Agency for Science, Technology and Research
SINGAPORE

A*STAR MINI SYMPOSIUM ON ENGINEERING BIOLOGY

OUTPACING MOORE'S LAW WITH SYNTHETIC BIOLOGY

DATE

February 2nd 2023

VENUE

Holiday Inn Singapore Atrium
Atrium Ballroom
317 Outram Rd
Singapore 169075
(Near Havelock MRT station)

Content

About the A*STAR Mini Symposium on Engineering Biology

As the world sets its sights on transforming towards a sustainable future, the stage is being set for engineering biology to play a pivotal role in the transition to a bioeconomy. Over the next decade, this cutting-edge field is poised to revolutionize our economy by applying the principles of genetics and biochemistry to real-world challenges, in line with the United Nations' 17 sustainable development goals. The unprecedented ease and accuracy of genetic manipulation offered by engineering biology offers promising solutions to pressing environmental and societal issues.

Join leaders from academia and industry as they come together to discuss cutting-edge advancements in engineering biology at this international symposium. Distinguished speakers from Australia and Singapore will present their achievements in foundational technologies, therapeutics, nutrition, green chemistry, and the translation of these technologies into practical applications.

With the theme of "Outpacing Moore's Law with Synthetic Biology," this event will delve into the latest developments in this rapidly advancing field, exploring how synthetic biology is poised to impact our lives in the near future. Attendees will have the opportunity to network with like-minded individuals and exchange ideas with experts from across the globe. This event aims to be a platform for meaningful scientific exchange and to pave the way to mutually beneficial collaborations.

Committee Chairperson

Dr. Melanie Weingarten, SIFBI

Committee Co-Chairperson

Dr. Yee Hwee Lim, ISCE^2

Programme Committee

Dr. Ee Lui Ang, SIFBI

Dr. Hao Fan, BII

Dr. Dave Ow, BTI

Dr. Fong Tian Wong, IMCB

Dr. Siti Nurhanna Riduan, Research Office

Dr. Kevin Chong, Research Office

Event Committee

Dr. Shirlena Soh, SIFBI

Dr. Geok Hong Soon, SIFBI

Ms. Mei Fang Teow, SIFBI

Ms. Vanessa Neo, SIFBI

Ms. Veronica Liew, SIFBI

Ms. Norjana Taib, Research Office

Ms. Debby Ong, SIFBI

Ms. Nafisah Binte Mohamad Ismail, Research Office

A*STAR Mini Symposium on Engineering Biology

"Outpacing Moore's Law with Synthetic Biology"

2nd February 2023

08:00-08:30	Arrival and Registration
08:30-08:35	Introduction by Symposium Committee Chairperson, **Dr. Melanie Weingarten**
08:35-08:45	Opening Address by Deputy Chief Executive (Research), A*STAR, **Prof. Andy Hor**

Session 1: Foundational Technologies in Engineering Biology

Moderator: Dr. Ee Lui Ang

08:45-09:15	Keynote Lecture by **Prof. Ian Paulsen, Macquarie University**
09:15-09:55	**Mr. Liwei Chen, GIS, A*STAR** *Writing in the Genome One Base at a Time with Transversion Base Editors* **Dr. Joy Xiang, IMCB, A*STAR** *Expansion of Repertoire of RNA Biosensors with DRIVER* **Dr. Yuangang Pan, IHPC, A*STAR** *Preference Guided Desired Data Generation* **Dr. Beverly Mok, IMCB, A*STAR** *Engineering of DNA Deaminases for CRISPR-Free Editing in Mitochondrial and Nuclear DNA*
09:55-10:15	**Block Q&A**
10:15-10:45	*Tea Break & Networking*

Session 2: Engineering Biology for Therapeutics and Nutrition

Moderator: Dr. Hao Fan

10:45-11:45	**Assoc Prof. Matthew Chang, US** *Engineering Microbes to Rewire Host-Microbiome Interactions* **Dr. Meiyappan Lakshmanan, BTI, A*STAR** *Integrative Multi-Omics Data Driven Approaches Guide Next Generation CHO Cell Line Development* **Dr. Simon Congqiang Zhang, SIFBI, A*STAR** *From Enzyme Discovery and Engineering to Natural Product Biosynthesis* **Asst Prof. Julius Fredens, NUS** *Phage Genome Engineering for All That is Good* **Dr. Naazneen Sofeo, SIFBI, A*STAR** *Customized Lipid Production in Yeast Using Tailored Enzymes*
11:45-12:05	**Block Q&A**
12:05-13:25	*Lunch & Networking*

A*STAR Mini Symposium on Engineering Biology

"Outpacing Moore's Law with Synthetic Biology"

2nd February 2023

Session 3: Going Green with Engineering Biology

Moderator: Dr. Yee Hwee Lim

13:30-14:30 **A/Prof. Sierin Lim, NTU**
Towards Carbon-Neutral Plastic Bioupcycling
Dr. Shreyas Supekar, BII, A*STAR
Engineering Enzymes for Improved Catalytic Efficiencies by Combining Structure-Based and Machine-Learning Approaches
Dr. Guangrong Peh, ISCE², A*STAR
Application of the Flavin-dependent Enzyme Prnc for Green Halogenation of Pyrrole Derivatives
Dr. Xixian Chen, SIFBI, A*STAR
Retrosynthetic Pathway Design and Enzyme Engineering for Natural Product Biosynthesis
Dr. Zhennan Liu, ISCE², A*STAR
Designer Metalloenzymes at the Interface between Biology and Chemistry

14:30-14:50 **Block Q&A**

14:50-15:20 *Tea Break & Networking*

Session 4: Translation of Engineering Biology to Industrial Applications

Moderator: Dr. Dave Ow

15:25-16:50 **Dr. Andrea Camattari, Gingko Bioworks**
Making Biology Easier to Engineer: Unlocking the Potential of Accelerated DBTL Cycle
Dr. Norbert Braun, Symrise
Synthetic Biology: A Game Changer for the Fragrance & Flavor Industry?
Dr. Han Ping Loh, BTI, A*STAR
CHO Platform for Producing Highly Potent Heparan Sulfate as Media Addictive for MSC Culture
Dr. Aparna Venkatesh, Bühler Asia Pte. Ltd.
A Stellar Approach to Bioprocessing Solutions for the Food Industry
Dr. Ichiro Hirao, Xenolis Pte Ltd
Designing Unnatural DNA Aptamers
Dr. Kostas Vavitsas, SINERGY
SINERGY: Supporting Synthetic Biology Innovation in Singapore

