

Genome Institute of Singapore (GIS)

Human Disease Modelling

Name	Project	Publications	Degree By
<p>Dr Ng Huck Hui 1) Executive Director, GIS & A*GA, A*STAR 2) Adj Prof at Dept Biochemistry, NUS 3) Adj Prof at SBS, NTU 4) Adj Senior Principal Scientist, SERI nghh@gis.a-star.edu.sg</p>	<p>Our ability to reprogram somatic cells to a pluripotent state, as well as our capability to isolate and propagate adult stem cells from human tissues are revolutionizing both our understanding of basic stem cell biology as well as approaches to disease modeling. In recent years, we have begun to witness the potential of stem cells in multiple applications ranging from regenerative therapy to disease modeling in a dish. To harness the full capacity of these stem cells, we aim to address two fundamental questions 1) how pluripotent and adult stem cells maintain their unique cell states, and 2) how we can leverage their propensities for controlled differentiation for the creation of next-generation cell and tissue models. We utilize advanced genetic approaches to identify and interrogate regulatory machineries governing the stem cell state. This is coupled with the development of novel cell culture approaches to generate 3D cellular models that demonstrate higher-order structure and a greater repertoire of relevant cell types to mimic the in vivo cell niche. We are particularly interested in applying these techniques to understand etiologies of neurodegenerative and metabolic diseases. Our ultimate goal is to harness the power of stem cells to derive more physiological disease models that can drive novel therapeutic discoveries and eventually actualize the goal of personalized medicine.</p>	<p>"Lab-grown mini-brains upgraded." Nat Cell Biol. 2017 Aug 31;19(9):1010-1012.</p> <p>"Midbrain-like Organoids from Human Pluripotent Stem Cells Contain Functional Dopaminergic and Neuromelanin-Producing Neurons." Cell Stem Cell. 2016 Aug 4;19(2):248-257.</p> <p>"Deterministic restriction on pluripotent state dissolution by cell-cycle pathways." Cell. 2015 Jul 30;162(3):564-79.</p>	<p align="center">NTU / NUS</p>
<p>Dr Torsten Wuestefeld Senior Research Scientist, GIS, A*STAR Wuestefeldt@gis.a-star.edu.sg</p>	<p>In vivo functional genetic screens to identify modulators of liver regeneration and disease, including NAFLD, liver cancer, fibrosis and cirrhosis. Liquid biopsy based diagnostic marker discovery for liver disease. (Liver) stem cells for cell based therapy.</p>	<p>"A Critical Role for Notch Signaling in the Formation of Cholangiocellular Carcinomas." Cancer Cell. 2016 Aug 8;30(2):353-356.</p> <p>"A MYC-aurora kinase A protein complex represents an actionable drug target in p53-altered liver cancer." Nat Med. 2016 Jul;22(7):744-53.</p> <p>"Erratum: mTOR regulates MAPKAPK2 translation to control the senescence-associated secretory phenotype." Nat Cell Biol. 2015 Oct;17(10):1370.</p>	
<p>Dr Swaine Chen 1) Senior Research Scientist, GIS, A*STAR 2) Ass Prof YLL SoM, NUS slchen@gis.a-star.edu.sg</p>	<p>Genomics of host-pathogen interactions for bacterial infections, including urinary tract infections and foodborne Group B Streptococcus infections; Synthetic biology and genome engineering in E. coli; Discovering novel mechanisms of antibiotic resistance in Gram negative bacteria and devising new strategies to combat antibiotic resistance.</p>	<p>"PRMT5 Circular RNA Promotes Metastasis of Urothelial Carcinoma of the Bladder through Sponging miR-30c to Induce Epithelial-Mesenchymal Transition." Clin Cancer Res. 2018 Oct 10.</p> <p>"A Sub-population of Group A Streptococcus Elicits a Population-wide Production of Bacteriocins to Establish Dominance in the Host." Cell Host Microbe. 2018 Mar 14;23(3):312-323.e6.</p> <p>"HLA-B*13:01 and the dapsone hypersensitivity syndrome." N Engl J Med. 2013 Oct 24;369(17):1620-8.</p>	<p align="center">NUS</p>

