467-023-42155-z

Zhang X, Yang B, Ni Q, Chen X. Materials engineering strategies for cancer vaccine adjuvant development. Chemical Society Reviews. (2023);52(9):2886-2910. doi:10.1039/d2cs00647b

Yang L, Lang Y, Wu H, et al. Engineered toll-like receptor nanoagonist binding to extracellular matrix elicits safe and robust antitumor immunity. ACS Nano. (2023);17(6):5340-5353. doi:10.1021/acsnano.2c08429

Ni Q, Zhang F, Liu Y, et al. A bi-adjuvant nanovaccine that potentiates immunogenicity of neoantigen for combination immunotherapy of colorectal cancer. Science Advances. (2020): 6(12). doi:10.1126/sciadv.aaw6071

OOI Eng Eong

Duke-NUS Medical School

Research Interests:
Innate Immunity RNA Biomarkers & Therapeutics
RNA-Protein Interactions

Ooi's laboratory is dedicated to advancing understanding in the field of dengue pathogenesis and immunity. This is achieved by integrating molecular virology and host response studies with epidemiological and experimental medicine research, including clinical trials. The team's research interests are multifaceted, focusing on the interactions between viral genomic RNA and host proteins that are crucial for disease pathogenesis. They also investigate the regulation of orthoflaviviral RNA translation mediated by the 5' and 3' untranslated regions (UTRs). Additionally, the laboratory is committed to enhancing the immunogenicity of RNA vaccines while simultaneously working to reduce their reactogenicity. Through these comprehensive efforts, the laboratory aims to fill significant knowledge gaps and contribute to the development of more effective therapeutic and preventive strategies against dengue.

Areas for collaboration:

- ❖ All areas of research interests in viral RNA

Selected Publications:

Choi ANX, Siriphanitchakorn T, Choy MM, et al. A prM mutation that attenuates dengue virus replication in human cells enhances midgut infection in mosquitoes. Science Translational Medicine. 2024;16(758). doi:10.1126/scitranslmed.adk4769

Zhong Y, Kang AYH, Tay CJX, et al. Correlates of protection against symptomatic SARS-CoV-2 in vaccinated children. Nature Medicine. (2024);30(5):1373-1383. doi:10.1038/s41591-024-02962-3

Ooi EE, Kalimuddin S. Insights into dengue immunity from vaccine trials. Science Translational Medicine. (2023);15(704). doi:10.1126/scitranslmed.adh3067

Ong EZ, Koh CWT, Tng DJH, et al. RNase2 is a possible trigger of acute-on-chronic inflammation leading to mRNA vaccine-associated cardiac complication. Med. (2023);4(6):353-360.e2. doi:10.1016/j.medj.2023.04.001

OOI Yaw Shin

Duke-NUS Medical School

Research Interests:
Bacterial and Viral RNAs Innate Immunity
RNA-Protein Interactions

Ooi's research group focuses on identifying and characterizing host factors essential for RNA virus infections. RNA viruses exploit cellular host factors, including RNA-binding proteins, to complete their infection cycle, while also evolving mechanisms to evade innate immune defenses. To explore these complex interactions, the group employs a multidisciplinary approach that integrates genome-scale CRISPR screening, bioinformatics, in vivo models, metabolomics, molecular virology, proteomics, and transcriptomics. Their work targets various RNA viruses, such as positive-sense arboviruses, negative-sense paramyxoviruses, and double-stranded orthoreoviruses, aiming to enhance understanding of RNA virus biology and discover new therapeutic targets.

Areas for collaboration:

- RNA virus-host interactions
- RNA binding proteins (pro-viral and anti-viral)
- Sensing of RNA viruses

Selected Publications:

Yousefi M, See WR, Aw-Yong KL, et al. GeneRaMeN enables integration, comparison, and meta-analysis of multiple ranked gene lists to identify consensus, unique, and correlated genes. Briefings in Bioinformatics. (2024);25(5). doi:10.1093/bib/bbae452

Yousefi M, Lee WS, Yan B, et al. TMEM41B and VMP1 modulate cellular lipid and energy metabolism for facilitating dengue virus infection. PLoS Pathogens. (2022);18(8):e1010763. doi:10.1371/journal.ppat.1010763

Shivaprasad S, Weng KF, Ooi YS, et al. Loquacious modulates flaviviral RNA replication in mosquito cells. PLoS Pathogens. (2022);18(4):e1010163. doi:10.1371/journal.ppat.1010163

Diep J, Ooi YS, Wilkinson AW, et al. Enterovirus pathogenesis requires the host methyltransferase SETD3. Nature Microbiology. (2019);4(12):2523-2537. doi:10.1038/s41564-019-0551-1

Ooi YS, Majzoub K, Flynn RA, et al. An RNA-centric dissection of host complexes controlling flavivirus infection. Nature Microbiology. (2019);4(12):2369-2382. doi:10.1038/s41564-019-0518-2

PASTORIN Giorgia

Faculty of Science

Research Interests:
Non-Coding RNAs
RNA Delivery

Pastorin's Lab focuses on creating innovative lipid-based and cell-based nanoformulations for targeted drug delivery. These formulations are designed to deliver mRNA, miRNA, or siRNA to specific tissues, enhancing their availability and efficacy. The lab's nanoformulations are suitable for lyophilization, which minimizes degradation of the loaded cargos, thereby improving the accessibility and stability of the dosage forms.

Areas for collaboration:

- Novel lipid-based and/or cell-based nanoformulations for mRNA, miRNA or siRNA delivery
- Lyophilization of RNA nanoformulations with minimal degradation of loaded cargo

Selected Publications:

Benetti AA, Tan EYZ, Chang ZW, et al. Design and characterization of a new formulation for the delivery of COVID-19-mRNA vaccine to the nasal mucosa. Vaccines. (2024);12(4):409. doi:10.3390/vaccines12040409.

Jesenko T, Brezar SK, Cemazar M, et al. Targeting Non-Coding RNAs for the development of novel hepatocellular carcinoma therapeutic approaches. Pharmaceutics. (2023);15(4):1249. doi:10.3390/pharmaceutics15041249

PATZEL Volker

Yong Loo Lin School of Medicine

Research Interests:
New Technologies RNA Biomarkers & Therapeutics
RNA Delivery

Volker's research centers on designing and delivering functional RNA structures for genetic therapy and vaccination. They study various RNAs, including antisense nucleic acids, RNAi effectors, and CRISPR sgRNA, and use algorithms to select active RNAs from large libraries. To improve RNA delivery, they have developed technologies to overcome cellular membrane barriers. A key innovation is SPRING DNA, a non-viral, dumbbell-shaped DNA vector that is non-immunogenic, enters nuclei faster than plasmid DNA and conventional dumbbells, and provides long-lasting gene expression. These vectors can be delivered naked, via lipid nanoparticles, or as conjugates. Their techniques are in pre-clinical trials for applications like gene complementation therapy, suicide gene therapy, genetic vaccination, and mitochondrial gene therapy.

Areas for collaboration:

- Designing and selecting functional RNA structures.
- Deliver genes of any size using non-immunogenic, redosable vectors that trigger long-lasting gene expression in vivo
- Cell type-specific gene activation using the RNA trans-splicing technology
- Mitochondrial delivery vector for nucleic acids (RNA/DNA).