16:50-17:10 **Block Q&A**

17:10-17:15 Closing Address by **Dr. Melanie Weingarten**

Session 1

Foundational Technologies in Engineering Biology

Prof. Ian Paulsen

Distinguished Professor
Macquarie University
Director
Australian Research Council Centre of Excellence in Synthetic Biology

Ian Paulsen is a world leading researcher in membrane transport, microbial genomics, metagenomics, systems biology, bioinformatics and synthetic biology. He is a former ARC Laureate Fellow. Ian is currently the Director of the $50 million ARC Centre of Excellence in Synthetic Biology and the Australian Genome Foundry. Other laurels include Distinguished Professor at Macquarie University, Fellow of the Australian Academy of Science and the Royal Society of New South Wales. Paulsen is an ISI Highly Cited Researcher, and Thomson Reuters have identified him as one of the world's 3000 most influential scientific minds. His has over 350 published papers and a H index of 126. His published work has received significant press attention, including two interview on the Channel 7 news in the last two years, as well as numerous radio and newspaper interviews, including in the ABC, Washington Post and New York Times.

The ARC Centre of Excellence in Synthetic Biology – Inspired by Nature, Designed by Science

Developing novel synthetic microbes for the sustainable production of biochemical, biofuels and bioplastics is critical for the emergence of a new global bioeconomy. I am the Director of the $50 million ARC Centre of Excellence in Synthetic Biology, a consortium across nine Australian universities and twenty industry partners, that seeks to build synthetic microbes that can convert agricultural biomass or waste streams into high-value chemicals. At Macquarie University, our synthetic biology voyage started with building two synthetic chromosomes as part of the Yeast 2.0 consortium, and has expanded to building new designer chromosomes, yeast morphological engineering, building synthetic symbioses and synthetic microbial communities, and re-engineering yeast to grow on waste streams.

Mr. Liwei Chen
Research Officer II
Genomic Institute of
Singapore (GIS), A*STAR

Liwei Chen is a Research Officer in the Laboratory of Synthetic Biology and Genome Editing Therapeutics in the Genome Institute of Singapore. He received his Bachelor's degree from The University of Chicago and Master's degree from Harvard University under the mentorship of Prof. David R. Liu. His work focuses on engineering CRISPR to make precise edits and has been licensed to biotechs working on developing genome editing technology in therapeutic and agricultural applications. He is a co-inventor in multiple patents and authored several papers across genome editing, chemical biology, and organic chemistry.

Writing in the Genome One Base at a Time with Transversion Base Editors

Every day, billions of mutations arise in your genome. The most common mutation is the single nucleotide polymorphism (SNP), in which a single base is substituted with another. While most mutations are innocuous and are quickly fixed by DNA repair, some can disrupt important cellular functions and activities in your cells, making you one of 350 million people worldwide with a genetic disease. Conventional Cas9 is inadequate in reversing SNPs. Base editors are.

I will cover the conception, development, and characterization of our C-to-G base editor (CGBE), which converts C to G in the human genome in a precise and programmable fashion. I will then touch on our endeavors in reversing disease associated SNPs. Finally, I will discuss our efforts in engineering base editors with new editing modalities to further augment our ability to write in the genome one base at a time.

Dr. Joy Xiang
Senior Research Fellow
Institute of Molecular and
Cell Biology (IMCB), A*STAR

Joy S. Xiang is a Senior Research Fellow in the Institute of Molecular and Cell Biology. During her PhD at Stanford University working under Prof. Christina Smolke, she developed high-throughput and automation platforms for engineering RNA switches and biosensors. Post-PhD, she joined the Molecular Engineering Lab to investigate RNA-targeting RNA-binding proteins. With the onset of COVID19, she profiled protein-RNA interactions of SARS-CoV-2, with mentorship from Prof. Gene Yeo in UC San Diego. Currently, she is studying protein-RNA interactions in RNA virus infections. Her interests also include developing RNA biosensors for diagnostics, sequencing technologies for studying ribonucleoprotein complexes, and RNA therapeutics.

Expansion of Repertoire of RNA Biosensors with DRIVER

Biosensors are key components in engineered biological systems, providing a means of measuring and acting upon the large biochemical space in living cells. However, generating small molecule sensing elements and integrating them into in vivo biosensors have been challenging. Here, using aptamer-coupled ribozyme libraries and a ribozyme regeneration method, de novo rapid in vitro evolution of RNA biosensors (DRIVER) enables multiplexed discovery of biosensors. With DRIVER and high-throughput characterization (CleaveSeq) fully automated on liquid-handling systems, we identify and validate biosensors against six small molecules, including five for which no aptamers were previously found. DRIVER-evolved biosensors are applied directly to regulate gene expression in yeast, displaying activation ratios up to 33-fold. DRIVER biosensors are also applied in detecting metabolite production from a multi-enzyme biosynthetic pathway. This work demonstrates DRIVER as a scalable pipeline for engineering de novo biosensors with wide-ranging applications in biomanufacturing, diagnostics, therapeutics, and synthetic biology.

Dr. Yuangang Pan
Research Scientist
Institute for High Performance Computing (IHPC), A*STAR

Yuangang Pan is working as a research scientist at A*STAR Centre for Frontier AI Research. He completed his Ph.D. degree in Computer Science in Mar 2020 from University of Technology Sydney (UTS), Australia. Before joining A*STAR, he was a postdoctoral research associate at the Australian Artificial Intelligence Institute at UTS. He has authored or co-authored papers on various top journals, such as JMLR, IEEE TIFS, IEEE TKDE, IEEE TNNLS, and ACM TOIS. His research interests include Preference Learning, Deep Generative Learning, and Deep Clustering.

Preference Guided Desired Data Generation

Synthetic biology refers to the systematic reverse engineering of biological systems toward specified functions. Existing synthetic technologies are mostly manual and emphasize domain experience. Although generative models significantly simplify the process of biological product design, they provide little control over the synthetics, posing strict restrictions. In this talk, I aim to build a directional generative framework (DGF) that introduces preference learning into synthetic biology to incorporate scientists' feedback. DGF is data-driven and designed to leverage patterns within existing biology datasets. More importantly, DGF provides flexible control interfaces, which adjust the generation direction merely based on scientists' preference over synthetics.

Dr. Beverly Mok
Research Fellow
Institute for Molecular and
Cell Biology (IMCB), A*STAR

Beverly Mok is a research fellow at the Molecular Engineering Lab in IMCB. She received her B.A from the University of Cambridge in 2015 and her PhD from Harvard University in 2022. In her graduate research with Professor David Liu, she developed the first reported genome editing agent (DdCBE) that performs precise DNA edits in human mitochondrial DNA. As a postdoctoral researcher at IMCB, Beverly is interested in utilizing PANCE and PACE to evolve different classes of DNA and RNA-modifying enzymes for applications in human therapeutics and biomanufacturing.