Dr Tam Wai Leong 1) Principal Investigator, GIS, A*STAR 2) Adj Asst Prof at Dept of Biochemistry, Yong Loo Lin School of Medicine, NUS 3) Adj Asst Prof at School of Biological Sciences, NTU 4) Principal Investigator, Cancer Science Institute of Singapore, NUS tamwl@gis.a-star.edu.sg	Novel therapeutic approaches to target cancer stem cells and cancer cell states and developing niche-targeting strategies in refractory cancers	"Chromosome 1q21.3 amplification is a trackable biomarker and actionable target for breast cancer recurrence." Nat Med. 2017 Nov;23(11):1319-1330.	NTU / NUS
		"Activation of PKA leads to mesenchymal-to-epithelial transition and loss of tumor-initiating ability." Science. 2016 Mar 4;351(6277):aad3680.	
		"Distinct EMT programs control normal mammary stem cells and tumour-initiating cells." Nature. 2015 Sep 10;525(7568):256-60.	

Microbial Genomics

Name	Project	Publications	Degree By
Dr Swaine Chen 1) Senior Research Scientist, GIS, A*STAR 2) Ass Prof YLL SoM, NUS slchen@gis.a-star.edu.sg	Genomics of host-pathogen interactions for bacterial infections, including urinary tract infections and foodborne Group B Streptococcus infections; Synthetic biology and genome engineering in E. coli; Discovering novel mechanisms of antibiotic resistance in Gram negative bacteria and devising new strategies to combat antibiotic resistance.	"PRMT5 Circular RNA Promotes Metastasis of Urothelial Carcinoma of the Bladder through Sponging miR-30c to Induce Epithelial-Mesenchymal Transition." Clin Cancer Res. 2018 Oct 10.	NUS
		"A Sub-population of Group A Streptococcus Elicits a Population-wide Production of Bacteriocins to Establish Dominance in the Host." Cell Host Microbe. 2018 Mar 14;23(3):312-323.e6.	
		"HLA-B*13:01 and the dapson hypersensitivity syndrome." N Engl J Med. 2013 Oct 24;369(17):1620-8.	
Dr Niranjan Nagarajan 1) Associate Director, GIS A*STAR 2) Assoc Prof at SOC, NUS 3) Assoc Prof at the Yong Loo Lin School of Medicine nagarajann@gis.a-star.edu.sg	Machine learning for uncovering biomarkers of treatment and response in cancer, Systems modelling of microbial communities, Microbial interactions in the skin microbiome, Evolution of antimicrobial resistance in the gut microbiome, Nanopore sequencing based analysis of complex microbiomes	"Oncogenic activation of the STAT3 pathway drives PD-L1 expression in natural killer/T-cell lymphoma." Blood. 2018 Sep 13;132(11):1146-1158.	NUS
		"IMMUNOLOGICAL COROLLARY OF THE PULMONARY MYCOBIOME IN BRONCHIECTASIS: THE CAMEB STUDY" Eur Respir J. 2018 Jul 27;52(1). pii: 1800766	
		"Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics" Cell. 2018 Apr 5;173(2):305-320.e10	

Computational Biology & Data Sciences

Name	Project	Publications	Degree By
Dr Jonathan Göke Senior Research Scientist, GIS, A*STAR gokej@gis.a-star.edu.sg	Machine Learning: prediction of clinical phenotypes using genomics data; super-fast algorithms for long read sequencing; probabilistic transcriptome assembly of repetitive elements. Computational methods for third generation sequencing	"Midbrain-like Organoids from Human Pluripotent Stem Cells Contain Functional Dopaminergic and Neuromelanin-Producing Neurons." Cell Stem Cell. 2016 Aug 4;19(2):248-257.	
		"Dynamic transcription of distinct classes of endogenous retroviral elements marks specific populations of early human embryonic cells." Cell Stem Cell. 2015 Feb 5;16(2):135-41	
		"X-exome sequencing of 405 unresolved families identifies seven novel intellectual disability genes." Mol Psychiatry. 2016 Jan;21(1):133-48	