Selected Publications:

Loh PS, Patzel V. Non-Covalent linkage of helper functions to Dumbbell-Shaped DNA vectors for targeted delivery. Pharmaceutics. (2023);15(2):370. doi:10.3390/pharmaceutics15020370

Yu H, Pan HM, Evalin N, Trau D, Patzel V. Capsule-like safe genetic Vectors—Cell-Penetrating Core–Shell particles selectively release functional small RNA and entrap its encoding DNA. ACS Applied Materials & Interfaces. (2018);10(25):21113-21124. doi:10.1021/acsami.8b04294

Poddar S, Loh PS, Ooi ZH, Osman F, Eul J, Patzel V. RNA structure design improves activity and specificity of trans-Splicing-Triggered cell death in a suicide gene therapy approach. Molecular Therapy — Nucleic Acids. (2018);11:41-56. doi:10.1016/j.omtn.2018.01.006

Jiang X, Yu H, Teo CR, et al. Advanced design of dumbbell-shaped genetic minimal vectors improves non-coding and coding RNA expression. Molecular Therapy. (2016);24(9):1581-1591. doi:10.1038/mt.2016.138

Yu H, Jiang X, Tan KT, Hang L, Patzel V. Efficient production of superior dumbbell-shaped DNA minimal vectors for small hairpin RNA expression. Nucleic Acids Research. 2015;43(18):e120. doi:10.1093/nar/gkv58

PEK Jun Wei

Faculty of Science

Research Interests:

Non-Coding RNAs RNA Localization and Transport

RNP Condensates

Pek's lab explores the roles of various aspects of RNA biology, including stable introns, circular RNA, translation, and small noncoding RNAs, in parental-child health. The lab is particularly interested in how noncoding RNAs and translation regulation influence oogenesis, spermatogenesis, and intergenerational inheritance. Additionally, Pek's lab investigates RNA regulation during stresses such as nutrient deprivation, aging, and metabolic stress. Currently, the lab focuses on RNA-protein condensate formation in relation to organelle functions and nuclear and cytoplasmic RNA processing.

Areas for collaboration:

- In vivo genetic studies in animal models and cells
- Cell biology of RNA localization and function

Selected Publications:

Chan SN, Pek JW. Can stable introns and noncoding RNAs be harnessed to improve health through activation of mitohormesis? BioEssays. (2024). doi:10.1002/bies.202400143

Pek JW. The idiosyncrasies of oocytes. Trends in Cell Biology. (2024). doi:10.1016/j.tcb.2024.07.006

Pek JW, Ng AYE. Q&A with Jun Wei Pek and Amanda Yunn Ee Ng. Cell Reports. (2024);43(6):114303. doi:10.1016/j.celrep.2024.114303

Ng AYE, Chan SN, Pek JW. Genetic compensation between ribosomal protein paralogs mediated by a cognate circular RNA. Cell Reports. (2024);43(5):114228. doi:10.1016/j.celrep.2024.114228

Ng AQE, Chan SN, Pek JW. Nutrient-dependent regulation of a stable intron modulates germline mitochondrial quality control. Nature Communications. (2024);15(1). doi:10.1038/s41467-024-45651-y

SINGH Brijesh Kumar

Duke-NUS Medical School

Research Interests:
RNA Biomarkers & Therapeutics
Transcriptomics and Bioinformatics Translation

Singh's research focuses on leveraging RNA biology to understand and treat metabolic and inflammatory diseases. The group is particularly interested in RNA-based therapeutics, such as siRNA and antisense oligonucleotides, to regulate pathways associated with obesity and steatotic liver disease. Their innovative approaches include liver-specific GalNAc conjugation to silence genes involved in inflammation and fibrosis in conditions like MASH and related metabolic disorders. They also utilize RNA sequencing to uncover non-coding RNAs and regulatory networks that drive disease progression. By integrating computational RNA design with chemical stabilization, they aim to develop targeted RNA therapeutics, bridging fundamental RNA biology with translational medicine.

Areas for collaboration:

- Investigate role of non-coding RNAs in regulating disease mechanisms
- Investigate RNA Modification and Epitranscriptomics in gene regulation and disease
- Develop RNA-Based therapeutics for various diseases and liver-specific delivery systems.

Selected Publications:

Widjaja AA, Lim WW, Viswanathan S, et al. Inhibition of IL-11 signalling extends mammalian healthspan and lifespan. Nature. (2024);632(8023):157-165. doi:10.1038/s41586-024-07701-9

Tripathi M, Gauthier K, Sandireddy R, et al. Estrogen receptor-related receptor (Esrra) induces ribosomal protein Rplp1-mediated adaptive hepatic translation during prolonged starvation. bioRxiv (Cold Spring Harbor Laboratory). (2024). doi:10.1101/2024.01.09.574937

Tripathi M, Gauthier K, Sandireddy R, et al. Esrra regulates Rplp1-mediated translation of lysosome proteins suppressed in metabolic dysfunction-associated steatohepatitis and reversed by alternate day fasting. Molecular Metabolism. (2024);87:101997. doi:10.1016/j.molmet.2024.101997

Zhang S, Guo Y, Fidelito G, et al. LINC00116-encoded microprotein mitoregulin regulates fatty acid metabolism at the mitochondrial outer membrane. iScience. (2023);26(9):107558. doi:10.1016/j.isci.2023.107558

Tripathi M, Singh BK, Zhou J, et al. Vitamin B12 and folate decrease inflammation and fibrosis in NASH by preventing syntaxin 17 homocysteinylation. Journal of Hepatology. (2022);77(5):1246-1255. doi:10.1016/j.jhep.2022.06.033

SO Jimmy Bok Yan

Yong Loo Lin School of Medicine

Research Interests:
Bacterial and Viral RNAs Non-Coding RNAs
RNA Biomarkers & Therapeutics

So's research group is interested in investigating the role of RNA biology in gastroesophageal cancers and obesity. Their work includes exploring tumor microenvironment changes, the prognostic significance of malignant ascites, and innovative surgical techniques like mediastinoscopic-assisted transhiatal esophagectomy. They also utilize artificial intelligence to improve diagnostic and therapeutic strategies. The group aims to translate these insights into enhanced diagnostic tools and therapeutic strategies, improving patient care.