Engineering of DNA Deaminases for CRISPR-Free Editing in Mitochondrial and Nuclear DNA

We recently reported the discovery of DddA, an interbacterial toxin that catalyzes the unprecedented deamination of cytidines within double-stranded DNA (dsDNA). All previously described cytidine deaminases operate on single-stranded DNA and thus when applied to genome editing require unwinding of dsDNA by macromolecules such as CRISPR-Cas9 complexed with a guide RNA. Challenges associated with guide RNA delivery into the mitochondria have thus far precluded base editing within mitochondrial DNA. We reasoned that the ability of DddA to act on dsDNA could circumvent this barrier. To overcome the inherent toxicity of DddA, we engineered split-DddA halves that are non-toxic and inactive until brought together on target DNA by adjacently bound programmable DNA-binding proteins. Fusions of the split-DddA halves, transcription activator-like effector array proteins, and a uracil glycosylase inhibitor resulted in RNA-free DddA-derived cytosine base editors (DdCBEs) that catalyse C•G-to-T•A conversions in human mtDNA and nuclear DNA with high target specificity and product purity. To improve editing efficiency and overcome the strict TC sequence-context constraint of DddA, we used phage-assisted non-continuous and continuous evolution (PANCE and PACE) to evolve DddA variants with improved activity and expanded targeting scope. DdCBEs are the first reported CRISPR-free base editors that enable precise manipulation of mtDNA, while remaining compatible with nuclear DNA editing. In addition, PANCE and PACE represent a versatile platform for directed evolution of other potential DNA- and RNA-modifying enzymes.

Session 2

Engineering Biology for Therapeutics and Nutrition

Assoc Prof. Matthew Chang

Dean's Chair Associate Professor
NUS Synthetic Biology for Clinical and Technological Innovation (SynCTI)
Synthetic Biology Translational Research Programme
Department of Biochemistry
Yong Loo Lin School of Medicine, NUS

Matthew Chang is Director of the Singapore Consortium for Synthetic Biology, Wilmar-NUS Corporate Laboratory, and NUS Synthetic Biology for Clinical and Technological Innovation, and Dean's Chair in Medicine and Associate Professor of Biochemistry and Synthetic Biology at the Yong Loo Lin School of Medicine at the National University of Singapore. His research focuses on studying the engineering of biology to develop autonomous, programmable cells for biomedical and biomanufacturing applications. He co-founded the Global Biofoundry Alliance and the Asian Synthetic Biology Association and currently serves as Co-Chair of the World Economic Forum's Global Future Council on Synthetic Biology.

Engineering Microbes to Rewire Host-Microbiome Interactions

The wealth of knowledge on the human microbiota composition and its roles in health and disease has recently spurred the development of novel therapeutic strategies. Moreover, with an array of genetic tools that are readily available, programmable genetic circuits can be designed, genomes can be edited and rewritten, and cells can be reprogrammed to foster novel microbiota-based interventions. In this talk, our recent work on engineering gut-resident microbes as versatile platforms equipped with clinically relevant functionalities will be presented. A particular emphasis will be placed on our efforts to transform gut microbes into live biotherapeutics with prophylactic and therapeutic efficacy against pathogenic infections and chronic metabolic diseases. This work provides a strong foundation for engineering microbes to modulate host-microbiome interactions and supports the use of live biotherapeutics as a viable strategy for clinical intervention.

Dr. Meiyappan Lakshmanan
Staff Scientist
Bioprocessing Technology Institute (BTI), A*STAR

Meiyappan Lakshmanan is currently a Staff Scientist and leads the Bioprocessing Data Integration group at Biorprocessing Technology Institute (BTI), A*STAR, Singapore. He has graduated with PhD in Chemical and Biomolecular Engineering from NUS in 2014 and has extensive experience in developing computational methods to analyze cellular metabolisms of mammalian systems by integrating diverse multi-omics data and genome-scale models with a particular focus to enhance bioprocessing aspects. He has coordinated and/or participated in various projects with internal and external (industrial) collaborators for enhancing mammalian cell-based bioprocessing. He has also published more than 30 peer-reviewed journal articles in these research areas (> 1100 citations; h-index: 18) and serve as a peer reviewer for more than 10 journals including Trends in Biotechnology, Genome Biology, Nucleic Acids Research, Bioinformatics and Cell Systems.

Integrative Multi-Omics Data Driven Approaches Guide Next Generation CHO Cell Line Development

Chinese hamster ovary (CHO) cells are the most prevalent mammalian cell factories for producing therapeutic biologics, due to its capacity for complex post-translational modifications, ability to grow well in suspension cultures and low susceptibility to human viral infections. Significant advances in various modules of the CHO cell line development and engineering have contributed to up to 100-fold increase in the product yields over the last three decades. In this talk, I will first present how mammalian systems biotechnology can decipher the genomic changes when a CHO cell becomes antibody producer. Next, I will present how such background knowledge can be used to drive the rational CHO cell line development by systematically combining the systematic assessment of multi-omic landscapes with genome engineering techniques.

Dr. Simon Congqiang Zhang

Junior Principal Investigator
Singapore Institute of Food and Biotechnology Innovation (SIFBI), A*STAR

Simon Zhang Congqiang received his PhD degree in 2014 in a joint program between National University of Singapore and Massachusetts Institute of Technology. He later joined Biotransformation Innovation Platform, A*STAR, as a founding member in 2015. He is now a PI in SIFBI leading a team working on multiple academic and industrial projects. His expertise is in metabolic engineering, synthetic biology, enzyme engineering, discovery and biosynthesis of natural products. He has published ~30 prestigious papers and filed 11 international patents (2 have been licensed) on industrial production of valuable terpenoids including carotenoids and apocarotenoids. He serves as the secretary of BioEnergy Society of Singapore, an editor of Frontiers in Bioengineering and Biotechnology and an active reviewer of many prestigious journals in synthetic biology (e.g., Nature Communications, Biotechnology Advances, Metabolic Engineering etc). He was awarded the prestigious Singapore Young Investigator Research Grant in 2019 and multiple national level competitive grants as PI or co-PI including Singapore Food Story IAF-PP, Applied Translation Research grant, A*STAR GAP projects, Singapore national synthetic biology program, INTRA-CREATE grant etc. He has been invited as a speaker in many international impactful conferences in Asia, EU and US.