<p>Dr Ken Sung Wing Kin 1) Senior Group Leader 2) Prof at SOC, NUS sungk@gis.a-star.edu.sg</p>	<p>Algorithms and Bioinformatics</p>	<p>"TranSurVeyor: an improved database-free algorithm for finding non-reference transpositions in high-throughput sequencing data." Nucleic Acids Res. 2018 Aug 22</p> <p>"Erratum: An intrinsic mechanism controls reactivation of neural stem cells by spindle matrix proteins." Nat Commun. 2017 Oct 31;8(1):1298.</p> <p>"An intrinsic mechanism controls reactivation of neural stem cells by spindle matrix proteins." Nat Commun. 2017 Jul 25;8(1):122.</p>	<p>NUS</p>
<p>Dr Niranjan Nagarajan 1) Associate Director, GIS A*STAR 2) Assoc Prof at SOC, NUS 3) Assoc Prof at the Yong Loo Lin School of Medicine nagaraiann@gis.a-star.edu.sg</p>	<p>Machine learning for uncovering biomarkers of treatment and response in cancer, Systems modelling of microbial communities, Microbial interactions in the skin microbiome, Evolution of antimicrobial resistance in the gut microbiome, Nanopore sequencing based analysis of complex microbiomes</p>	<p>"Oncogenic activation of the STAT3 pathway drives PD-L1 expression in natural killer/T-cell lymphoma." Blood. 2018 Sep 13;132(11):1146-1158.</p> <p>"IMMUNOLOGICAL COROLLARY OF THE PULMONARY MYCOBIOME IN BRONCHIECTASIS: THE CAMEB STUDY" Eur Respir J. 2018 Jul 27;52(1). pii: 1800766</p> <p>"Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics" Cell. 2018 Apr 5;173(2):305-320.e10</p>	<p>NUS</p>
<p>Dr Shyam Prabhakar 1) Senior Group Leader, Computational & Systems Biology, GIS 2) Assoc. Director, Integrative Genomics prabhakars@gis.a-star.edu.sg</p>	<p>We use single cell transcriptomics (including imaging-based spatial omics), algorithm development (machine learning), analysis of large datasets and targeted validation assays to uncover disease mechanisms, develop new molecular diagnostics and identify novel drug targets. The projects span a range from basic science and technology development to translational and commercial applications. Phenotypic focus areas include autism, colorectal and lung cancer, chronic myeloid leukemia, depression, type 1 diabetes, ageing and rheumatoid arthritis. We are looking for smart recruits on the wet lab as well as the dry lab side with any interest in technology and algorithm development as well as applications in precision medicine.</p>	<p>"Reference component analysis of single-cell transcriptomes elucidates cellular heterogeneity in human colorectal tumors." Nat Genet. 2017 May;49(5):708-718.</p> <p>"Histone Acetylome-wide Association Study of Autism Spectrum Disorder." Cell. 2016 Nov 17;167(5):1385-1397.e11</p> <p>"Sensitive detection of chromatin-altering polymorphisms reveals autoimmune disease mechanisms." Nat Methods. 2015 May;12(5):458-64.</p>	
<p>Dr. Anders Jacobsen Skanderup 1) Senior Research Scientist, GIS, A*STAR 2) Adj. Asst. Prof. at Dept of Computer Science, NUS skanderupami@gis.a-star.edu.sg</p>	<p>Bioinformatics / Computational Biology; Precision Medicine and Big Data; Cancer; Machine Learning / Deep Learning of genomics and clinical data; Tumor microenvironment.</p>	<p>"Mutation hotspots at CTCF binding sites coupled to chromosomal instability in gastrointestinal cancers." Nat Commun. 2018 Apr 18;9(1):1520.</p> <p>"Long noncoding RNA EGFR-AS1 mediates epidermal growth factor receptor addiction and modulates treatment response in squamous cell carcinoma." Nat Med. 2017 Oct;23(10):1167-1175.</p> <p>"Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas." N Engl J Med. 2015 Jun 25;372(26):2481-98.</p>	<p>NUS</p>