Areas for collaboration:

- Non-coding RNAs in gastroesophageal cancers and obesity
- Bacterial and Viral RNAs in gastroesophageal cancers and obesity
- RNA biomarkers and therapeutics for gastroesophageal cancers and obesity

Selected Publications:

Zhao JJ, Ong CAJ, Srivatsava S, et al. Spatially resolved niche and tumor microenvironmental alterations in gastric cancer peritoneal metastases. Gastroenterology. (2024). doi:10.1053/j.gastro.2024.08.007

Huang KK, Ma H, Chong RHH, et al. Spatiotemporal genomic profiling of intestinal metaplasia reveals clonal dynamics of gastric cancer progression. Cancer Cell. (2023);41(12):2019-2037.e8. doi:10.1016/j.ccell.2023.10.004

Totoki Y, Saito-Adachi M, Shiraishi Y, et al. Multiancestry genomic and transcriptomic analysis of gastric cancer. Nature Genetics. (2023);55(4):581-594. doi:10.1038/s41588-023-01333-x

Gwee YX, Chia DKA, So J, et al. Integration of genomic biology into therapeutic strategies of gastric Cancer peritoneal metastasis. Journal of Clinical Oncology. (2022);40(24):2830. doi:10.1200/jco.21.02745

Sundar R, Huang KK, Kumar V, et al. Epigenetic promoter alterations in GI tumour immune-editing and resistance to immune checkpoint inhibition. Gut. (2021);71 (7):1277-1288. doi:10.1136/gutjnl-2021-324420

SOONG Tuck Wah

Yong Loo Lin School of Medicine

Research Interests:
RNA Modification
RNA Processing

Soong's lab investigates the diversification of calcium channel structure and function through alternative splicing and RNA editing, examining their roles in neurological disorders like anxiety and fear, as well as cardiovascular disorders such as hypertension and heart failure. The lab focuses on the RNA splice code of voltage-gated calcium channels and their cell-specific expressions in health and disease contexts. Additionally, they explore the physiological significance of alternative splicing and RNA editing of CaV channels in hippocampal learning and memory, cerebellar motor learning, and their influence on circadian rhythm, feeding behavior, and obesity.

Areas for collaboration:

- Functionalizing discovery in RNA-biology related research that affect excitability of cells such as muscle, neurons or pancreatic β-cells using Langendorff system to isolate cardiomyocytes and Pressure myography to measure arterial muscle contractility
- Investigate functional changes in cells (e.g. muscles and neurons) that are subject to electrogenic changes or excitability at the membrane through Patch-clamp electrophysiological rigs

Selected Publications:

Huang H, Rui D MA, Chan DWS, et al. Targeting heterozygous dominant negative variant of KCNA2 using Gapmer antisense oligonucleotides (ASO) for the treatment of drug-resistant epilepsy. Molecular Therapy — Nucleic Acids. (2024);35(4):102316. doi:10.1016/j.omtn.2024.102316

Zhai J, Navakkode S, Yeow SQZ, et al. Loss of Ca V 1.3 RNA editing enhances mouse hippocampal plasticity, learning, and memory. Proceedings of the National Academy of Sciences. (2022);119(32). doi:10.1073/pnas.2203883119

Huang H, Tay SH, Ng W, Ng SY, Soong TW. Targeting novel human transient receptor potential ankyrin 1 splice variation with splice-switching antisense oligonucleotides. Pain. 2021;162(7):2097-2109. doi:10.1097/j.pain.0000000000002216

Huang H, Kapeli K, Jin W, et al. Tissue-selective restriction of RNA editing of CaV1.3 by splicing factor SRSF9. Nucleic Acids Research. (2018);46(14):7323-7338. doi:10.1093/nar/gky348

Hu Z, Li G, Wang JW, et al. Regulation of blood pressure by targeting CA V 1.2-Galectin-1 protein interaction. Circulation. 2018;138(14):1431-1445. doi:10.1161/circulationaha.117.03123

SUN Alfred Xuyang

Duke-NUS Medical School

Research Interests:
Non-Coding RNAs RNA Biomarkers & Therapeutics
RNP Condensates

Sun's lab is focused on the intersection of RNA biology and neurodegeneration, building on its established expertise in neurodegenerative research. The lab is keen to expand its exploration into how RNA molecules and processes influence neurodegenerative diseases. By delving deeper into the roles and mechanisms of various RNA species in neural cells, Sun's lab aims to enhance understanding of the molecular underpinnings of neurodegeneration.

Areas for collaboration:

- Long reads sequencing
- Spatial RNA analysis

Selected Publications:

Toh HSY, Choo XY, Sun AX. Midbrain organoids—development and applications in Parkinson's disease. Oxford Open Neuroscience. (2023);2. doi:10.1093/oons/kvad009

Zhou ZD, Saw WT, Ho PGH, et al. The role of tyrosine hydroxylase–dopamine pathway in Parkinson's disease pathogenesis. Cellular and Molecular Life Sciences. (2022);79(12). doi:10.1007/s00018-022-04574-x

Jo J, Yang L, Tran H, et al. Lewy body–like inclusions in human midbrain organoids carrying glucocerebrosidase and A-Synuclein mutations. Annals of Neurology. (2021);90(3):490-505. doi:10.1002/ana.26166

Sun AX, Yuan Q, Fukuda M, et al. Potassium channel dysfunction in human neuronal models of Angelman syndrome. Science. (2019);366(6472):1486-1492. doi:10.1126/science.aav5386

Zhou W, Ma D, Sun AX, et al. PD-linked CHCHD2 mutations impair CHCHD10 and MICOS complex leading to mitochondria dysfunction. Human Molecular Genetics. (2018);28(7):1100-1116. doi:10.1093/hmg/ddy413

TAN Kar Tong

Faculty of Science

Research Interests:
RNA Modifications RNA Processing
Transcriptomics and Bioinformatics

Tan's lab leverages high-throughput sequencing technologies and extensive genomics datasets to explore complex biological questions through large-scale genome mining. Focusing on discovering missing somatic alterations in cancer, the lab addresses cases where patients lack detectable alterations, hypothesizing these may reside in challenging-to-analyze, repetitive genome regions. They develop computational methods and employ long-read sequencing technologies to uncover these DNA alterations. Further, they also develop methods and technologies to identify rare somatic variations in aging and pre-cancerous tissues.

Additionally, Tan's lab aims to advance RNA-based therapeutics, drawing inspiration from successful RNA vaccines. They use genome mining to identify valuable RNA elements, engineering new therapeutics. The lab also investigates somatic mutations in aging-related diseases, developing methods to understand their impact across diverse tissues.

Areas for collaboration:

- Computational Genomics and Bioinformatics
- Long-read DNA and RNA-sequencing
- Evolution of RNA processing pathways

Selected Publications:

Tan KT, Ding LW, Wu CS, Tenen DG, Yang H. Repurposing RNA sequencing for discovery of RNA modifications in clinical cohorts. Science Advances. (2021);7(32). doi:10.1126/sciadv.abd2605

Lin Y, Tan KT, Liu J, Kong X, Huang Z, Xu XQ. Global profiling of Rbm24 bound RNAs uncovers a multi-tasking RNA binding protein. The International Journal of Biochemistry & Cell Biology. (2017);94:10-21. doi:10.1016/j.biocel.2017.11.002

Yu H, Jiang X, Tan KT, Hang L, Patzel V. Efficient production of superior dumbbell-shaped DNA minimal vectors for small hairpin RNA expression. Nucleic Acids Research. (2015);43(18):e120. doi:10.1093/nar/gkv583

Poon KL, Tan KT, Wei YY, et al. RNA-binding protein RBM24 is required for sarcomere assembly and heart contractility. Cardiovascular Research. (2012);94(3):418-427. doi:10.1093/cvr/cvs095

TAN Yong Zi

Faculty of Science

Research Interests:
RNA Structure and Modeling

Tan's research group employs cryogenic electron microscopy (cryo-EM) to investigate the structure and function of membrane proteins significant in human diseases. They also develop cryo-EM methods to address biological research challenges. In relation to RNA, the group uses cryo-EM to determine the structures of RNA molecules and their binding proteins to understand their functions. They have successfully resolved experimental structures with RNA bound, such as ribosomes, and have developed various cryo-EM methods applicable to RNA and RNA-binding proteins.

