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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，实现编码基因的确证与校正、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）

1. **Yang MK#**, Yang YH#, Chen Z, Zhang J, Lin Y, Wang Y, Xiong Q, Li T, Ge F, Bryant DA, Zhao JD (2014) Proteogenomic analysis and global discovery of post-translational modifications in prokaryotes. *Proc Natl Acad Sci U S A* 111: E5633-E5642.

2. **Mingkun Yang**, Xiaohuang Lin, Xin Liu, Jia Zhang and Feng Ge\* (2018) Genome Annotation of a Model Diatom *Phaeodactylum tricornutum* Using an Integrated Proteogenomic Pipeline. *Molecular Plant*. Oct 8;11(10):1292-1307.

3. **Yang MK**, Wang Y, Chen Y, Cheng ZY, Gu J, Deng JY, Bi LJ, Chen CB, Mo R, Wang XD, Ge F (2015) Succinylome analysis reveals the involvement of lysine succinylation in metabolism in pathogenic *Mycobacterium tuberculosis* H37Rv. *Molecular & Cellular Proteomics*, 14: 796-811.

4. Liu FY#, **Yang MK#**, Wang XD#, Yang SS, Gu J, Zhou J, Zhang XE, Deng JY, Ge F (2014) Acetylome analysis reveals diverse functions of lysine acetylation in *Mycobacterium tuberculosis*. *Molecular & Cellular Proteomics*, 13: 3352-3366.

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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7. Xin Liu#, **Mingkun Yang**#, Yan Wang, Zhuo Chen, Jia Zhang, Xiaohuang Lin, Feng Ge,\* and Jindong Zhao\*. (2018) Effects of PSII Manganese-Stabilizing Protein Succinylation on Photosynthesis in the Model Cyanobacterium *Synechococcus* sp. PCC 7002. *Plant and Cell Physiology*, Jul 1;59(7):1466-1482.

8. **Yang MK**#, Qiao ZX#, Zhang WY, Xiong Q, Zhang J, Li T, Ge F, Zhao JD (2013) Global phosphoproteomic analysis reveals diverse functions of Serine/Threonine/Tyrosine phosphorylation in the model cyanobacterium *Synechococcus* sp. strain PCC 7002. *Journal of Proteome Research*, 12: 1909-1923.

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.

10. Chen Z#, **Yang MK**#, Li CY, Wang Y, Zhang J, Wang DB, Zhang XE, Ge F (2014) Phosphoproteomic analysis provides novel insights into stress responses in *Phaeodactylum tricornutum*, a model diatom. *Journal of Proteome Research*, 13: 2511-2523.

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).

13. Silin Ren#, **Mingkun Yang**#, Yu Li, Feng Zhang, Zhuo Chen, Jia Zhang, Guang Yang, Yuewei Yue, Siting Li, Feng Ge & Shihua Wang. (2016) Global Phosphoproteomic Analysis Reveals the Involvement of Phosphorylation in Aflatoxins Biosynthesis in the Pathogenic Fungus *Aspergillus flavus*. *Scientific Reports*, 6:34078.