From Enzyme Discovery and Engineering to Natural Product Biosynthesis

Isoprenoids, or terpenoids, constitute possibly the largest group of natural products (>95,000). Structural diversity of terpenoids contributes to wide applications ranging from pharmaceuticals (e.g., Taxol), nutraceuticals (e.g., astaxanthin), flavors and fragrances (e.g., linalool), polymer molecules (e.g., isoprene) and biofuels (e.g., farnesene). Unlike plant terpenes that are well studied, fungal terpenes and their synthases remain largely untapped. My team has developed an integrated platform for the discovery of novel fungal terpene synthases (TPSs). Coupling bioinformatics and experiments, we have successfully predicted several unique clusters of putative isofunctional TPSs (e.g., protoilludene, viridiflorol) and identified a highly active and specific linalool synthase and an TPS produce a novel spirobicyclo terpene. We also crystalized the fungal linalool synthase and studied the mechanism for its specificity by mutational experiments and molecular docking.

Also, we developed a multidimensional heuristic process (MHP) to efficiently synthesize these molecules in Escherichia coli. Built on statistical analysis and modular metabolic engineering methods, MHP is a systematic approach to optimize the performance of biosynthetic pathways, especially effective on complex systems (>10 enzymes). With MHP and enzyme engineering, we have several high-value flavor, fragrance and nutraceutical molecules at high yields and titres including astaxanthin (>1000 $/kg), lycopene, linalool, α-ionone (>5,000 €/kg), geranyl acetate, nerolidol (~500 $/kg) and viridiflorol etc. Currently, we are working on using CO2-derived acetate and ethanol as carbon source to produce value-added products, including food ingredients such as single-cell protein and polyunsaturated lipids.

Asst Prof. Julius Fredens

Assistant Professor
Department of Biochemistry
Yong Loo Lin School of Medicine,
NUS

Julius Fredens received his PhD from University of Southern Denmark, where he worked on proteomics in C. elegans but – more importantly – was introduced to synthetic biology through iGEM. With this newly found interest, he joined Jason Chin's lab at LMB in Cambridge for his postdoc, where he co-authored the first synthetic E. coli genome. He has recently started a group at NUS, working on engineering bacteriophages for various purposes.

Phage Genome Engineering for All That is Good

Bacteriophages are beautiful little bio-micromachines with the intrinsic ability to kill or transduce target bacteria with very high efficiency and specificity. Due to their relative simplicity and incredibly high proliferation rate, they have proven extraordinarily useful for phage display, and they are being explored as therapeutic agents as well as bio-detectors. With our ever-expanding toolbox for deep genetic engineering and the vast diversity of phages in nature (parts), bacteriophages represent are great system for conducting synthetic biology with clinical and technical applications in the age of high-throughput biology.

Dr. Naazneen Sofeo
Research Fellow
Singapore Institute of Food and Biotechnology Innovation (SIFBI), A*STAR

Naazneen Sofeo is a Research Fellow at Singapore Institute of Food and Biotechnology Innovation (SIFBI), A*STAR. She did her Bachelors in Engineering (Biotechnology) from India and earned her doctorate in Biochemistry from Iowa State University, USA. Naazneen is interested in enzyme and strain engineering and has worked with bacteria, yeasts, filamentous fungi, and plants. Currently she is working on multiple projects at SIFBI, ranging from protein production in filamentous fungi to custom lipid production in yeasts. She has been awarded with both local and international grants to pursue her work in lipid synthetic biology. She was recently awarded a prestigious international grant from the Good Food Institute and the A*STAR Career Development Fund Award. She was a recipient of Print and Grace Powers Hudson Scholarship during her Ph. D and had received the University level Gold Medal during her Bachelor studies. Apart from research, she loves to volunteer as mentor for young school and undergraduate students and inspire them to pursue science and research.

Customized Lipid Production in Yeast Using Tailored Enzymes

Majority of food oils and fats are currently derived from animal and plant sources. The OECD-FAO agricultural outlook report for 2021-2030 projects highest growth rate (of 10%) for fat consumption over the next ten years. Challenges like limited availability of agricultural land and the polluting effect of the animal rearing industry on the environment, urgently call for an alternative platform for production of different oils and fats to cater to this increasing demand. Oleaginous yeasts can be up to 70% lipids in dry weight of which 80-90% is triacylglycerols (TAGs). These are an important nutritional source. Fermentation of oleaginous yeasts can be a potential alternative source for animal fat analogues. The stereospecificity and composition of fatty acids in TAGs determines the physical properties of fat in food. This shows that careful selection of fatty acids at the different sn-1/2/3 positions of TAG can lead to different kinds of fat products. Hence, it is important to understand the substrate specificity of enzymes involved in TAG biosynthesis pathway. Combining the approach of machine learning, computational modelling, targeted mutagenesis and heterologous expression we are creating strains with varied lipid production. Another bottleneck in microbial fermentation of lipids is the input substrate cost, and using waste streams can lower this. By using adaptive evolution, we have also improved the growth and productivity of lipids in yeasts growing on such waste streams. Eventually these custom lipids could potentially be used as a taste and nutrient enhancing ingredient.

Session 3

Going Green with
Engineering Biology

Assoc Prof. Sierin Lim
Associate Professor
School of Chemistry, Chemical Engineering and Biotechnology, NTU

Sierin Lim is an Associate Professor of Bioengineering at the School of Chemistry, Chemical Engineering and Biotechnology at Nanyang Technological University, Singapore (NTU). Her research group focuses on the design and engineering of hybrid nano/microscale devices from biological parts for applications in health and the environment. Specifically, her Bioengineered and Applied Nanomaterials Lab (BeANs Lab) uses protein cages as the building blocks and a platform for formulation and delivery of active molecules to the skin. Her lab also explores the utility of protein cages to enhance contrast in imaging atherosclerotic plaques. In her Molecular & Cellular Bioengineering Lab (MCBe Lab), she leads a program in engineering PETase to upcycle plastic waste to oil, cellulose, and cannabinoids using cyanobacteria, cellulose bacteria, and yeast. She is currently serving as the Associate Dean of Global Partnerships at the NTU Graduate College. She earned her B.S. in Chemical Engineering and Ph.D. in Biomedical Engineering from University of California Los Angeles (UCLA).