Areas for collaboration:

- High resolution imaging of RNA related macromolecules through cryo-EM

Selected Publications:

Aiyer S, Baldwin PR, Tan SM, et al. Overcoming resolution attenuation during tilted cryo-EM data collection. Nature Communications. (2024);15(1). doi:10.1038/s41467-023-44555-7

Tan YZ, Rubinstein JL. Through-grid wicking enables high-speed cryoEM specimen preparation. Acta Crystallographica Section D Structural Biology. (2020);76(11):1092-1103. doi:10.1107/s2059798320012474

Tan YZ, Baldwin PR, Davis JH, et al. Addressing preferred specimen orientation in single-particle cryo-EM through tilting. Nature Methods. (2017);14(8):793-796. doi:10.1038/nmeth.4347

Davis JH, Tan YZ, Carragher B, Potter CS, Lyumkis D, Williamson JR. Modular assembly of the bacterial large ribosomal subunit. Cell. (2016);167(6):1610-1622.e15. doi:10.1016/j.cell.2016.11.020

TANG Hong-Wen

Duke-NUS Medical School

Research Interests:
RNA Modification RNA Processing
Transcriptomics and Bioinformatics

Tang's research aims to elucidate how oncogenic signalling pathways reprogram RNA metabolism during aging and tumorigenesis. Specifically, the research group seeks to uncover the regulatory mechanisms driving tumorigenesis and the onset of cancer cachexia, with a focus on how advanced tumors induce muscle wasting. They also aim to characterize the effects of aging on muscle physiology and identify potential molecular targets for mitigating sarcopenia, the age-related degeneration of muscle mass and function.

Areas for collaboration:

- Study muscle related diseases using various models (I.e. fly, mouse, and human model systems)

Selected Publications:

Goh KY, Lee WX, Choy SM, et al. FOXO-regulated DEAF1 controls muscle regeneration through autophagy. Autophagy. (2024):1-23. doi:10.1080/15548627.2024.2374693

Cho S, Lee G, Pickering BF, et al. mTORC1 promotes cell growth via m6A-dependent mRNA degradation. Molecular Cell. 2021;81(10):2064-2075.e8. doi:10.1016/j.molcel.2021.03.010

Tang HW, Weng JH, Lee WX, et al. mTORC1-chaperonin CCT signaling regulates m 6 A RNA methylation to suppress autophagy. Proceedings of the National Academy of Sciences. 2021;118(10). doi:10.1073/pnas.2021945118

Tang HW, Hu Y, Chen CL, et al. The TORC1-Regulated CPA complex rewires an RNA processing network to drive autophagy and metabolic reprogramming. Cell Metabolism. 2018;27(5):1040-1054.e8. doi:10.1016/j.cmet.2018.02.023

Guo J, Tang HW, Li J, Perrimon N, Yan D. Xio is a component of the Drosophila sex determination pathway and RNA N 6 -methyladenosine methyltransferase complex. Proceedings of the National Academy of Sciences. (2018);115(14):3674-3679. doi:10.1073/pnas.1720945115

TAY Andy Kah Ping

College of Design and Engineering

Research Interests:

RNA Biomarkers & Therapeutics RNA Delivery

RNA Localization and Transport

Tay's lab has developed a nano-electroporation method to deliver naked RNA into cells for tracking intracellular stability, transport and degradation. We have also established a library of barcoded inorganic nanoparticles for tissue-specific delivery of RNA. Finally, Tay's lab has human immune organoid model that can be used for testing RNA-based therapeutics.

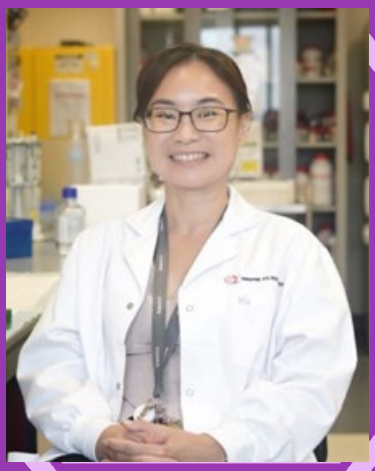
Areas for collaboration:

- Nano-electroporation for intracellular RNA delivery
- DNA-barcoded nanoparticle library for tissue-specific in vivo RNA delivery
- Human immune organoid for testing RNA therapeutics

Selected Publications:

Quek YJ, Tay A. Nanoscale methods for longitudinal extraction of intracellular contents. Advanced Materials. (2024);36(25). doi:10.1002/adma.202314184

Kumar ARK, Shou Y, Chan B, L K, Tay A. Materials for improving immune cell transfection. Advanced Materials. (2021);33(21). doi:10.1002/adma.202007421



TAY Hwee Goon

Duke-NUS Medical School

Research Interests:
RNA Biomarkers & Therapeutics
RNA Delivery

Tay's lab focuses on developing RNA therapeutics for retinal diseases, including age-related macular degeneration (AMD) and inherited retinal diseases. A key area of their research is identifying RNA biomarkers for diagnosing early retinal diseases, such as AMD, to better understand disease progression. Through these efforts, the lab aims to advance therapeutic strategies and improve early diagnostic capabilities for retinal conditions.

Areas for collaboration:

- Screening of LNP libraries and testing of LNP formulated RNA therapeutics in iPSC lines obtained from retina disease patients.
- Determine the routes of ocular administration (intravitreal or subretinal) for RNA therapeutics in pre-clinical animal models

Selected Publications:

Abdel-Razek O, Marzouk A, MacKinnon M, et al. Calcium signaling mediates proliferation of the precursor cells that give rise to the ciliated left-right organizer in the zebrafish embryo. Frontiers in Molecular Biosciences. (2023);10. doi:10.3389/fmolb.2023.1292076

Tun SBB, Shepherdson E, Tay HG, Barathi VA. Sub-Retinal Delivery of Human Embryonic Stem Cell Derived Photoreceptor Progenitors in *rd10* Mice. Journal of Visualized Experiments. (2023);(200). doi:10.3791/65848

Ng XY, Peh GSL, Yam GHF, Tay HG, Mehta JS. Corneal Endothelial-like Cells Derived from Induced Pluripotent Stem Cells for Cell Therapy. International Journal of Molecular Sciences. (2023);24(15):12433. doi:10.3390/ijms241512433

Tay HG, Andre H, Chrysostomou V, et al. Photoreceptor laminin drives differentiation of human pluripotent stem cells to photoreceptor progenitors that partially restore retina function. Molecular Therapy. (2023);31(3):825-846. doi:10.1016/j.ymthe.2022.12.012

TAY Yvonne

Yong Loo Lin School of Medicine

Research Interests:
Non-Coding RNAs RNA Processing
RNA-Protein Interactions

Tay's lab investigates mechanisms beyond genomic alterations that modify gene function and contribute to tumorigenesis, focusing on post-transcriptional regulation by RNA binding proteins and non-coding RNAs. The lab studies non-coding RNAs and the untranslated regions (UTRs) of protein-coding mRNAs. Their research has three main focus areas: deconvoluting RNA:RNA networks in cancer to understand their role in carcinogenesis, exploring the interactions between RNA:RNA and RNA:protein, and examining crosstalk between these post-transcriptional networks and RNA processing pathways like alternative splicing and polyadenylation. Their long-term goal is to translate their research discoveries into new RNA-based cancer diagnostics and therapeutics.

