



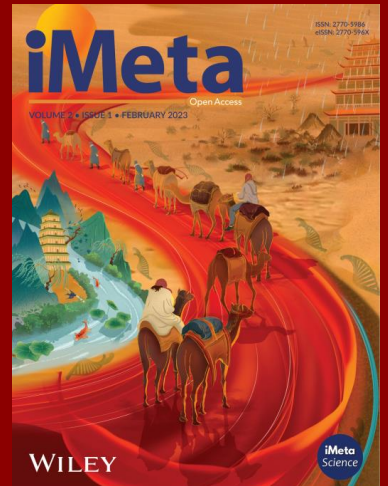
# 优势酶结构驱动的微生物组靶向功能调控 ——以脲酶为例

赵圣国<sup>1</sup>, 仲慧月<sup>1</sup>, 贺越<sup>1</sup>, 李晓姣<sup>1</sup>, 朱莉<sup>2</sup>, 熊展博<sup>1</sup>, 张晓音<sup>1</sup>, 郑楠<sup>1</sup>, Diego P Morgavi<sup>3</sup>, 王加启<sup>1</sup>

<sup>1</sup> 中国农业科学院北京畜牧兽医研究所

<sup>2</sup> 兰州大学

<sup>3</sup> 法国农业食品与环境研究院



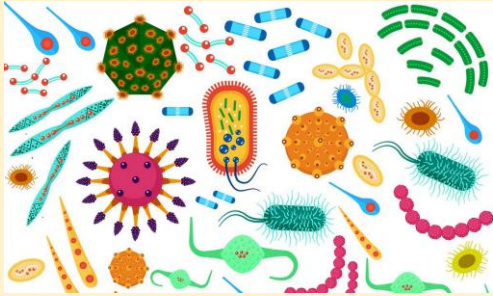
Shengguo Zhao, Huiyue Zhong, Yue He, Xiaojiao Li, Li Zhu, Zhanbo Xiong, Xiaoyin Zhang, et al. 2025. Leveraging core enzyme structures for microbiota targeted functional regulation: Urease as an example. *iMeta* 4: e70032.

