

## Joint Projects

1.	Homomorphic Encryption for Privacy-Preserving Analytics and Learning	2
2.	Dissecting the molecular functions of CLPTM1L as a lipid-flippase with oncogenic roles	4
3.	Investigating Cytokine Receptor Biogenesis and Protein Quality Control in Immune Cells during <i>Enterococcus faecalis</i> Infection	6



## 1. Homomorphic Encryption for Privacy-Preserving Analytics and Learning

Date Posted	5 July 2024		
Home University	Nanyang Technological University		
Partner University	Technical University of Munich		
Supervisors	Home	Partner	
Name	Jun Zhao	Amr Alanwar	
School	College of Computing and Data Science (CCDS)	School of Computation, Information and Technology	
Email	junzhao@ntu.edu.sg	<u>alanwar@tum.de</u>	
Website	https://personal.ntu.edu.sg/ju nzhao/	https://www.professoren.tum .de/en/alanwar-amr	
Project Description (200-300 words)	College of Computing and Data Science (CCDS)School of Computation, Information and Technologyjunzhao@ntu.edu.sgalanwar@tum.dehttps://personal.ntu.edu.sg/iu nzhao/https://www.professoren.tum .de/en/alanwar-amrIn an era where data privacy concerns coincide with an unprecedented surge in data analytics and machine learning applications, securing computational methods that protect user privacy is paramount. Homomorphic Encryption (HE) presents a formidable solution by enabling operations directly on encrypted data, thereby ensuring data privacy remains intact during processing. This PhD project focuses on enhancing HE for efficient implementation in machine learning tasks, specifically through optimizing matrix multiplication—a critical operation in numerous algorithms, including neural networks.The specific tasks are as follows: • Task 1 on Algorithms for Homomorphic Encryption- 		



	The successful development of efficient HE algorithms for matrix multiplication could revolutionize the field of privacy- preserving analytics by making it feasible to implement these methods in real-world machine learning tasks. This has profound implications for sectors where data sensitivity is paramount, such as healthcare and finance, allowing for the broad adoption of Al solutions without compromising user privacy.
Program/Center Website(s)	NA
Additional Information (e.g., files with project details)	NA



2. Dissecting the molecular functions of CLPTM1L as a lipid-flippase with oncogenic roles

Date Posted	1 July 2024	
Home University	Nanyang Technological University	
Partner University	Technical University of Munich	
Supervisors	Home	Partner
Name	Guillaume Thibault	Matthias J Feige
School	Biological Sciences	Natural Sciences
Email	thibault@ntu.edu.sg	matthias.feige@tum.de
Website	www.thibaultlab.com	www.bio.nat.tum.de/cell/home
Project Description (200-300 words)	Guillaume Thibault Matthias J Feige   Biological Sciences Natural Sciences   thibault@ntu.edu.sg matthias.feige@tum.de   www.thibaultlab.com www.bio.nat.tum.de/cell/home   CLPTM1L is a protein that has recently been described as a lipid flippase that can thus change the composition of both leaflets of biological membranes (Wang et al., PNAS, 2022). At the same time multiple studies point towards   CLPTM1L being involved in the development of different forms of cancer, e.g. cervical cancer (Koel et al., Hum Mol Genet, 2023) and lung cancer (Mandour et al., Adv Resp Med, 2020). The links between the molecular functions of CLPTM1L and its role in cancer development have remained unclear and will be explored during this project.   Specifically, we will:   Analyze the flippase functions of CLPTM1L: Using lipidomics of different cellular organelles, we will assess if CLPTM1L overexpression or knockout changes the lipid composition of cell organelles.   Define the CLPTM1L-affected proteome: Lipid composition of membranes can affect membrane protein stability and/or their signalling which may be related to a role of CLPTM1L in cancer. Using CLPTM1L overexpression or knockout we will define by proteomics and RNAseq which proteins and /or pathways are affected in cells.   Perform drug screens to modulate CLPTM1L function:   Based on the aforementioned parts of the project, we will aim to develop a high-throughput capable screen for the functions of CLPTM1L taking its role in cancer development into account.	



	Together, this project will define the functions of an ill- defined but strongly cancer related lipid flippase and set the basis for inhibitor screens for this protein.
Program/Center Website(s)	NA
Additional Information (e.g., files with project details)	NA



3. Investigating Cytokine Receptor Biogenesis and Protein Quality Control in Immune Cells during *Enterococcus faecalis* Infection

Date Posted	1 July 2024		
Home University	Nanyang Technological University		
Partner University	Technical University of Munich		
Supervisors	Home	Partner	
Name	Guillaume Thibault	Matthias J Feige	
School	Biological Sciences	Natural Sciences	
Email	thibault@ntu.edu.sg	matthias.feige@tum.de	
Website	www.thibaultlab.com	www.bio.nat.tum.de/cell/home	
Project Description (200-300 words)	The endoplasmic reticulum ( biogenesis and quality contro- proteins, including cytokine r cell signaling. Disruptions in can lead to misfolding and m affecting immune responses. investigate the mechanisms and PQC in immune cells du infection, leveraging single-c seq) data to uncover novel ir Using advanced techniques immunology, we will analyze control of cytokine receptors, cytokines in immune cells fro preliminary scRNA-seq data cell populations and pathway infection. We will focus on th biogenesis and quality contro Specifically, we will: <b>Characterize the ER Stress</b> <b>Mechanisms</b> : Identify and a cytokine and receptor bioger <b>Investigate Cytokine Recep</b> <i>E. faecalis</i> infection impacts expression of cytokine recep siRNA approaches. <b>Rational Engineering of Cy</b> cytokine receptors with enha	ER) plays a pivotal role in the ol of secreted and membrane eceptors critical for immune protein quality control (PQC) alfunction of these receptors, . This project aims to of cytokine receptor biogenesis ring <i>Enterococcus faecalis</i> ell RNA sequencing (scRNA- hsights. in protein biogenesis and the production and quality such as IL-12Rα, but also om infected tissues. Our have identified key immune vs affected by <i>E. faecalis</i> e ER's role in managing the ol of these receptors. <b>Response and PQC</b> halyze PQC factors affecting hesis during infection. <b>Cor Biogenesis</b> : Explore how the biogenesis and cell surface tors, using CRISPR/Cas9 and	



	under ER stress conditions to improve immune responses during bacterial infections.
	This project will provide insights into protein quality control, cytokine receptor biogenesis, and immune responses during bacterial infections. By combining expertise from both labs, we aim to develop innovative therapeutic strategies targeting the ER to enhance immune function and combat infections.
Program/Center Website(s)	NA
Additional Information (e.g., files with project details)	NA