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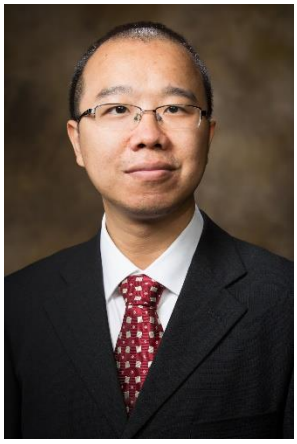
Department of Chemistry and Biochemistry
Colloquium Speaker



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"Genetic Code Expansion for Protein Acetylation Studies"

Abstract:

The reversible acetylation of lysine residues is one of the most abundant protein post-translational modifications (PTMs) in nature, and plays important roles in a wide range of biological processes such as DNA-protein interaction, transcription, translation, protein stability, stress response, apoptosis, cellular differentiation, and circadian rhythm. With advanced mass spectrometry techniques, a large dataset of acetylated lysine residues has been established. However, only few studies have been performed to validate and characterize these putative acetylation targets, largely due to the challenge to produce homogeneously acetylated protein at specific positions. To overcome this problem, genetic code expansion has been applied in protein acetylation studies. Here, we will summarize our recent development of 1) an optimized highly efficient system to incorporate acetyllysine directly into selected sites of target proteins; 2) a genetic incorporation system for thio-acetyllysine which is a non-deacetylatable analog of acetyllysine. This system will help us monitor long-lasting effects of lysine acetylation without concerning about the deacetylation of proteins by endogenous deacetylases in cells; 3) a system to simultaneously incorporate both acetyllysine and phosphoserine at two specific positions in a single protein, which provides a powerful tool to study crosstalk between acetylation and phosphorylation.

Monday January 25th, 2021
4:00 pm
Virtual Talk via WebEx

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