<https://doi.org/10.1002/imt2.70032>



# 研究背景

## 微生物群功能调控



### 传统调控:

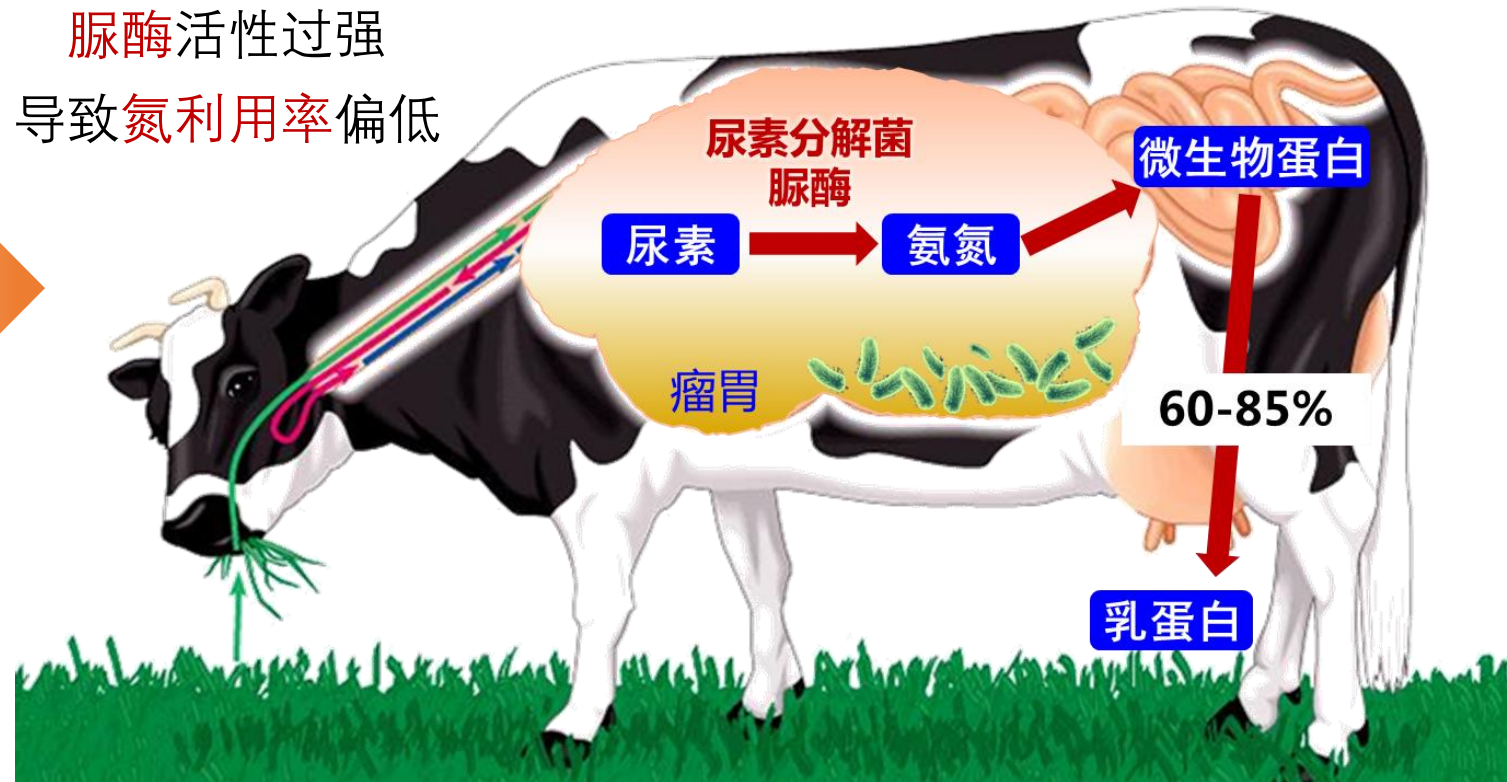
- 广谱抗生素
- 益生菌
- 饮食干预

### 局限性:

- 靶向性不强
- 非靶标扰动

## 瘤胃微生物群分解尿素的调控

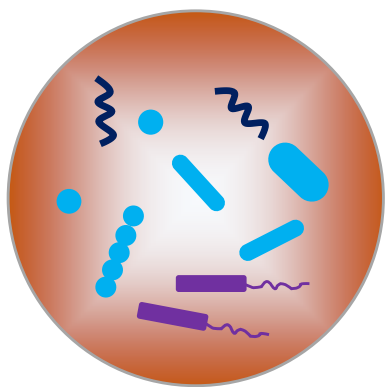
脲酶活性过强  
导致氮利用率偏低



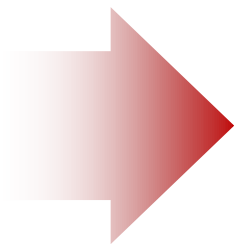


# 简介

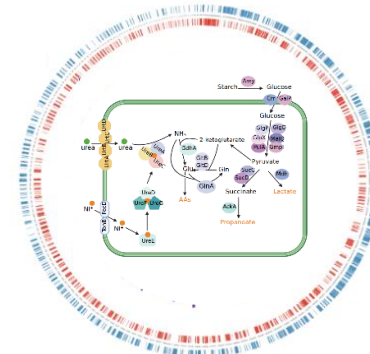
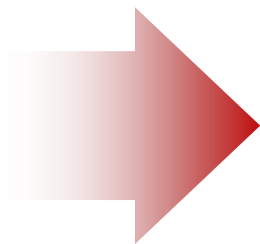
## 优势酶结构驱动的微生物组靶向功能调控



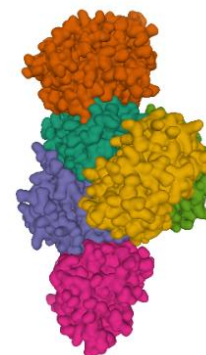
微生物群



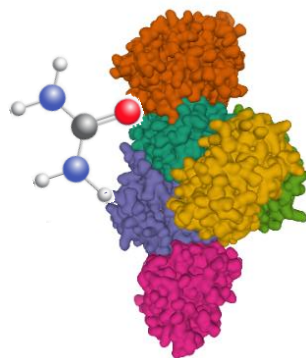
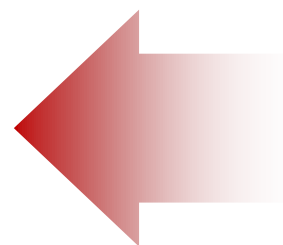
优势酶鉴定



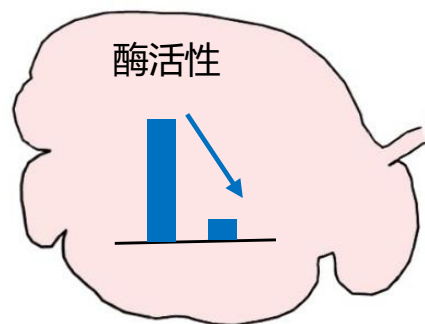
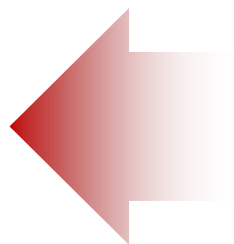
基因组与代谢



