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主要研究领域和方向: (1)以蛋白质的翻译后修饰组学研究为核心和特色, 发现并鉴定新的蛋白质翻译后修饰, 探索蛋白质翻译后修饰的生物学功能及其调控的作用机制; (2)利用高通量质谱技术进行基因组重注释研究, 实现编码基因的确认与校正、发现新的编码基因以及发现蛋白质特有的翻译后修饰现象等。

相关的代表性论文 ( #共同第一)

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5. Jia Zhang#, **Ming-kun Yang#**, Honghui Zeng, and Feng Ge\*. (2016) GAPP: A Proteogenomic Software for Genome Annotation and Global Profiling of Post-translational Modifications in Prokaryotes. *Molecular & Cellular Proteomics*, 15(11):3529-3539.
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9. Mo R#, **Yang MK#**, Chen Z#, Cheng ZY, Yi XL, Li CY, He CL, Xiong Q, Chen H, Wang Q, Ge F (2015) Acetylome analysis reveals the involvement of lysine acetylation in photosynthesis and carbon metabolism in the model cyanobacterium *Synechocystis* sp. PCC 6803. *Journal of Proteome Research*, 14: 1275-1286.
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11. Yanyan Ma#, **Mingkun Yang#**, Xiaohuang Lin, Xin Liu, Hui Huang, and Feng Ge. (2017) Malonylome Analysis Reveals the Involvement of Lysine Malonylation in Metabolism and Photosynthesis in Cyanobacteria. *Journal of Proteome Research*, 16(5): 2030-2043.
12. **Mingkun Yang#**, Hui Huang# and Feng Ge\*. (2019) Lysine Propionylation is a Widespread Post-Translational Modification Involved in Regulation of Photosynthesis and Metabolism in Cyanobacteria. *International Journal of Molecular Sciences*. Sep 26;20(19).
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