Towards Carbon-Neutral Plastic Bioupcycling

The world produces about 400 million tons of plastic waste every year1. Of the plastic waste, the rate of plastic bottle consumption is estimated at 1 M units/minute which makes up approximately 5 million tons of waste annually. As natural plastic degradation takes hundreds of years, plastic waste reduction and conversion are of increasing significance. Currently, plastic waste is reduced or recycled (10%) through physical and chemical methods which are not sustainable. Thus, there is an urgent need for an environmentally sustainable solution to reduce plastic waste. Upcycling is the transformation of waste or unwanted products into material of greater value and therefore represents a valuable avenue for plastic waste reduction if it can be done through ecologically sound methods.

Our programme aims to reduce poly(ethylene terephthalate) (PET) waste (currently amounting to ~7% of the world's plastic demand2) by engineering enzymes and microbes that convert PET into compounds of industrial value. PET-degrading microbes have already been isolated from various environmental samples3,4. Though these were shown to be able to degrade PET, there is limited mechanistic understanding of the processes that enable PET utilization.

One of the best understood systems is found in the bacterium, Ideonella sakaiensis. It utilizes PET as a carbon source by secreting a PET degrading enzyme, PET hydrolase (PETase), which breaks down PET5. Exploiting this and other microbes for PET waste degradation could be an environmentally sustainable method of reducing waste. However, genetic tools for engineering these environmental isolates for such a purpose are unavailable and attempts at engineering PET-degrading enzymes (e.g., PETase and cutinase) have been met with limited success.

Our goal is to convert PET to their monomers, TPA and EG, that can then be used as carbon feedstocks while recapturing CO2 from fermentation, thus achieving carbon neutrality (i.e., not net carbon release). We will accomplish this by engineering both enzymes and microbial hosts (i.e., chassis) for improved PET degradation and conversion to value-added molecules through (1) directed evolution and mutagenesis methods that improve PETase kinetic parameters for greater catalytic efficiency, and (2) synthetic biology and metabolic engineering approaches for utilization of the PET monomers. TPA and EG will be then used as feedstocks for three engineered chassis to produce value-added compounds (e.g., L-DOPA, free fatty acids (FFA), cellulose, polyunsaturated fatty acid (PUFA)). PET utilization modules (PUMs) will be designed for easy integration to three industrially relevant microbes. These strains are selected for their carbon sequestration, cellulose production and lipid accumulation capabilities, respectively, thus enabling an integrated bioprocess and closed-loop usage of PET waste as carbon feedstock in biotransformation processes. The integration of the carbon-fixing cyanobacteria in the process allows CO2 produced by growth of the other two microbes to be captured, thus upcycling PET in a carbon-neutral and sustainable way.

References

1 Our Planet is Choking on Plastic, <https://www.unep.org/interactives/beat-plastic-pollution/ > (2022).

2 *World Plastics Production 1950-2015*, <https://committee.iso.org/files/live/sites/tc61/files/The%20Plastic%20Industry%20Berlin%20Aug%202016%20-%20Copy.pdf>

3 Muhonja, C. N., Makonde, H., Magoma, G. & Imbuga, M. Biodegradability of polyethylene by bacteria and fungi from Dandora dumpsite Nairobi-Kenya. *PLoS One* **13**, e0198446, doi:10.1371/journal.pone.0198446 (2018).

4 Urbanek, A. K., Rymowicz, W. & Mironczuk, A. M. Degradation of plastics and plastic-degrading bacteria in cold marine habitats. *Appl Microbiol Biotechnol* **102**, 7669-7678, doi:10.1007/s00253-018-9195-y (2018).

5 Yoshida, S. *et al.* A bacterium that degrades and assimilates poly(ethylene terephthalate). *Science* **351**, 1196, doi:https://doi.org/10.1126/science.aad6359 (2016).

Dr. Shreyas Supekar

Senior Post-Doctoral
Research Fellow
Bioinformatics Institute (BII),
A*STAR

Shreyas Supekar is a postdoctoral fellow at BII working in the group of Dr. Hao Fan. Shreyas has been at A*STAR for three years and is actively involved in several projects in the fields of enzyme engineering, drug design, and structural biology. He has a background in computational biophysics and computational biomolecular simulations. He is also actively employing AI/ML methods in his projects to improve the predictive power of computational models. He received his Ph.D. in computational biocatalysis while working on proton-coupled electron transport in cytochrome c oxidase at the Technical University of Munich (TUM), Germany.

Engineering Enzymes for Improved Catalytic Efficiencies by Combining Structure-Based and Machine-Learning Approaches

In this project, we built high-throughput protein-ligand interaction models which were used to train machine learning models to reproduce experimental catalytic activity. The trained models were found to predict catalytic activities for galactose oxidase with an accuracy of ~90%. Further, we also employed a fragment-based approach to predict new substrates for galactose oxidase. The previously trained machine learning models were employed to screen the predicted substrates to yield a handful of chemicals suitable for galactose oxidase chemistry.

Dr. Guangrong Peh
Scientist I
Institute of Sustainability for Chemicals, Energy and Environment (ISCE^2), A*STAR

Guangrong Peh was born in Singapore and received his honours degree from the National University of Singapore. He received his PhD from the University of Pittsburgh in 2016 under the mentorship of Paul E. Floreancig. Upon completion of his doctoral studies, he joined GlaxoSmithKline (GSK) plc as a process chemist. His current position is research scientist at the Institute of Sustainability for Chemicals, Energy and Environment (ISCE^2). His research interests include the development of reactions for chemoenzymatic synthesis of bioactive compounds and the development of green sustainable catalysis processes.

Application of the Flavin-dependent Enzyme Prnc for Green Halogenation of Pyrrole Derivatives

Halogenation of pyrroles requires harsh reagents and often results in uncontrolled poly-halogenated products. To date, there have been limited reports of green alternative enzymatic protocols to access this privilege pyrrolic scaffold. Herein, we report the first flavin-dependent halogenase, PrnC which is able to act on free-standing pyrroles to yield novel halogenated products. The PrnC gene has been genetically modified for robust heterologous expression as soluble proteins for kinetic studies as well as for in-vitro studies of a diverse mini-library consisting of pyrrolic compounds. In particular, the PrnC enzyme was used in the late-stage directing group free chlorination of the agrochemical fungicide, Fludioxonil.