Genomic Medicine

Name	Project	Publications	Degree By
<p>Dr Foo Jia Nee 1) Senior Research Scientist, GIS, A*STAR 2) Asst Professor, Lee Kong Chian School of Medicine, NTU foojn@gis.a-star.edu.sg</p>	<p>Evaluating somatic mosaicism in diseased brain tissue; Genetics; Neuroscience</p> <p>There is increasing evidence to suggest that somatic mutations that occur during post-zygotic cell division may predispose to neurological disorders. Moreover, age-related somatic mutations have also been postulated to play a role in neurodegeneration. The degree of mosaicism may underlie variation in disease severity and age of onset. Using tissues from the Imperial College Parkinson's Disease and Multiple Sclerosis brain bank, we will analyze post-mortem brain tissue from deceased patients that have previously been diagnosed with neurodegenerative diseases such as Parkinson's disease, Alzheimer's disease and Multiple Sclerosis as well as from healthy controls. The student will work on detecting somatic mutations and expression differences at high sensitivity using the latest single-cell genomic technologies (DNA/RNA sequencing) at LKCMedicine, NTU and the Genome Institute of Singapore, A*STAR.</p>	<p>"Systematic evaluation of CRISPR-Cas systems reveals design principles for genome editing in human cells." Genome Biol. 2018 May 29;19(1):62.</p> <p>"Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci." Nat Genet. 2017 Jul;49(7):993-1004</p> <p>"HLA-B*13:01 and the dapsone hypersensitivity syndrome." N Engl J Med. 2013 Oct 24;369(17):1620-8</p>	<p>NTU</p>
<p>Dr Liu Jianjun 1) Deputy Executive Director, GIS, A*STAR 2) Professor, YLL School of Medicine, NUS 3) Adj Senior Principal Research Scientist, SERI liuj3@gis.a-star.edu.sg</p>	<p>Genetic and genomic studies of human disease, pharmacogenomics, large-scale population sequencing, and electronic medical record (EMR)-based omics analysis.</p>	<p>"Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics." Cell. 2018 Apr 5;173(2):305-320.e10</p> <p>"Discovery of six new susceptibility loci and analysis of pleiotropic effects in leprosy." Nat Genet. 2015 Mar;47(3):267-71.</p> <p>"HLA-B*13:01 and the dapsone hypersensitivity syndrome." N Engl J Med. 2013 Oct 24;369(17):1620-8</p>	<p>NUS</p>
<p>Dr Khor Chiea Chuen 1) Group Leader, GIS, A*STAR 2) Adjunct Clinician Scientist, SERI khorrcc@gis.a-star.edu.sg</p>	<p>Glaucoma is one of the commonest causes of irreversible blindness worldwide. The project will focus on dissecting the molecular genetic basis of glaucoma using whole exome sequencing. The student will gain experience in learning how to process a large amount of next generation sequencing data and analyzing it to obtain biological insights into the disease process of glaucoma. The second part of the project will entail functional biological experiments to discern the contribution of mutations discovered via</p>	<p>"Frequent transmission of the Mycobacterium tuberculosis Beijing lineage and positive selection for the EsxW Beijing variant in Vietnam." Nat Genet. 2018 Jun;50(6):849-856.</p> <p>"Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci." Nat Genet. 2017 Jul;49(7):993-1004</p> <p>"Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study." Lancet Oncol. 2016 Sep;17(9):1240-7</p>	
<p>Dr Roger Foo 1) Group Leader, GIS, A*STAR 2) Assoc Prof at YLLSoM, NUS foosyr@gis.a-star.edu.sg</p>	<p>Cardiovascular epigenetics and chromatin biology in heart failure and cardiovascular disease.</p>	<p>"Correction: Population genomics in South East Asia captures unexpectedly high carrier frequency for treatable inherited disorders." Genet Med. 2018 Aug 8.</p> <p>"Targeting Chondroitin Sulfate Glycosaminoglycans to Treat Cardiac Fibrosis in Pathological Remodeling." Circulation. 2018 Jun 5;137(23):2497-2513.</p> <p>"Single cardiomyocyte nuclear transcriptomes reveal a lincRNA-regulated de-differentiation and cell cycle stress-response in vivo." Nat Commun. 2017 Aug 9;8(1):225.</p>	<p>NUS</p>