酶蛋白结构



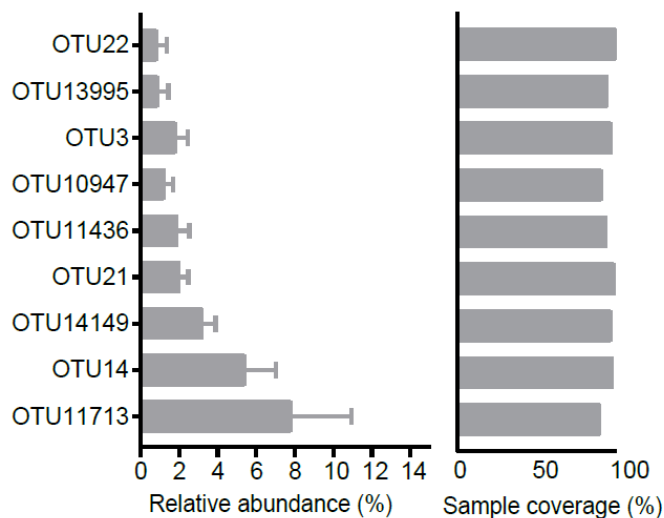
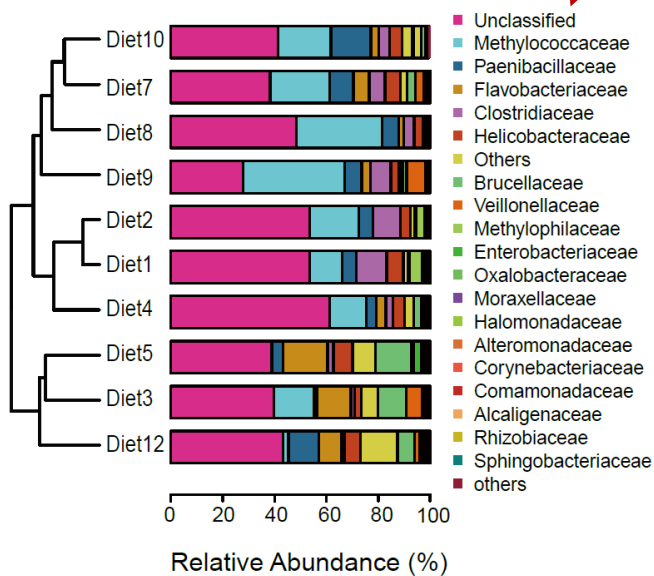
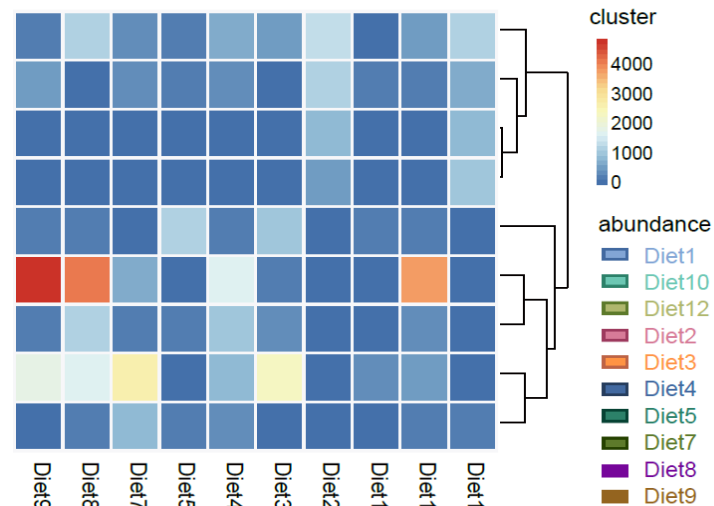
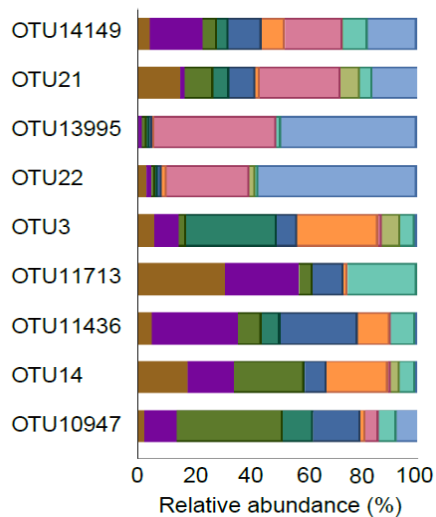
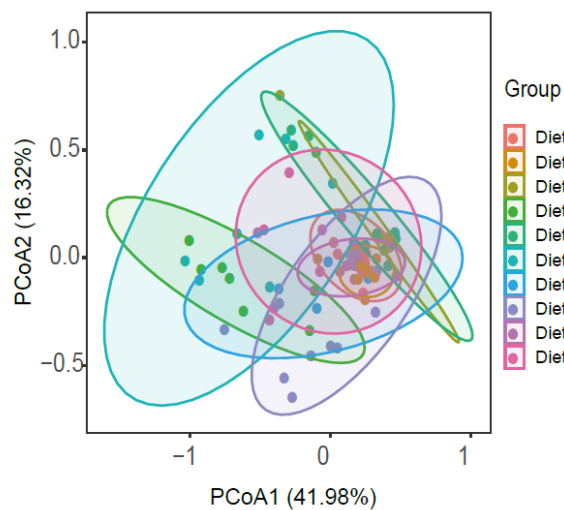
虚拟筛选抑制剂