Dr. Xixian Chen
Junior Principal Investigator
Singapore Institute of Food and Biotechnology Innovation (SIFBI), A*STAR

Xixian Chen graduated from National University of Singapore with Chemical Engineering and Life Science degrees. She was awarded Singapore-MIT Alliance fellowship for her PhD study on metabolic engineering and synthetic biology. After PhD, Xixian pursued her postdoc studies under Singapore-MIT Alliance Research and Technology innovation grant and developed industrial strains and processes to produce nutraceuticals, pharmaceuticals and hormonal proteins. Subsequently, she joined Biotransformation Innovation Platform (BioTrans) in A*STAR. As a pioneering member in the platform, she has built up research capabilities in the field of enzyme engineering and metabolic engineering, and forged collaborations with local universities as well as European research institutes. Xixian's main expertise includes enzyme expression and activity optimization, and integration enzyme engineering strategies with metabolic engineering to improve bioproduction. She has >10 patents and technology disclosures, and published in high-impact journals such as Nature Communications, Metabolic engineering and ACS Synthetic Biology etc. Xixian has received competitive Young Investigator Research Grant from A*STAR Advanced Manufacturing and Engineering. With a strong passion for applied research, Xixian also collaborates with various industrial partners to improve sustainable food production and to develop industrially viable bioprocesses.

Retrosynthetic Pathway Design and Enzyme Engineering for Natural Product Biosynthesis

Metabolic engineering has become an attractive method for the efficient production of natural products. However, one important pre-requisite is to establish the biosynthetic pathways. Many commercially interesting molecules cannot be biosynthesized as their native biochemical pathways are not fully elucidated. Cis-α-irone, a top-end perfumerymolecule, is an example. To address this challenge, retrobiosynthetic pathway design by employing promiscuous enzymes provides an alternative solution. In this work, we have designed a synthetic pathway to produce cis-α-irone with a promiscuous methyltransferase (pMT). Using structure-guided enzyme engineering strategies, we have improved pMT activity and specificity towards cis-α-irone by >10,000-fold and >1000-fold, respectively. About 120 mg l cis-α-irone is produced by one-step biotransformation of synthetic psi-ionone. By incorporating one of the optimized methyltransferases into our engineered microbial cells, ~86 mg l cis-α-irone is produced from glucose in a 5 l bioreactor. Our work illustrates that integrated retrobiosynthetic pathway design and enzyme engineering can offer opportunities to expand the scope of natural molecules that can be biosynthesized.

Dr. Zhennan Liu

Scientist I
Institute of Sustainability for Chemicals, Energy and Environment (ISCE^2), A*STAR

Zhennan Liu received her B.Sc (Hons) in Chemistry & Biological Chemistry from Nanyang Technological University in 2014. She was awarded National Science Scholarship in 2015 and went on to undertake PhD studies at University of California at Berkeley, supervised by Prof. John Hartwig. During her PhD study, her research interest focused on the development of artificial metalloenzymes (ArMs) for unnatural reactions, the in vivo engineering and catalysis of ArMs, and the integration of ArMs with a natural biosynthetic pathway. In 2021, Zhennan joined Institute of Sustainability for Chemicals, Energy And Environment, extending her research interests in engineering metalloenzymes as sustainable catalysts for application in the fine chemicals sector.

Designer Metalloenzymes at the Interface between Biology and Chemistry

Organic chemists and synthetic biologists have long used mostly orthogonal technologies to access small molecules like pharmaceuticals and commodity chemicals. Recently, growing concerns about sustainability of existing manufacturing processes spur the quest for cleaner and more efficient synthetic transformations and pathways. Biocatalysis offers unique advantages such as mild reaction conditions, high catalytic efficiency, and unparalleled levels of selectivity control, but it is inherently limited by the reactions known to nature, and therefore the ability to access vast swathes of chemical space. One emerging solution to the problem is to integrate the versatility and scope of chemical catalysis into the realm of biocatalysis. Nature uses metalloenzymes as organometallic catalysts, in which the metal cofactors impart unique reactivity and expand the range of chemistry that the combination of 20 canonical amino acids can afford. By anchoring synthetic metal cofactors into protein scaffolds to create new abiotic reactivity, the designer metalloenzyme has demonstrated potential in accessing chemical space that would not be possible with natural biosynthetic machinery alone.

Session 4

Translation of Engineering Biology to Industrial Applications

Dr. Andrea Camattari
Senior Director of Organism Engineering
Ginkgo Bioworks (USA)

After his PhD in industrial biotechnology at the University of Milano-Bicocca in Milan, Italy, **Andrea Camattari** joined the Bioprocessing Technology Institute in Singapore as research scientist. In 2010, he moved to the Austrian Centre of Industrial Biotechnology (ACIB) in Graz, while at the same time fulfilling a role as assistant professor at TU Graz. He returned in Singapore as a group leader at the Biotransformation Innovation Platform, before joining the private sector as a project manager at Evonik GmbH. In 2020 he joined Ginkgo Bioworks in Boston (MA), first as a principal organism engineer and more recently as senior director of organism engineering.

Making Biology Easier to Engineer: Unlocking the Potential of Accelerated DBTL Cycle

The Design-Build-Test-Learn (DBTL) cycle is a key concept of synthetic biology, borrowed from traditional engineering disciplines and representing an increasingly adopted metabolic engineering framework for a more systematic and efficient approach to strain development than historical efforts in a variety of industrial domains.

At Ginkgo Bioworks, DBTL cycles are considered a key element to fulfill our mission to make biology easier to engineer. In this context, the pivotal concept of Cell Development Kits (CDKs) has been introduced: by analogy with Software Development Kits (SDKs), allowing software houses to streamline their platform development, we aim to greatly accelerate strain development by ultimately generating a data-driven ecosystem for constantly understanding and improving performance.

Another key development we are implementing at Ginkgo Bioworks is directly related to the predictability of resource (and time) allocation for our platform, as a direct consequence of CDK workflows. A fundamental issue for innovation in biotechnology is related to the difficulty to scale operations maintaining an ever-improving virtuous cycle: applying the CDK concept, it is possible to apply and benefit from concepts of lean industry 4.0, since process modularity allows to finally consider and assimilate a biotech process to large-scale manufacturing.

Dr. Norbert Braun

Vice President Innovation & QC, Scent & Care, Asia Pacific
Symrise Asia Pacific Pte. Ltd.

Norbert A. Braun studied Chemistry and Biology and obtained his "Staatsexamen" in 1994 from the Universität Hohenheim, Stuttgart (Germany). In 1997 he received his Ph.D. in Organic Chemistry from the same university. From 1997 to 1999 he was a Postdoctoral Research Associate at Rice University, Houston, Texas (USA) and Université Claude Bernard, Lyon (France). In 1999, Dr. Braun joined Dragoco now Symrise, Holzminden (Germany) where he held various positions in Fragrance Research and was actively involved in the merger of Dragoco and Haarmann & Reimer. In 2005 he moved to Singapore to establish the APAC Innovation team covering Applied Research, Encapsulation, Analytical, and Formulation. He is currently Vice President Innovation & QC for Scent & Care, Asia Pacific, and a member of the global Innovation leadership team at Symrise. He is the author/coauthor of >50 scientific publications and patents. His research interest centers on natural and synthetic aroma molecules.

