Hong Kong University of Science and Technology
Department of Chemical & Biological Engineering

Synthetic gene expression control systems in bacteria

Dr. Sang Woo Seo

Department of Chemical and Biological Engineering, Seoul National University

I, , Gwanak-ro, Gwanak-Gu, Seoul, 08826, Korea

TEL: +82-2-880-2274, FAX: +82-2-880-7295

Email: swseo@snu.ac.kr

Date : **30 November (Monday)**

Time : **10:00 – 11:30 am**

Venue : **Rm 2303 (near Lift 17/18), HKUST**

Abstract

In this talk, we introduce newly developed synthetic gene expression control systems in bacteria. First, we demonstrate that a synthetic protein quality control (ProQC) system that enables translation only when both ends of mRNAs are present and followed by circularization based on sequence-specific RNA–RNA hybridization can be applied for various metabolic engineering applications. Second, to control the gene expression level precisely, we introduce tunable CRISPRi systems at both transcriptional and translational levels by engineering sgRNA and crRNA. Finally, we suggest a new expression platform for polycistronic gene expression by using synthetic translational coupling system. We believe these tools can be applied to improve the efficiencies of metabolic pathways.

References:

Nat. Chem. Biol. 17:421-427 (2021)
Nucleic Acids Res. 51(9):4650-4659 (2023)
Nat. Commun. 15:5319 (2024)
*Metab. Eng.*88:148-159 (2025)

Biography

Dr. SangWoo Seo is a Professor and Vice Chair for Research in the Department of Chemical and Biological Engineering at Seoul National University (SNU), South Korea, where he also chairs the Interdisciplinary Program in Bioengineering and directs the Institute of Bioengineering. He earned his B.S. (2007) and Ph.D. (2012) in Chemical Engineering from POSTECH, developing synthetic biology tools in *E. coli*, and completed postdoctoral training in Bioengineering at UC San Diego, reconstructing transcriptional regulatory networks through multi-omics analysis. His research group develops novel synthetic biology tools, redesigns biological systems for producing chemicals, fuels, pharmaceuticals, and therapeutics and for environmental and biomedical applications, and elucidates complex regulatory networks using NGS-based multi-omics approaches. His group works with a range of host organisms, including *E. coli* (including the probiotic strain Nissle 1917), *Vibrio natriegens, Corynebacterium glutamicum, Bacillus, methanotrophs, Saccharomyces cerevisiae, Yarrowia lipolytica, Pichia pastoris*, and mammalian cells.