Dr Li Jingmei 1) Senior Research Scientist, GIS, A*STAR 2) Adj. Asst. Prof. at Dept of Surgery, NUS lijm1@gis.a-star.edu.sg	Cancer genetics and epidemiology; Public health; Women's health	"A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer." Nat Genet. 2018 Jul;50(7):968-978	NUS
		"Systematic evaluation of CRISPR-Cas systems reveals design principles for genome editing in human cells." Genome Biol. 2018 May 29;19(1):62.	
		"Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics." Cell. 2018 Apr 5;173(2):305-320.e10	

Genomic Technology

Name	Project	Publications	Degree By
Dr. Chen Kok Hao GIS Fellow chenkh@gis.a-star.edu.sg	Spatial transcriptomics; Bio-imaging	"Reference component analysis of single-cell transcriptomes elucidates cellular heterogeneity in human colorectal tumors." Nat Genet. 2017 May;49(5):708-718.	
		"A Young Man With Epigastric Pain After Extracorporeal Shock Wave Lithotripsy." Gastroenterology. 2018 Jul;155(1):27-28.	
		"RNA imaging. Spatially resolved, highly multiplexed RNA profiling in single cells." Science. 2015 Apr 24;348(6233):aaa6090.	
Dr Wan Yue 1) Senior Research Scientist, GIS, A*STAR 2) Adj Asst Prof Dept of Biochemistry, YLLSoM, NUS 3) Adj Prof, NTU wany@gis.a-star.edu.sg	Identifying large scale RNA-RNA interactions in transcriptomes; Identifying functional RNA elements in dengue and Zika viruses	"Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci." Nat Genet. 2017 Jul;49(7):993-1004.	NTU / NUS
		"Late-stage tumors induce anemia and immunosuppressive extramedullary erythroid progenitor cells." Nat Med. 2018 Oct;24(10):1536-1544	
		"Landscape and variation of RNA secondary structure across the human transcriptome." Nature. 2014 Jan 30;505(7485):706-9.	
Dr Tan Meng How 1) Senior Research Scientist, GIS, A*STAR 2) Asst Prof at SCBE NTU tanmh@gis.a-star.edu.sg	Development and applications of genome and transcriptome engineering technologies based on CRISPR-Cas; Development and applications of nanopore third generation sequencing technologies for the interrogation of RNA modifications	"SRSF9 selectively represses ADAR2-mediated editing of brain-specific sites in primates." Nucleic Acids Res. 2018 Aug 21;46(14):7379-7395.	NTU
		"Systematic evaluation of CRISPR-Cas systems reveals design principles for genome editing in human cells." Genome Biol. 2018 May 29;19(1):62.	
		"Dynamic landscape and regulation of RNA editing in mammals." Nature. 2017 Oct 11;550(7675):249-254.	
Dr. Goh Wee Siong GIS Fellow wsgoh@gis.a-star.edu.sg	High-resolution RNA-modification sequencing to study the impact of epitranscriptomics on human diseases	"piRNA-directed cleavage of meiotic transcripts regulates spermatogenesis." Genes Dev. 2015 May 15;29(10):1032-44.	
		"Starvation-induced transgenerational inheritance of small RNAs in C. elegans." Cell. 2014 Jul 17;158(2):277-287.	
		"A genome-wide RNAi screen identifies factors required for distinct stages of C. elegans piRNA biogenesis." Genes Dev. 2014 Apr 1;28(7):797-807.	