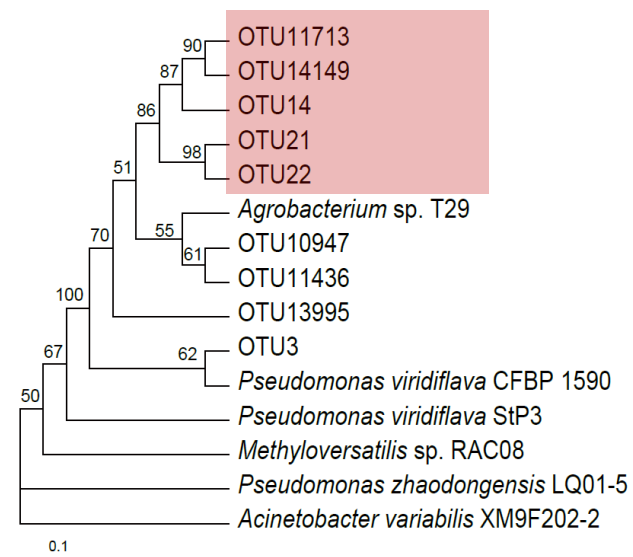
功能验证



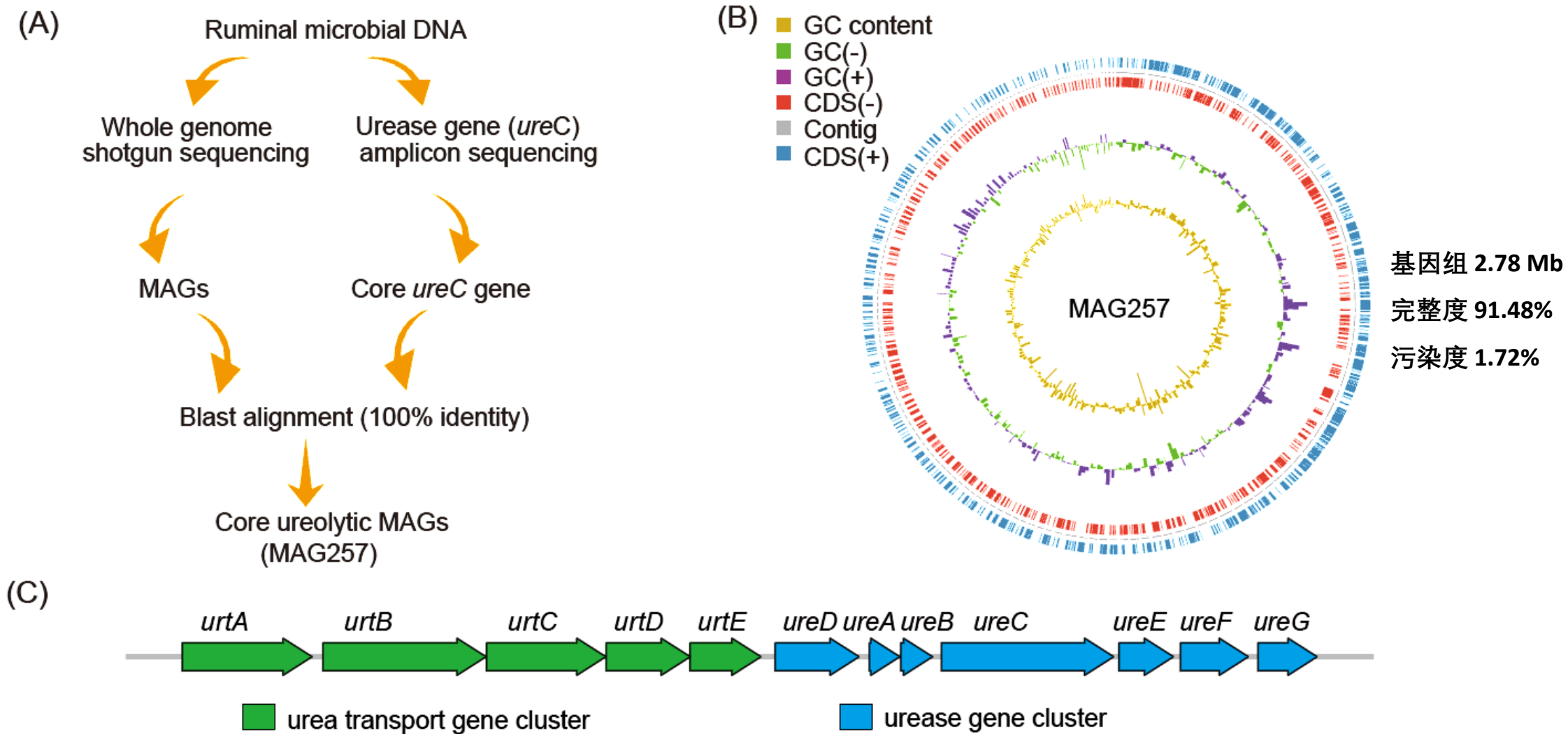
# 瘤胃微生物优势脲酶的鉴定



相对丰度>1%， 样本覆盖率>85%



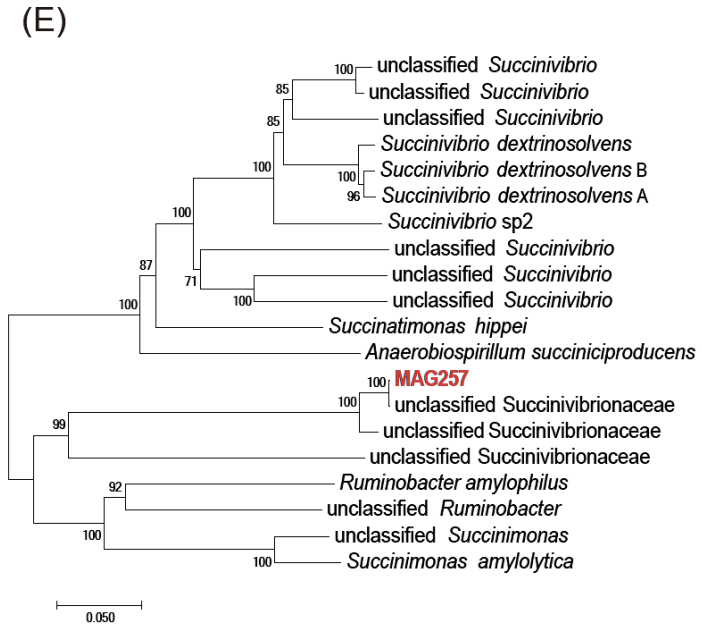
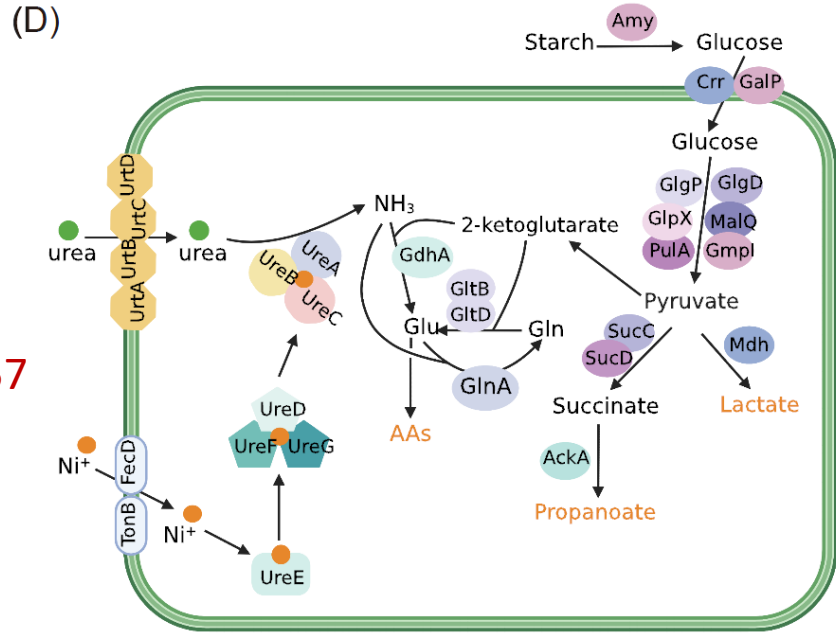
# 优势脲酶所在基因组的鉴定