Areas for collaboration:

- RNA processing
- Non-coding RNAs
- RNA-protein interactions

Selected Publications:

Li Z, Zhang B, Chan JJ, et al. An isoform-resolution transcriptomic atlas of colorectal cancer from long-read single-cell sequencing. Cell Genomics. (2024);4(9):100641. doi:10.1016/j.xgen.2024.100641

Lee YF, Phua CZJ, Yuan J, et al. PARP4 interacts with hnRNPM to regulate splicing during lung cancer progression. Genome Medicine. (2024);16(1). doi:10.1186/s13073-024-01328-1

Long Y, Zhang B, Tian S, et al. Accurate transcriptome-wide identification and quantification of alternative polyadenylation from RNA-seq data with APAIQ. Genome Research. (2023);33(4):644-657. doi:10.1101/gr.277177.122

Chan JJ, Zhang B, Chew XH, et al. Pan-cancer pervasive upregulation of 3' UTR splicing drives tumourigenesis. Nature Cell Biology. (2022);24(6):928-939. doi:10.1038/s41556-022-00913-z

Desi N, Tong QY, Teh V, et al. Global analysis of RNA-binding proteins identifies a positive feedback loop between LARP1 and MYC that promotes tumorigenesis. Cellular and Molecular Life Sciences. (2022);79(3). doi:10.1007/s00018-021-04093-1

TOH Wei Seong

Yong Loo Lin School of Medicine

Research Interests:
RNA Biomarkers & Therapeutics

Toh's lab focuses on understanding the mechanisms for degeneration, and developing multidisciplinary strategies for regeneration, of tissues of the musculoskeletal system. They have established in vitro assays, and animal models to advance the study of aging-associated musculoskeletal diseases such as osteoarthritis, intervertebral disc degeneration, and sarcopenia. Additionally, Toh's lab is exploring the development of RNA therapeutics for orthopaedic applications, aiming to translate these insights into effective treatments for musculoskeletal diseases, and ultimately improving patient outcomes.

Areas for collaboration:

- Development of RNA therapeutics for orthopaedic applications
- Animal models to demonstrate the safety and efficacy of RNA therapeutics

Selected Publications:

Zhang S, Wong KL, Ren X, et al. Mesenchymal stem cell exosomes promote functional osteochondral repair in a clinically relevant porcine model. The American Journal of Sports Medicine. (2022);50(3):788-800. doi:10.1177/03635465211068129

Zhang S, Teo KYW, Chuah SJ, Lai RC, Lim SK, Toh WS. MSC exosomes alleviate temporomandibular joint osteoarthritis by attenuating inflammation and restoring matrix homeostasis. Biomaterials. (2019);200:35-47. doi:10.1016/j.biomaterials.2019.02.006

Zhang S, Chuah SJ, Lai RC, Hui JHP, Lim SK, Toh WS. MSC exosomes mediate cartilage repair by enhancing proliferation, attenuating apoptosis and modulating immune reactivity. Biomaterials. (2017);156:16-27. doi:10.1016/j.biomaterials.2017.11.028

TOO Heng Phon

Yong Loo Lin School of Medicine

Research Interests:
Non-Coding RNAs
RNA Biomarkers & Therapeutics

Too's lab has broadened its research focus from investigating microRNA as biomarkers to include other RNA species such as long non-coding RNA (lncRNA) and transfer RNA (tRNA). The lab is actively exploring the potential of RNA as a moiety for non-viral transfection of stem cells, with applications in oncology and regenerative medicine.

Areas for collaboration:

- miRNA
- Liquid biopsy
- In vitro RNA delivery

Selected Publications:

Chai YL, Strohm L, Zhu Y, et al. Extracellular Vesicle-Enriched MIRNA-Biomarkers show improved utility for detecting Alzheimer's disease dementia and medial temporal atrophy. Journal of Alzheimer S Disease. (2024);99(4):1317-1331. doi:10.3233/jad-230572

Zou R, Loke SY, Tang YC, et al. Development and validation of a circulating microRNA panel for the early detection of breast cancer. British Journal of Cancer. (2022);126(3):472-481. doi:10.1038/s41416-021-01593-6

Cheong JK, Tang YC, Zhou L, Cheng H, Too HP. Advances in quantifying circulatory microRNA for early disease detection. Current Opinion in Biotechnology. (2022);74:256-262. doi:10.1016/j.copbio.2021.12.007

So JBY, Kapoor R, Zhu F, et al. Development and validation of a serum microRNA biomarker panel for detecting gastric cancer in a high-risk population. Gut. (2020);70(5):829-837. doi:10.1136/gutjnl-2020-322065

Ying L, Du L, Zou R, et al. Development of a serum miRNA panel for detection of early stage non-small cell lung cancer. Proceedings of the National Academy of Sciences. (2020) ;117(40):25036-25042. doi:10.1073/pnas.2006212117

VENKITARAMAN Ashok

Cancer Science Institute of Singapore

Research Interests:
RNA Localization and Transport
RNA Modification RNA Processing

Ashok's lab seeks to understand the mechanisms underlying susceptibility to cancer, and to exploit this knowledge in innovative approaches for early clinical intervention in the commonest human cancers. In studying cancer susceptibility, Ashok's lab has uncovered mechanisms governing RNA processing, modification and intracellular localization that impact genome stability. Their ongoing research has established new approaches to study RNA localization, to identify RNA-protein interactions that mediate biological processes, and to target these interactions using structure-guided ligand discovery.

Areas for collaboration:

- Multiple isogenic cell models genetically engineered using CRISPR/Cas9 or /Cas13 systems
- Imaging platform for intracellular RNA localization
- Analysis of bulk and scRNA seq data

Selected Publications:

Najafabadi MG, Gray GK, Kong LR, et al. A transcriptional response to replication stress selectively expands a subset of Brca2-mutant mammary epithelial cells. Nature Communications. (2023);14(1). doi:10.1038/s41467-023-40956-w

Renaudin X, Lee M, Shehata M, Surmann EM, Venkitaraman AR. BRCA2 deficiency reveals that oxidative stress impairs RNaseH1 function to cripple mitochondrial DNA maintenance. Cell Reports. (2021);36(5):109478. doi:10.1016/j.celrep.2021.109478

Emery A, Hardwick BS, Crooks AT, et al. Target identification for small-molecule discovery in the FOXO3a tumor-suppressor pathway using a biodiverse peptide library. Cell Chemical Biology. (2021);28(11):1602-1615.e9. doi:10.1016/j.chembiol.2021.05.009

Shivji MKK, Renaudin X, Williams ÇH, Venkitaraman AR. BRCA2 regulates transcription elongation by RNA polymerase II to prevent R-Loop accumulation. Cell Reports. (2018);22(4):1031-1039. doi:10.1016/j.celrep.2017.12.086

Wickramasinghe VO, Gonzàlez-Porta M, Perera D, et al. Regulation of constitutive and alternative mRNA splicing across the human transcriptome by PRPF8 is determined by 5' splice site strength. Genome Biology. (2015);16(1). doi:10.1186/s13059-015-0749-3

WANG Jiong-Wei

Yong Loo Lin School of Meicine

Research Interests:
Non-Coding RNAs
RNA Biomarkers & Therapeutics RNA Delivery

Wang's research group is interested in exploring RNA therapeutics to combat cardiovascular and metabolic diseases. Their work involves developing non-coding RNAs, siRNAs, mRNAs, and gene editing tools with nanoparticle delivery systems, including both synthetic nanoparticles and natural ones like extracellular vesicles, to enhance the precision and efficacy of these therapies. By leveraging these advanced delivery methods, the group aims to improve targeted treatment outcomes and contribute significantly to the field of precision medicine for complex cardiovascular and metabolic conditions.