Synthetic Biology: A Game Changer for the Fragrance & Flavor Industry?

Fragrances and flavors are an integral part of our daily life. Imagine consumer products like shower gels, fabric softeners, fine fragrances or your favorite beverage and snacks without a scent or flavor.

Fragrances and flavors are designed using a wide variety of aroma molecules. The demand from consumers for sustainable and renewable products using other feedstock instead of crude oil is ever-growing. Will synthetic biology be a viable option beside green chemistry to address these needs?

The lecture will not only give insights of current market products using synthetic biology but also address different drivers and roadblocks in the flavor and fragrance industry. In addition, we will highlight why existing and new analytical tools should be leveraged during product development via synthetic biology.

Dr. Han Ping Loh
Research Fellow
Bioprocessing Technology Institute (BTI), A*STAR

Han Ping Loh is a Research Fellow at Bioprocessing Technology Institute (BTI). Han Ping graduated with a B.Sc. from the School of Biological Sciences in NTU and was awarded the A*STAR Graduate Scholarship to pursue his doctoral degree under the supervision of Prof. Peter Preiser and Prof. Laurent Renia. His doctoral research focused on the study of multigene families in Plasmodium parasites and its impact on immune evasion. He then joined the lab of Dr. Yang Yuansheng in BTI, working extensively on mammalian cell synthetic biology. His research focus is to engineer CHO cell lines for producing high value materials such as heparan sulfate.

CHO Platform for Producing Highly Potent Heparan Sulfate as Media Addictive for MSC Culture

Heparan sulfate (HS) plays a vital role in mediating important biological interactions and is a high value material in many applications. HS stabilizes the interaction between growth factors and its receptor, thereby allowing it to be used as a media addictive to lower the amount of growth factor used in media. Currently, the production of HS still depends on the use of animal derived raw materials which are prone to contamination. Attempts to produce recombinant HS is hampered by the template-independent synthesis of HS, which involves a vast number of enzymes, making it difficult to produce desirable HS structures that bind optimally to specific targets. In this seminar, we present our Chinese hamster ovary (CHO) platform for the expression of highly potent heparin sulfate for use as media addictive in MSC culture. Using this platform, we have identified optimal combinations of genes that are essential for producing HS that can bind FGF2 and promote MSC growth in culture.

Dr. Aparna Venkatesh
Regional Innovation Lead
Bühler Group

Aparna Venkatesh is the Innovation Lead at Bühler for the region of Southeast Asia & Oceania. In this role, she leads innovation strategy in emerging opportunities for sustainable foods and scouts for novel agri-food technology applications with external partners in the ecosystem to develop purposeful and high-impact transformations for the future of food. Her career spanned a decade in the public sector with A*STAR. As head of A*STAR Enterprise's Agri-Food and Nutrition division, Aparna played a key role in supporting the scientific, business, regulatory and strategy aspects of building up Singapore's alternative protein capabilities, enabling local food production as part of the nation's food resilience agenda. She holds a Bachelor's degree in Biological Sciences from NTU, Singapore, and a PhD in immunology from the Università degli Studi di Milano Bicocca, Italy.

A Stellar Approach to Bioprocessing Solutions for the Food Industry

Bühler is committed to having solutions ready to feed 10b people while enabling 35% less land usage by 2050. Bioprocessing approaches will be a crucial element in future food systems if we manage to address quality, cost and availability. The talk will focus on a novel technological solution targeting to improve the efficiency by 15-20% of bioprocesses at scale and in a strain-independent manner on seven organism families, operated in continuous bypass or single flow-through mode. The Stellar™ technology is based on nanosecond pulsed electric field to improve the cultivation and fermentation efficiency of unicellular organisms without biologically altering them.

Dr. Ichiro Hirao
Chief Scientific Officer
Xenolis Pte. Ltd.

Ichiro Hirao is Chief Scientific Officer of Xenolis Pte. Ltd. He obtained his Ph.D. from the Chemistry Department at Tokyo Institute of Technology in 1983. From 1984, he worked at the University of Tokyo as a research associate. In 1992, he became an associate professor at Tokyo University of Pharmacy and Life Sciences. In 1995, he moved to Dr. Andrew Ellington's laboratory at Indiana University. Dr. Ellington is a pioneer of nucleic acid aptamers. In 1997, he joined the Japan Science and Technology Agency (JST) as a group leader, to start a new project for genetic alphabet expansion technologies. In 2002, he continued his work as a professor at The University of Tokyo. From 2006 to 2015, he managed a synthetic biology team at RIKEN, where his team established a genetic alphabet expansion technology and a high-affinity DNA aptamer generation method. In 2015, he moved to IBN (IBB), A*STAR in Singapore, with his team member. In April 2022, he founded a startup company, Xenolis Pte. Ltd., in Singapore, together with Michiko Hirao (Kimoto), to commercialize their novel DNA aptamer and unnatural base pair technologies.

Designing Unnatural DNA Aptamers

To increase the molecular diversity and functionality of nucleic acids, our team is creating a novel technology, genetic alphabet expansion, by introducing artificial extra nucleobases (unnatural bases) as new letters. We developed unnatural bases, Ds and Px, which specifically form the unnatural Ds–Px pair, functioning in replication as a third base pair. The sequence diversity of conventional 20-base DNA fragments with four natural letters, A, G, C, and T, is 420 = 1.1 × 1012. In contrast, by introducing two new letters, Ds and Px, the sequence diversity of 20-base DNA fragments with six letters increases to 620 = 3.7× 1015. We applied this unnatural base pair system to DNA aptamer technology.

DNA aptamers are short single-stranded DNA fragments that bind specifically to targets, such as small molecules, proteins, and cells, including toxic or non-immunogenic compounds, and thus can be used as next-generation antibodies. Aptamers are generated by an evolutionary engineering method called SELEX, using a large oligonucleotide library with random sequences. However, the molecular diversity of the nucleic acid library with four letters is limited, as compared to that of proteinous antibodies with 20 different letters of amino acids. In addition, these 4-letter nucleotides are relatively hydrophilic, which is a disadvantage for interactions with the hydrophobic regions of targets. To address this issue, we developed a novel DNA aptamer generation method (ExSELEX, genetic alphabet expansion for SELEX) by introducing new letters of nucleotides with hydrophobic unnatural bases. The introduction of a few unnatural-base components greatly augmented the aptamers' affinities, which were 100- to 1,000-fold higher than those of the conventional 4-letter DNA aptamers. Here, I will introduce this novel aptamer technology for diagnostic and therapeutic applications.