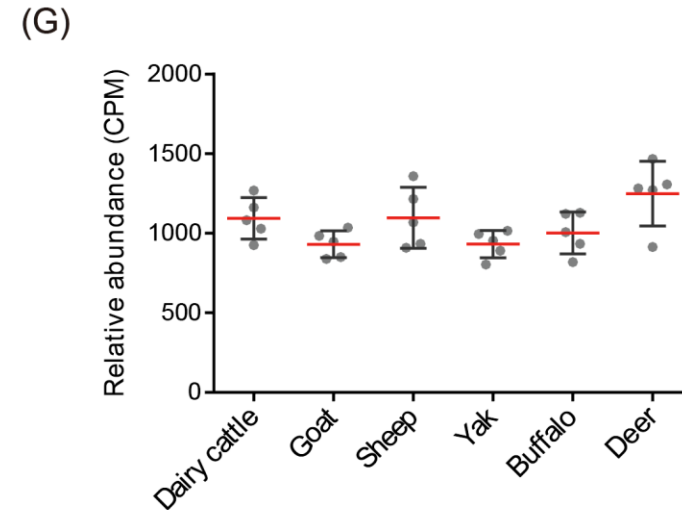


# 优势脲酶所在基因组的特征

MAG257  
代谢

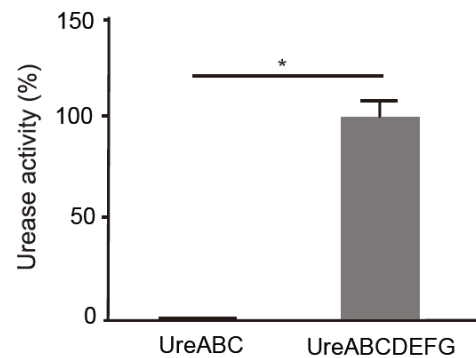
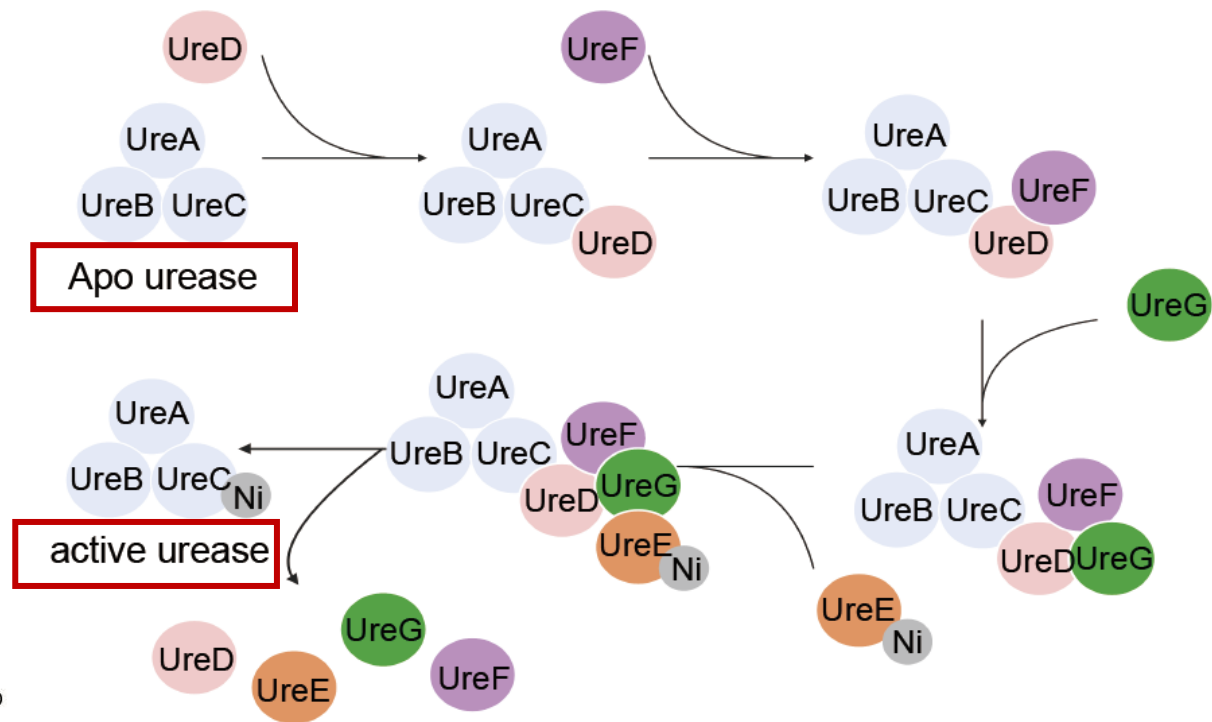
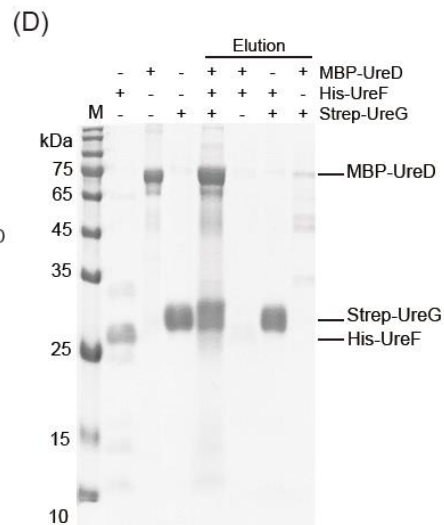
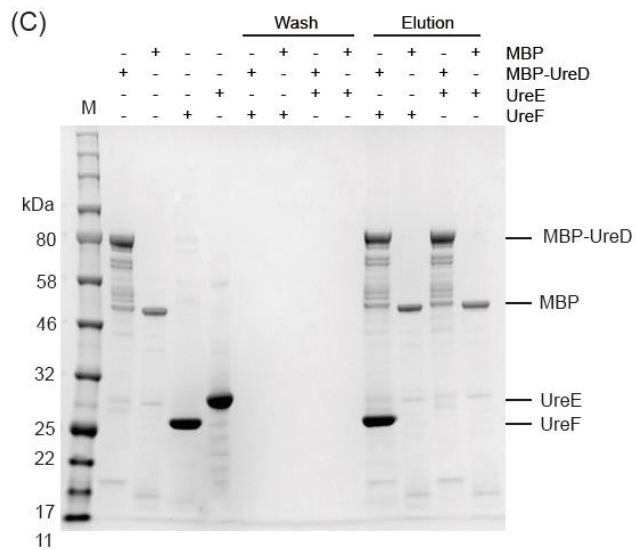
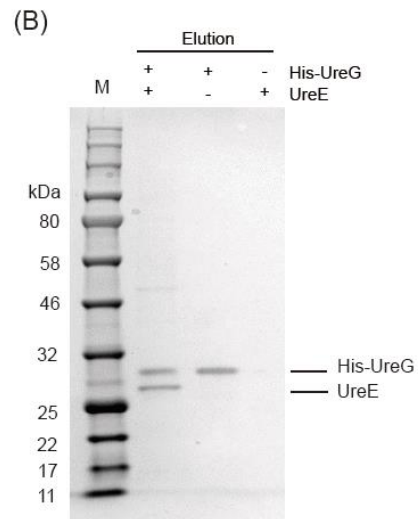
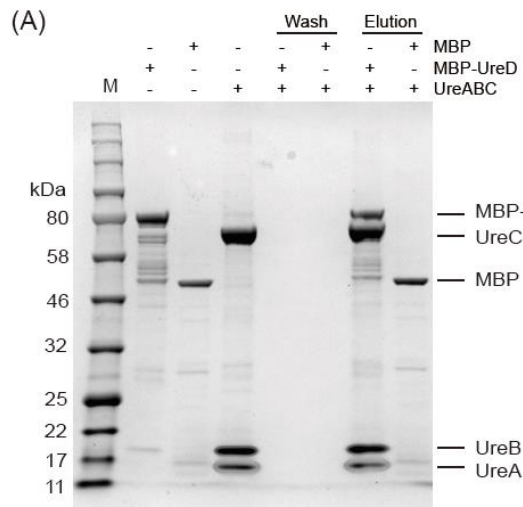