Areas for collaboration:

- RNA delivery
- RNA modification
- Gene therapy
- Preclinical testing

Selected Publications:

Tong L, Wang Q, Zhang Y, et al. Myocardial delivery of miR30d with peptide-functionalized milk-derived extracellular vesicles for targeted treatment of hypertrophic heart failure. Biomaterials. (2024);316:122976. doi:10.1016/j.biomaterials.2024.122976

Lin Y, Liu J, Chong SY, et al. Dual-Function nanoscale coordination polymer nanoparticles for targeted diagnosis and therapeutic delivery in atherosclerosis. Small. (2024). doi:10.1002/smll.202401659

Chong SY, Wang X, Van Bloois L, et al. Injectable liposomal docosahexaenoic acid alleviates atherosclerosis progression and enhances plaque stability. Journal of Controlled Release. (2023);360:344-364. doi:10.1016/j.jconrel.2023.06.035

Tong L, Zhang S, Liu Q, et al. Milk-derived extracellular vesicles protect intestinal barrier integrity in the gut-liver axis. Science Advances. (2023);9(15). doi:10.1126/sciadv.ade5041

De Castilla PEM, Tong L, Huang C, et al. Extracellular vesicles as a drug delivery system: A systematic review of preclinical studies. Advanced Drug Delivery Reviews. (2021);175:113801. doi:10.1016/j.addr.2021.05.011

WANG Yibin

Duke-NUS Medical School

Research Interests:
Non-Coding RNAs RNA Biomarkers & Therapeutics
RNA-Protein Interactions

Wang's group is dedicated to RNA-focused research, exploring several key areas related to heart diseases. Their work includes investigating RNA-splicing regulation in the pathogenesis of heart failure and the maturation of cardiomyocytes during development. The group also utilizes advanced technologies to profile RNA-protein interactions, contributing to systems biology network discovery. Furthermore, they examine long non-coding RNA (lncRNA) mediated regulation of ribosome biogenesis, both in developmental processes and disease contexts. Through these research avenues, Wang's group aims to develop new therapeutic modalities that address different aspects of heart diseases.

Areas for collaboration:

- Transcriptomic bioinformatics
- RNA-protein prediction
- RNA based imaging technologies
- RNA based therapeutics

Selected Publications:

Gao C, Wang Y. A New linc(-RNA) Between NFAT/MEF2 and Cardiac Hypertrophy. Circulation Research. (2024);135(3):450-452. doi:10.1161/circresaha.124.324794

Huang J, Lee JZ, Rau CD, et al. Regulation of postnatal cardiomyocyte maturation by an RNA splicing regulator RBFOX1. Circulation. (2023);148(16):1263-1266. doi:10.1161/circulationaha.122.061602

Yu J, Wang W, Yang J, et al. LNCRNA PSR regulates vascular remodeling through encoding a novel protein arteridin. Circulation Research. (2022);131(9):768-787. doi:10.1161/circresaha.122.321080

Gong X, Tian M, Cao N, et al. Circular RNA circEsyt2 regulates vascular smooth muscle cell remodeling via splicing regulation. Journal of Clinical Investigation. (2021);131(24). doi:10.1172/jci147031

Rau CD, Lusis AJ, Wang Y. Systems genetics for Mechanistic discovery in heart diseases. Circulation Research. (2020);126(12):1795-1815. doi:10.1161/circresaha.119.315863

WANG Zhisong

Faculty of Science

Research Interests:
New Technologies RNA Biomarkers & Therapeutics
RNA Delivery

Wang's research interest is development of advanced DNA molecular motors and their biomedical applications, with the major targeted areas as biosensing (for RNA, DNA, and protein biomarkers) and potentially also active drug delivery. Wang's lab has developed two platforms that may help RNA research.

Platform 1: Force-scalable DNA nano-mechanical devices (muscle-like and powered by small DNA molecular motors) capable of non-invasive or high-throughput force-dependent manipulation of single RNA, DNA or protein molecules. This platform is a low-cost but high-throughput method for studying RNA biology without using expensive optical/magnetic tweezers, it can be used for ultrasensitive single-molecule mechanochemical sensing (e.g., miRNA biomarkers), force-dependent drug screening, potentially also used for active drug delivery through dense tumour tissues.

Platform 2: Nano-robotic platforms (based on DNA origami-molecular motor integration) which can be used as a nano-robotic tool for RNA research and for RNA sensing.

Areas for collaboration:

- Single-molecule mechanical study of RNA biology
- Ultrasensitive single molecule mechanochemical sensing (e.g., miRNA biomarkers)
- Force-dependent drug screening
- Active drug delivery through dense tumour tissues
- Nano-robotic tool for RNA research and for RNA sensing

Selected Publications:

Anderson T, Wu W, Sirbu O, et al. A Light-Powered Single-Stranded DNA Molecular Motor with Colour-Selective Single-Step Control. Angewandte Chemie International Edition. (2024);63(32). doi:10.1002/anie.202405250

Siti W, Too HL, Anderson T, Liu XR, Loh IY, Wang Z. Autonomous DNA molecular motor tailor-designed to navigate DNA origami surface for fast complex motion and advanced nanorobotics. Science Advances. (2023);9(38). doi:10.1126/sciadv.adi8444

Liu XR, Loh IY, Siti W, Too HL, Anderson T, Wang Z. A light-operated integrated DNA walker–origami system beyond bridge burning. Nanoscale Horizons. (2023);8(6):827-841. doi:10.1039/d2nh00565d

WEI Jiangbo

Faculty of Science

Research Interests:
New Technologies RNA Modification
RNA-Chromatin Interactions

Wei's lab investigates the context-dependent regulation of gene expression mediated by RNA modifications, emphasizing their interplay with epigenetic mechanisms and potential epigenetic inheritance during cell state transitions. The team examines how RNA modifications and their associated effectors respond to cellular signaling, external stimuli, and drug treatments, with the aim of identifying synthetic lethal interactions between specific biological processes and distinct RNA modifications. Additionally, Wei's lab develops novel chemical and biophysical tools to profile RNA properties, such as modifications, structures, condensates, and interactions with other biomolecules, ultimately aiming to modulate these properties at transcript or site resolution.