Dr. Kostas Vavitsas
Consortium Manager
Singapore Consortium for
Synthetic Biology (SINERGY)

Kostas Vavitsas is the Manager of the Singapore Consortium for Synthetic Biology. He received his PhD in Biotechnology from the University of Copenhagen, Denmark, and has held research positions at the University of Queensland, Australia, and the University of Athens, Greece. Kostas has worked as science writer and editor, and was previously a freelance consultant in Biotechnology and Synthetic Biology.

SINERGY: Supporting Synthetic Biology Innovation in Singapore

Synthetic biology is a maturing scientific discipline that combines science and engineering in order to design and build new biological parts, devices and systems. Synthetic biology offers enormous opportunities to benefit society with promising applications in areas such as energy, healthcare and the environment. The Singapore Consortium for Synthetic Biology, SINERGY, aims to consolidate Singapore's capabilities in synthetic biology and harness synergies across industry sectors to create a vibrant and globally connected bio-based economy in Singapore. Efforts to foster interactions and co-development between the industry, universities and research institutes will encourage user-inspired research, augment manpower development, as well as speed up the translation of expertise in synthetic biology for industry applications.

Poster Exhibition

Presenter	Title
Dr. Madhaiyan Munusamy & Mr. Joshua Casey Darian (SIFBI)	Phylogeny and Diversity of Biosynthetic Gene Clusters from NPL Fungal Genomes
Dr. Dillon Tay (ISCE²) & Dr. Shi Jun Ang (IHPC)	Deep Generative Modelling for Natural Product Discovery
Mr. Leo Jerome De Souza (SIT)	Growth Factors Engineering
Dr. Yifeng Wei (SIFBI)	Discovery of Bacteriophage 2-Aminoadenosine Biosynthetic Enzymes and Application to Unnatural Nucleoside Synthesis
Ms. Ying Sin Koo (ISCE²)	Discovery of Unexplored Polyethylene Terephthalate (PET) Degrading Enzymes
Dr. Lokanand Koduru (IMCB)	*In silico* Approaches to Natural Product Discovery and Chassis Improvement
Dr. Vishnu Vadanan Sundaravadanan (NTU)	Bioengineered Magnetic Bacterial Cellulose Membrane
Dr. Dillon Tay (ISCE²) & Ms. Jhoann M.T. Miyajima (BII)	Directed Evolution and Predictive Modelling of Galactose Oxidase
Dr. Fong Tian Wong (IMCB)	A General Multi-Pronged Activation Approach for Natural Product Discovery in Actinomycetes
Dr. Shohei Kitano (NUS)	*Saccharomyces cerevisiae* Chromosome Redesigned for Engineering Niology
Dr. Winston Koh (IBB)	The Freedom to Innovate: How AI and Synthetic Biology Unlocks a New Enzyme Mutant-Verse
Dr. Elena Heng (IMCB)	Characterization of Cas toolbox for Streptomycetes Genome Editing
Mr. Abdurrahman Adam (NTU)	Process Evaluation of PET Plastic Degradation Using STAR PETase

Poster Exhibition

Presenter	Title
Dr. Say Kong Ng (BTI)	A HEK293 Expression System for the Stable Production of Glycoproteins
Dr. Beverly Mok (IMCB)	CRISPR-Free Base Editors with Enhanced Activity and Expanded Targeting Scope in Mitochondrial and Nuclear DNA
Dr. Koon Jiew Chua (NUS)	An Engineered Probiotic Produces a Type III Interferon IFNL1 and Reduces Inflammations in *in vitro* Inflammatory Bowel Disease Models
Dr. Tamilvendan Manavalan & Ms. Chu Hui Ting (SIFBI)	Engineering *Aspergillus oryzae* as a Host for Precision Fermentation
Dr. Zhiwei Song (BTI)	Production of Human Milk Oligosaccharides (HMOs) using Glycoengineered CHO Cells
Dr. Nikhil Aggarwal (NUS)	Rapid and Sensitive Nucleic Acid Detection Using Flap Endonucleases and CRISPR-Cas12
Dr. Farid John Ghadessy (IMCB)	Plastic Degrading Enzyme Engineering
Dr. Meiyappan Lakshmanan (BTI)	Multi-Omic Data-Driven Ration Development of CHO Cell Lines
Dr. Joy Xiang (IMCB)	SARS-CoV-2 Protein-RNA Interactions Contribute to Viral Fitness and Shape Host Transcriptome
Dr. Yossa Dwi Hartono (BII & NUS)	Regioselective Cannabinoid Production by Enzyme Engineering
Dr. Si-En Poh (IMCB)	*Malassezia furfur* Secreted Aspartyl Protease 1 (MfSAP1) and Its Role in Extracellular Matrix Degradation

About the Singapore Integrative Biosystems & Engineering Research (SIBER), A*STAR

Engineering biology is the design, manipulation, and engineering of purposeful biological systems, using engineering techniques including genetic engineering, biotechnology, and biochemistry for useful applications. Advances in engineering biology is set to be the key enabling technology for biomanufacturing with the potential to address key global challenges in energy, healthcare, and the environment, and to transform manufacturing approaches for advanced therapeutics, chemicals, and food.

The Singapore Integrative Biosystems & Engineering Research (SIBER) was established in 2021 as one of A*STAR's Strategic Research Programmes to build the next generation of enabling technologies in engineering biology and to address crucial gaps in biomanufacturing. Through this, A*STAR supports and funds research in engineering biology, and SIBER serves as a multi-disciplinary initiative that integrates A*STAR's capabilities in engineering biology, bioinformatics, artificial intelligence, machine learning, and automation for biosystems design. With the goal of developing novel end-to-end capabilities for manipulating and engineering biological systems, SIBER aims to apply these capabilities to provide solutions, such as the creation of innovative small molecule drugs and sustainable biofuels, to real-world problems.

SIBER is a collaborative effort that involves the Singapore Institute of Food and Biotechnology Innovation (SIFBI), Institute of Molecular & Cell Biology (IMCB), Singapore Institute of Manufacturing Technology (SIMTech), Institute of High Performance Computing (IHPC), Genome Institute of Singapore (GIS), Bioinformatics Institute (BII), Institute of Sustainability for Chemicals, Energy, and Environment (ISCE2), and Advanced Remanufacturing and Technology Centre (ARTC).

Agency for
Science, Technology
and Research

SINGAPORE