脲酶活性  
宏蛋白质



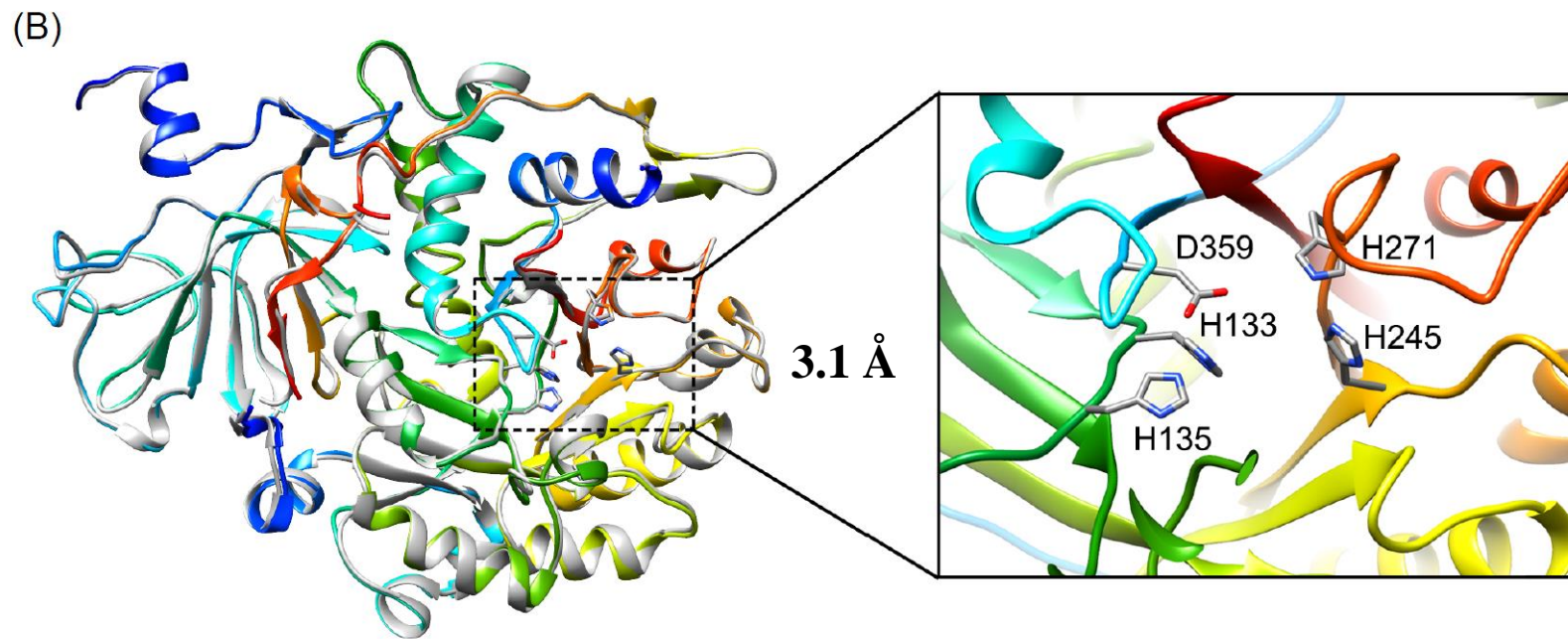
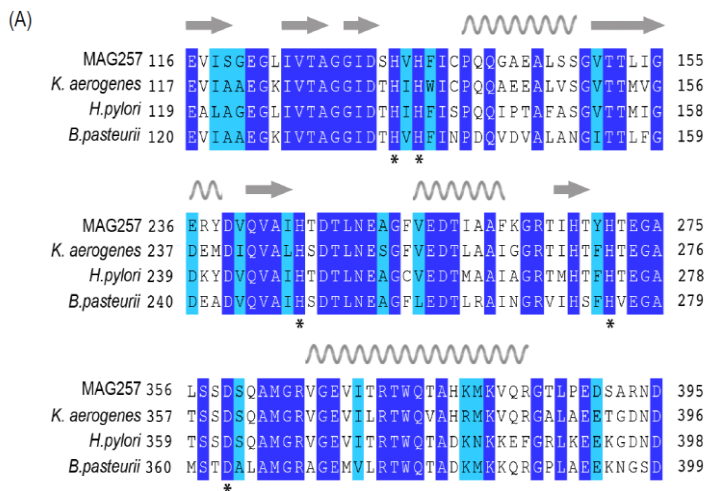