<p>Dr Niranjan Nagarajan 1) Associate Director, GIS A*STAR 2) Assoc Prof at SOC, NUS 3) Assoc Prof at the Yong Loo Lin School of Medicine nagarajann@gis.a-star.edu.sg</p>	<p>Machine learning for uncovering biomarkers of treatment and response in cancer, Systems modelling of microbial communities, Microbial interactions in the skin microbiome, Evolution of antimicrobial resistance in the gut microbiome, Nanopore sequencing based analysis of complex microbiomes</p>	<p>"Oncogenic activation of the STAT3 pathway drives PD-L1 expression in natural killer/T-cell lymphoma." <i>Blood</i>. 2018 Sep 13;132(11):1146-1158.</p> <p>"IMMUNOLOGICAL COROLLARY OF THE PULMONARY MYCOBIOME IN BRONCHIECTASIS: THE CAMEB STUDY" <i>Eur Respir J</i>. 2018 Jul 27;52(1). pii: 1800766</p> <p>"Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics" <i>Cell</i>. 2018 Apr 5;173(2):305-320.e10</p>	<p>NUS</p>
<p>Dr Yu Qiang 1) Senior Group Leader, GIS, A*STAR 2) Adj Prof at YLL School of Medicine, NUS yug@gis.a-star.edu.sg</p>	<p>Cancer Therapeutics; Biomarker and Targets Discovery and Development.</p>	<p>"KDM4B-regulated unfolded protein response as a therapeutic vulnerability in PTEN-deficient breast cancer." <i>J Exp Med</i>. 2018 Sep 28. pii: jem.20180439.</p> <p>"Chromosome 1q21.3 amplification is a trackable biomarker and actionable target for breast cancer recurrence." <i>Nat Med</i>. 2017 Nov;23(11):1319-1330</p> <p>"IRAK1 is a therapeutic target that drives breast cancer metastasis and resistance to paclitaxel." <i>Nat Commun</i>. 2015 Oct 27;6:8746.</p>	<p>NUS</p>
<p>Dr Shyam Prabhakar 1) Senior Group Leader, Computational & Systems Biology, GIS 2) Assoc. Director, Integrative Genomics prabhakars@gis.a-star.edu.sg</p>	<p>We use single cell transcriptomics (including imaging-based spatial omics), algorithm development (machine learning), analysis of large datasets and targeted validation assays to uncover disease mechanisms, develop new molecular diagnostics and identify novel drug targets. The projects span a range from basic science and technology development to translational and commercial applications. Phenotypic focus areas include autism, colorectal and lung cancer, chronic myeloid leukemia, depression, type 1 diabetes, ageing and rheumatoid arthritis. We are looking for smart recruits on the wet lab as well as the dry lab side with any interest in technology and algorithm development as well as applications in precision medicine.</p>	<p>"Reference component analysis of single-cell transcriptomes elucidates cellular heterogeneity in human colorectal tumors." <i>Nat Genet</i>. 2017 May;49(5):708-718.</p> <p>"Histone Acetylome-wide Association Study of Autism Spectrum Disorder." <i>Cell</i>. 2016 Nov 17;167(5):1385-1397.e11</p> <p>"Sensitive detection of chromatin-altering polymorphisms reveals autoimmune disease mechanisms." <i>Nat Methods</i>. 2015 May;12(5):458-64.</p>	

