South Korea

HAN-P-23

Seokhee Kim

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Website	https://shkim115.wixsite.com/skimlab
Research Field(s)	biosynthesis, peptide natural products, targeted in vivo hypermutation, continuous directed evolution

Academic Career

B.S., 2001, Seoul National University; Ph.D., 2008, Harvard University (advisor: Daniel Kahne); Postdoctoral Training, 2008-2014, MIT (Advisor: Robert T. Sauer); Assistant/Associate Professor, 2014-current, Seoul National University

Selected Publications

1. Evolutionary spread of distinct O-methyltransferases guides the discovery of unique isoaspartate-containing peptides, pamtides. Lee, H., et al. Adv. Sci., 11, 2305946 (2024)
2. Exploring the Diverse Landscape of Biaryl-Containing Peptides Generated by Cytochrome P450 Macrocyclases. Nam, H., et al. J. Am. Chem. Soc., 145, 22047-22057 (2023)
3. Discovery and Biosynthesis of Cihunamides, Macrocyclic Antibacterial RiPPs with a Unique C-N Linkage Formed by CYP450 Catalysis. An, J.S., et al. Angew. Chem. Int. Ed., 62, e202300998 (2023)
4. A dual gene-specific mutator system installs all transition mutations at similar frequencies in vivo. Seo, D., et al. Nucleic Acids Res., 51, e59 (2023)
5. Development of a genome-targeting mutator for the adaptive evolution of microbial cells. Eom, G., et al. Nucleic Acids Res., 50, e38 (2022)
6. Molecular mechanism underlying substrate recognition of the peptide macrocyclase PsnB. Song, I., et al. Nat. Chem. Biol., 17, 1123-1131 (2021)
7. Gene-specific mutagenesis enables rapid continuous evolution of enzymes in vivo. Park, H. and Kim, S. Nucleic Acids Res., 49, e32 (2021)
8. Genome Mining Reveals High Topological Diversity of ω-Ester-Containing Peptides and Divergent Evolution of ATP-Grasp Macrocyclases. Lee, H., et al. J. Am. Chem. Soc., 142, 3013-3023 (2020)

Why My Lab?

Students in my lab conduct multidisciplinary research using various tools in molecular biology, biochemistry, enzymology, chemical biology, bioinformatics, bacterial genetics, and structural biology. We frequently use genome mining, bioinformatic analyses, protein expression/purification, in vitro reconstitution of enzyme reactions, HPLC/mass/NMR-based peptide characterization, enzyme engineering, NGS analyses, and etc.