# 优势脲酶的蛋白互作

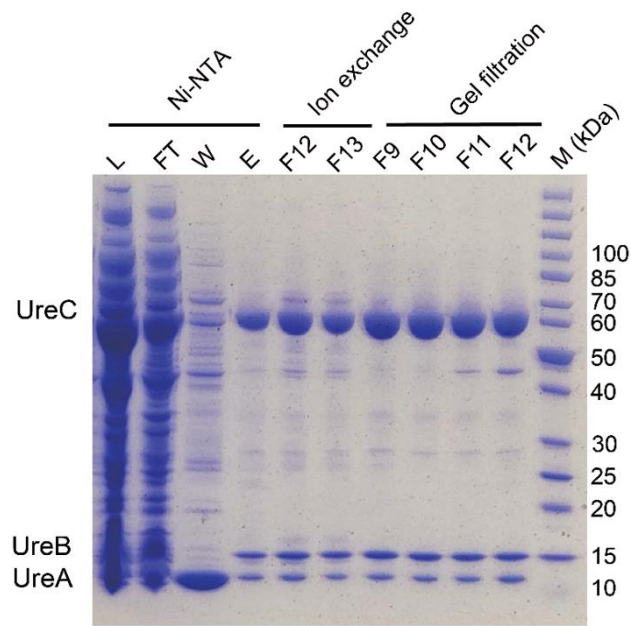




# 优势脲酶的蛋白质结构特征

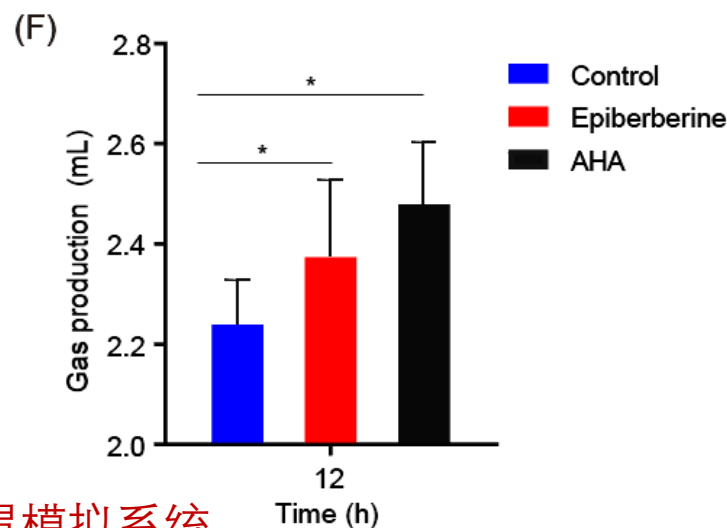
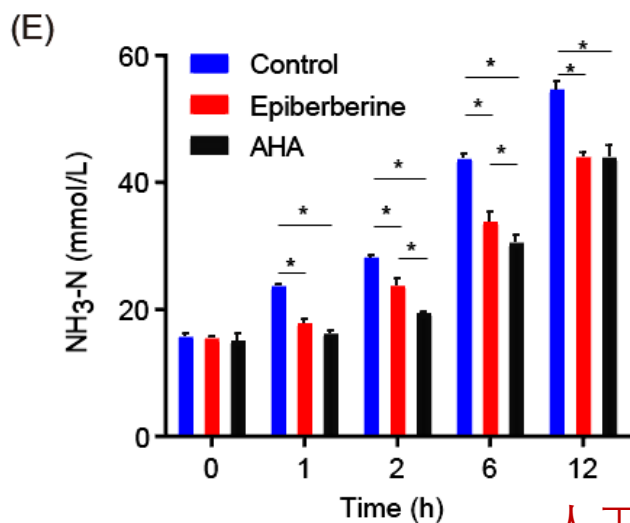
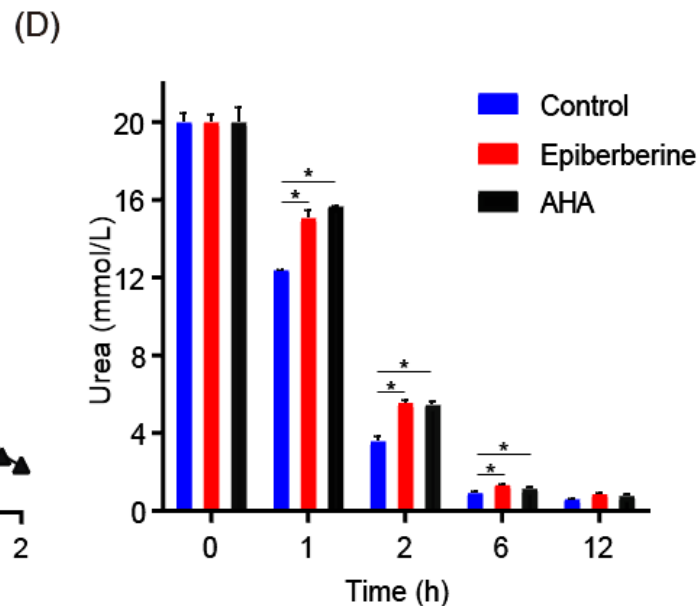
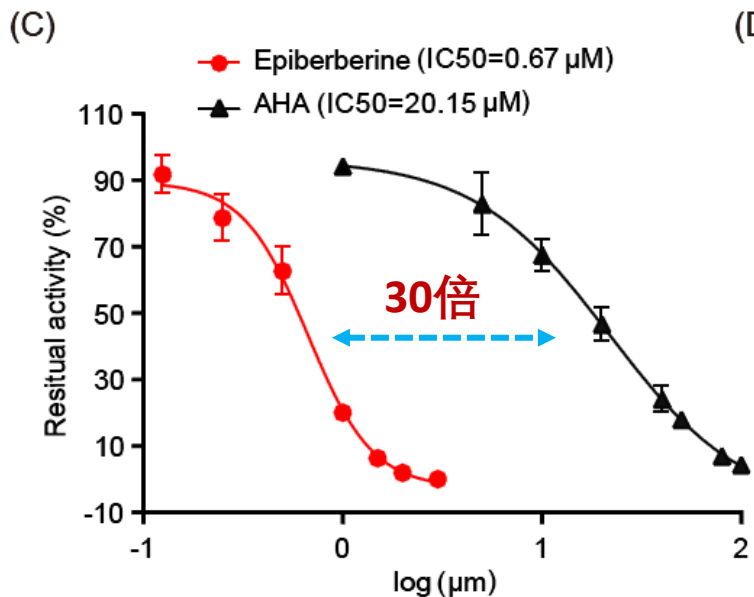
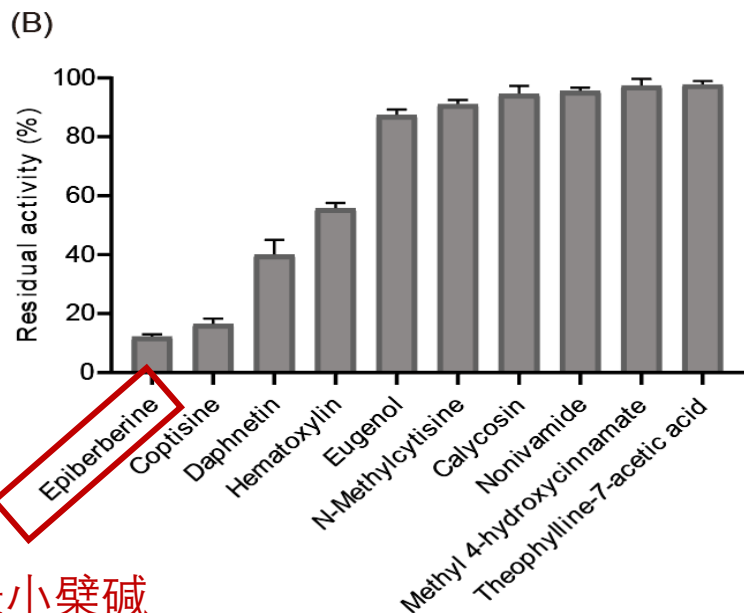
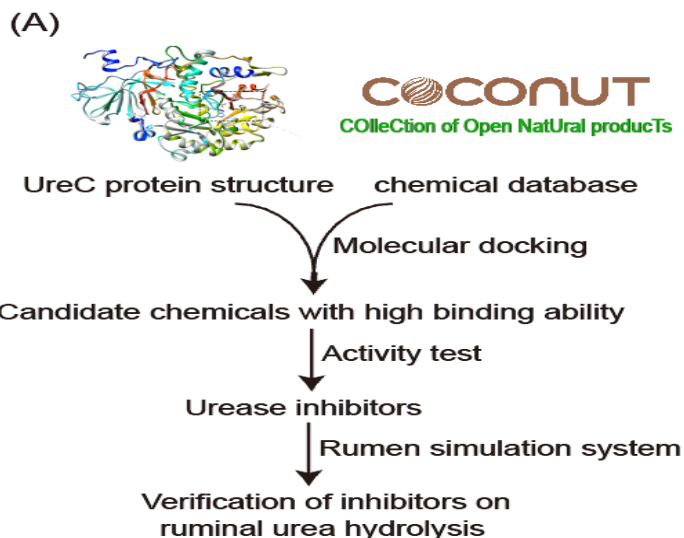