Areas for collaboration:

- Sequencing methods for challenging RNA modifications
- Small molecule approaches to study RNA interactions
- Exploring RNA modification models for functional studies

Selected Publications:

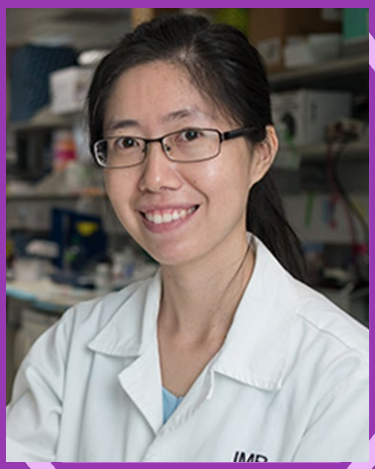
Wei J, Yu X, Yang L, et al. FTO mediates LINE1 m 6 A demethylation and chromatin regulation in mESCs and mouse development. Science. (2022);376(6596):968-973. doi:10.1126/science.abe9582

Wei J, Liu F, Lu Z, et al. Differential M6A, M6AM, and M1A demethylation mediated by FTO in the cell nucleus and cytoplasm. Molecular Cell. (2018);71(6):973-985.e5. doi:10.1016/j.molcel.2018.08.011

He PC, Wei J, Dou X, et al. Exon architecture controls mRNA m 6 A suppression and gene expression. Science. (2023);379(6633):677-682. doi:10.1126/science.abj9090

Zhang J, Wei J, Sun R, et al. A lncRNA from the FTO locus acts as a suppressor of the m6A writer complex and p53 tumor suppression signaling. Molecular Cell. (2023);83(15):2692-2708.e7. doi:10.1016/j.molcel.2023.06.024

Zou Z, Wei J, Chen Y, et al. FMRP phosphorylation modulates neuronal translation through YTHDF1. Molecular Cell. (2023);83(23):4304-4317.e8. doi:10.1016/j.molcel.2023.10.028



XUE Shifeng

Faculty of Science

Research Interests:
Non-Coding RNAs RNA Modification
Transcriptomics and Bioinformatics

Xue's research group is focused on the study of epigenetic repression, particularly through the investigation of epigenetic repressors. They explore how only a small fraction of the genome remains active at any given time while silencing elements such as transposable elements. The group is particularly interested in rare diseases with mutations in epigenetic regulators. Utilizing genomic, biochemical, and cell biology techniques, Xue's team seeks to uncover the molecular mechanisms behind these conditions, with the ultimate goal of developing therapeutic options for affected patients. Using mice, zebrafish and human cells as models, their research spans developmental biology, epigenetics, congenital diseases, and molecular biology.

Areas for collaboration:

- Transgenerational inheritance
- RNA-chromatin interactions

Selected Publications:

Del Fierro AT, Hamer BD, Benetti N, et al. SMCHD1 has separable roles in chromatin architecture and gene silencing that could be targeted in disease. Nature Communications. (2023;14(1). doi:10.1038/s41467-023-40992-6

Khan H, Koh G, Chong AEQ, et al. A novel variant in AFF3 underlying isolated syndactyly. Clinical Genetics. (2022);103(3):341-345. doi:10.1111/cge.14254

Xue S, Ly TTN, Vijayakar RS, et al. HOX epimutations driven by maternal SMCHD1/LRIF1 haploinsufficiency trigger homeotic transformations in genetically wildtype offspring. Nature Communications. (2022);13(1). doi:10.1038/s41467-022-31185-8

Leppek K, Fujii K, Quade N, et al. Gene- and Species-Specific HOX mRNA translation by ribosome expansion segments. Molecular Cell. (2020);80(6):980-995.e13. doi:10.1016/j.molcel.2020.10.023

Gordon CT, Xue S, Yigit G, et al. De novo mutations in SMCHD1 cause Bosma arhinia microphthalmia syndrome and abrogate nasal development. Nature Genetics. (2017);49(2):249-255. doi:10.1038/ng.3765

YANG Daiwen

Faculty of Science

Research Interests:
RNA Delivery RNA Structure and Modeling
RNA-Protein Interactions

My research focuses on the structure and dynamics of protein and its complex with RNA or DNA; we developed virus-like particles as a device to deliver biomolecules including protein, peptide, and RNA.

Areas for collaboration:

- NMR for structure determination and dynamics characterization
- Virus-like particles for delivering RNA

Selected Publications:

Zhang J, Fan JS, Li S, et al. Structural basis of DNA binding to human YB-1 cold shock domain regulated by phosphorylation. *Nucleic Acids Research*. 2020;48(16):9361-9371. doi:10.1093/nar/gkaa619

YANG Li

Cancer Science Institute of Singapore

Research Interests:
New Technologies RNA Biomarkers & Therapeutics
RNA Structure and Modelling

Li's lab focuses on RNA structure prediction and design through computational approaches. The lab's research integrates co-evolutionary analysis with advanced deep learning methods to enhance RNA structure prediction. Additionally, the lab aims to design RNA sequences and structures with customized properties using deep learning-based generative models. Through these complementary approaches, the team aims to unlock the full potential of RNA molecules for applications in medicine and biotechnology.

Areas for collaboration:

- Deep learning-based RNA structure modelling
- Computational RNA structure and sequence design

Selected Publications:

Zheng W, Wuyun Q, Li Y, Zhang C, Freddolino PL, Zhang Y. Improving deep learning protein monomer and complex structure prediction using DeepMSA2 with huge metagenomics data. Nature Methods. (2024);21(2):279-289. doi:10.1038/s41592-023-02130-4

Li Y, Zhang C, Feng C, Pearce R, Freddolino PL, Zhang Y. Integrating end-to-end learning with deep geometrical potentials for ab initio RNA structure prediction. Nature Communications. (2023);14(1). doi:10.1038/s41467-023-41303-9

Li Y, Zhang C, Yu DJ, Zhang Y. Deep learning geometrical potential for high-accuracy ab initio protein structure prediction. iScience. (2022);25(6):104425. doi:10.1016/j.isci.2022.104425

Zhou X, Li Y, Zhang C, Zheng W, Zhang G, Zhang Y. Progressive assembly of multi-domain protein structures from cryo-EM density maps. Nature Computational Science. (2022);2(4):265-275. doi:10.1038/s43588-022-00232-1

Li Y, Zhang C, Bell EW, et al. Deducing high-accuracy protein contact-maps from a triplet of coevolutionary matrices through deep residual convolutional networks. PLoS Computational Biology. (2021);17(3):e1008865. doi:10.1371/journal.pcbi.1008865

YU Hao

Faculty of Science

Research Interests:
RNA Modification RNA-Chromatin Interactions
RNA-Protein Interactions

Yu's lab focuses on understanding flowering plants as critical sources of food, medicine, and energy. By exploring the molecular mechanisms of plant development in changing environments, the lab seeks to address key challenges in food supply, medicine, energy, and environmental protection. The research aims to unravel complex regulatory networks of plant growth and apply this knowledge to improve human wellbeing. Current projects include studying RNA modifications, molecular trafficking, and phytohormone signaling, understanding the floral transition, molecular breeding of novel crop varieties for urban farming, and developing plant-based biomanufacturing platforms.

