

세미나 초록

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발표 주제	비천연아미노산을 이용한 효소개량 기술
발표 내용	<p>The two main protein engineering strategies, rational design and directed evolution, have found widespread applications in improving or altering the intrinsic activities of numerous enzymes. But, these strategies are primarily based on nature's alphabet of twenty canonical amino acids (cAAs). Because of the limited chemical and physical repertoire of cAAs, not surprisingly, enzymes recruit reactive cofactors and post-transnationally modify existing amino acids in the active site. The advancements in the genetic code expansion allow enhanced protein properties by introducing unique functional groups beyond nature's limited building blocks. To this end, a series of orthogonal amino-acyl transfer RNA (tRNA) synthetase (aaRS)/tRNA pairs have been developed to encode distinct non-canonical amino acids (ncAAs) in vivo. Over the last two decades, more than 200 ncAAs have been genetically encoded in prokaryotes and eukaryotes. Apart from protein modification and antibody development for pharmaceutical use, ncAAs have been widely applied in enzyme engineering research to illustrate the enzyme mechanisms, enhance enzyme activity, and even generate new catalytic mechanisms into protein scaffolds. In this presentation, I will present our recent efforts to enhance functionality of enzyme through ncAA-based engineering approach.</p>