Precision Oncology

Name	Project	Publications	Degree By
Dr DasGupta Ramanuj 1) Group Leader, GIS, A*STAR 2) Adj A/Prof, CSI NUS dasguptar@gis.a-star.edu.sg	Use of single cell '-omic' technologies to identify mechanisms of drug resistance and metastasis in epithelial cancers	"Demographic and Treatment Variables Influencing Outcome for Localized Paratesticular Rhabdomyosarcoma: Results From a Pooled Analysis of North American and European Cooperative Groups." J Clin Oncol. 2018 Oct 23;JCO2018789388. "Long noncoding RNA EGFR-AS1 mediates epidermal growth factor receptor addiction and modulates treatment response in squamous cell carcinoma." Nat Med. 2017 Oct;23(10):1167-1175. "Phenotype-driven precision oncology as a guide for clinical decisions one patient at a time." Nat Commun. 2017 Sep 5;8(1):435.	NUS
Dr Yu Qiang 1) Senior Group Leader, GIS, A*STAR 2) Adj Prof at YLL School of Medicine, NUS, NUS yug@gis.a-star.edu.sg	Cancer Therapeutics; Biomarker and Targets Discovery and Development.	"KDM4B-regulated unfolded protein response as a therapeutic vulnerability in PTEN-deficient breast cancer." J Exp Med. 2018 Sep 28. pii: jem.20180439. "Chromosome 1q21.3 amplification is a trackable biomarker and actionable target for breast cancer recurrence." Nat Med. 2017 Nov;23(11):1319-1330 "IRAK1 is a therapeutic target that drives breast cancer metastasis and resistance to paclitaxel. Nat Commun. 2015 Oct 27;6:8746.	NUS
Dr Tam Wai Leong 1) Principal Investigator, GIS, A*STAR 2) Adj Asst Prof at Dept of Biochemistry, Yong Loo Lin School of Medicine, NUS 3) Adj Asst Prof at School of Biological Sciences, NTU 4) Principal Investigator, Cancer Science Institute of Singapore, NUS	Novel therapeutic approaches to target cancer stem cells and cancer cell states and developing niche-targeting strategies in refractory cancers	"Chromosome 1q21.3 amplification is a trackable biomarker and actionable target for breast cancer recurrence." Nat Med. 2017 Nov;23(11):1319-1330. "Activation of PKA leads to mesenchymal-to-epithelial transition and loss of tumor-initiating ability." Science. 2016 Mar 4;351(6277):aad3680. "Distinct EMT programs control normal mammary stem cells and tumour-initiating cells." Nature. 2015 Sep 10;525(7568):256-60.	NTU / NUS

Synthetic Biology

Name	Project	Publications	Degree By
Dr Chew Wei Leong GIS Fellow chewwl@gis.a-star.edu.sg	Gene-editing; Gene therapy; Synthetic Biology; Immunology; Biotech.	"Corrigendum: Engineering and optimising deaminase fusions for genome editing." Nat Commun. 2017 Oct 9;8:16169 "Insulin-Like Growth Factor 1 Receptor-Dependent Pathway Drives Epicardial Adipose Tissue Formation After Myocardial Injury." Circulation. 2017 Jan 3;135(1):59-72. "In vivo gene editing in dystrophic mouse muscle and muscle stem cells." Science. 2016 Jan 22;351(6271):407-411.	
Dr Tan Meng How 1) Senior Research Scientist, GIS, A*STAR 2) Asst Prof at SCBE NTU tanmh@gis.a-star.edu.sg	Development and applications of genome and transcriptome engineering technologies based on CRISPR-Cas; Development and applications of nanopore third generation sequencing technologies for the interrogation of RNA modifications	"SRSF9 selectively represses ADAR2-mediated editing of brain-specific sites in primates." Nucleic Acids Res. 2018 Aug 21;46(14):7379-7395. "Systematic evaluation of CRISPR-Cas systems reveals design principles for genome editing in human cells." Genome Biol. 2018 May 29;19(1):62. "Dynamic landscape and regulation of RNA editing in mammals." Nature. 2017 Oct 11;550(7675):249-254.	NTU