Areas for collaboration:

- RNA modification mechanisms
- Interaction between epigenetics and epitranscriptomics
- RNA-binding proteins

Selected Publications:

Zhang B, Zhang S, Wu Y, et al. Defining context-dependent m6A RNA methylomes in Arabidopsis. Developmental Cell. (2024);59(20):2772-2786.e3. doi:10.1016/j.devcel.2024.06.012

Li ST, Ke Y, Zhu Y, et al. Mass spectrometry-based proteomic landscape of rice reveals a post-transcriptional regulatory role of N6-methyladenosine. Nature Plants. (2024);10(8):1201-1214. doi:10.1038/s41477-024-01745-5

Wu X, Su T, Zhang S, et al. N6-methyladenosine-mediated feedback regulation of abscisic acid perception via phase-separated ECT8 condensates in Arabidopsis. Nature Plants. (2024);10(3):469-482. doi:10.1038/s41477-024-01638-7

Shen L, Ma J, Li P, Wu Y, Yu H. Recent advances in the plant epitranscriptome. Genome Biology. (2023);24(1). doi:10.1186/s13059-023-02872-6

Wong CE, Zhang S, Xu T, et al. Shaping the landscape ofN6-methyladenosine RNA methylation in Arabidopsis. PLANT PHYSIOLOGY. (2023);191(3):2045-2063. doi:10.1093/plphys/kiad010

ZHOU Yilong

Cancer Science Institute of Singapore

Research Interests:
RNA-Protein Interactions
RNP Condensates

Zhou's lab investigates the dynamics of RNA flux in mammalian cells, including RNA-protein interactions and RNA-protein phase separation, under stress and disease conditions. More specifically, they are interest in understanding how cells respond to dangerous RNA species, such as endogenous damaged RNA and exogenous virus RNA. They developed a new biomolecular condensates isolation method called "FANCI" and identified a unique subtype of RNA condensates known as DHX9 stress granules (SGs) in the cells. These DHX9 SGs sequester damaged intron RNA in the cytosol and activate a series of protective stress responses.

Areas for collaboration:

- Biomolecular condensates purification
- In vivo and In vitro phase separation assay
- RNA-protein interactions

Selected Publications:

Zhou Y, Panhale A, Shvedunova M, et al. RNA damage compartmentalization by DHX9 stress granules. Cell. (2024);187(7):1701-1718.e28. doi:10.1016/j.cell.2024.02.028

Wang L, Zhou Y, Chen Z, et al. PLCβ2 negatively regulates the inflammatory response to virus infection by inhibiting phosphoinositide-mediated activation of TAK1. Nature Communications. (2019);10(1). doi:10.1038/s41467-019-08524-3

Zhou Y, He C, Yan D, et al. The kinase CK1ε controls the antiviral immune response by phosphorylating the signaling adaptor TRAF3. Nature Immunology. (2016);17(4):397-405. doi:10.1038/ni.3395

ZHU Ru-Yi

Faculty of Science

Research Interests:
RNA Biomarkers & Therapeutics RNA Delivery
RNA Modification

Zhu's research is focused on developing novel chemistries for post-transcriptional RNA modifications aimed at RNA therapeutics. The team designs small-molecule probes to investigate how RNA interacts with other biomolecules, including RNA, proteins, and small molecules. They are particularly interested in identifying selective RNA-binding small molecules that could serve as potential drug candidates targeting RNA and as innovative molecular tools for RNA regulation.

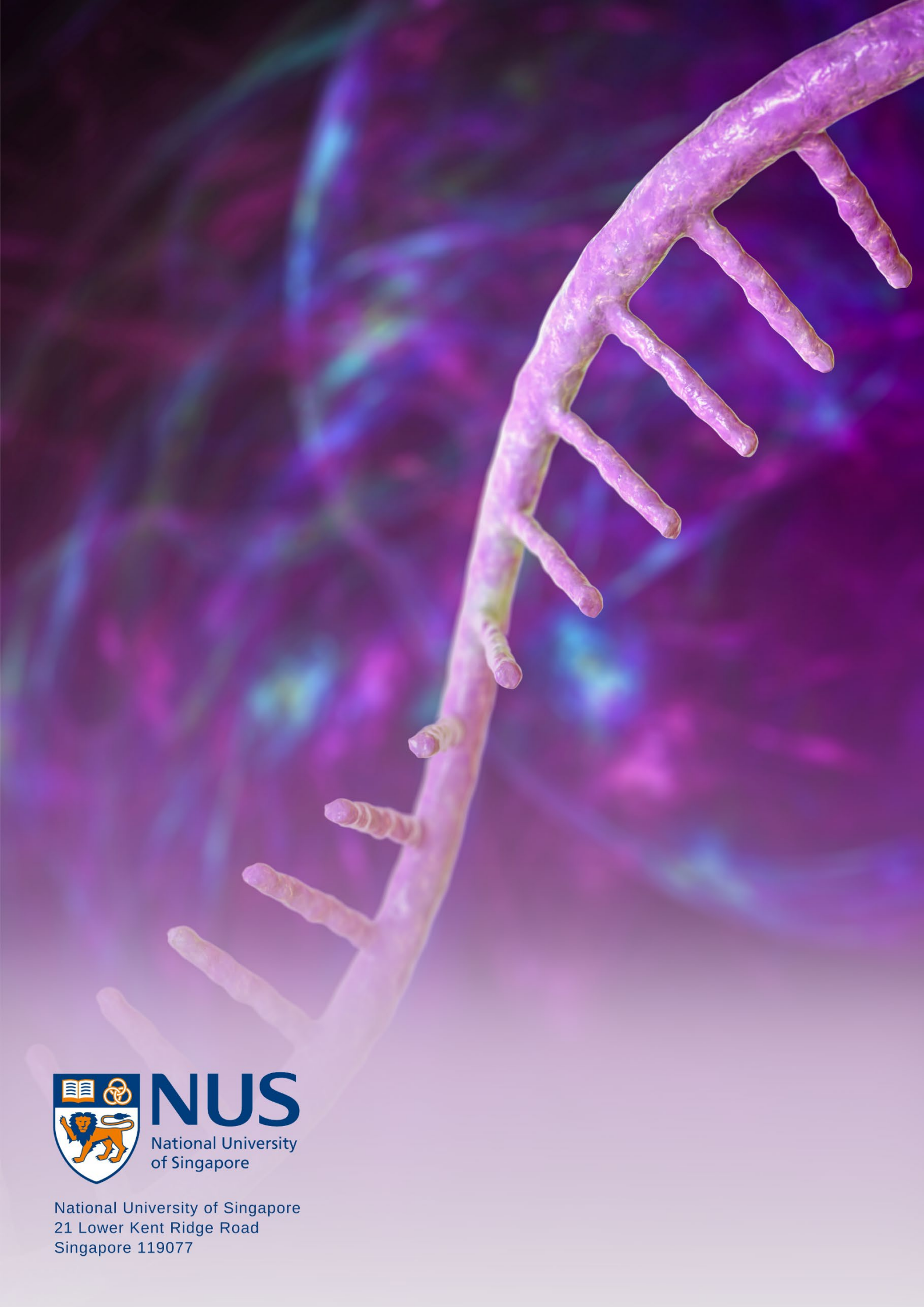
Areas for collaboration:

- Post-transcriptional RNA modifications to enhance RNA stability, delivery using small molecules and reduce immunogenicity
- Design small-molecule probes to study RNA interaction with biomolecules and other small molecules.
- Looking for collaborations to test our modification methods in various settings

Selected Publications:

Kha TK, Shi Q, Pandya N, Zhu RY. Multifaceted nucleic acid probing with a rationally upgraded molecular rotor. Chemical Science. (2024);15(13):5009-5018. doi:10.1039/d4sc00141a

Guo J, Chen S, Onishi Y, et al. RNA control via Redox-Responsive acylation. Angewandte Chemie International Edition. (2024);63(21). doi:10.1002/anie.20240217



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