冷冻电镜 脲酶UreC蛋白





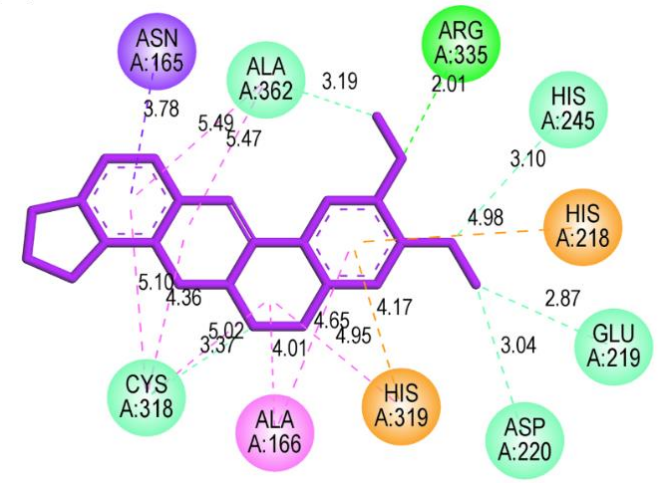
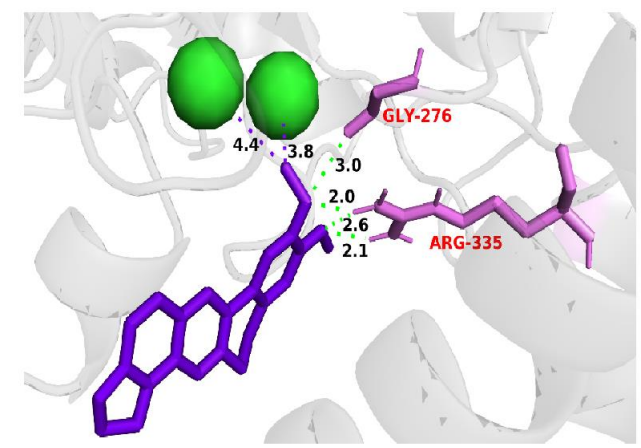
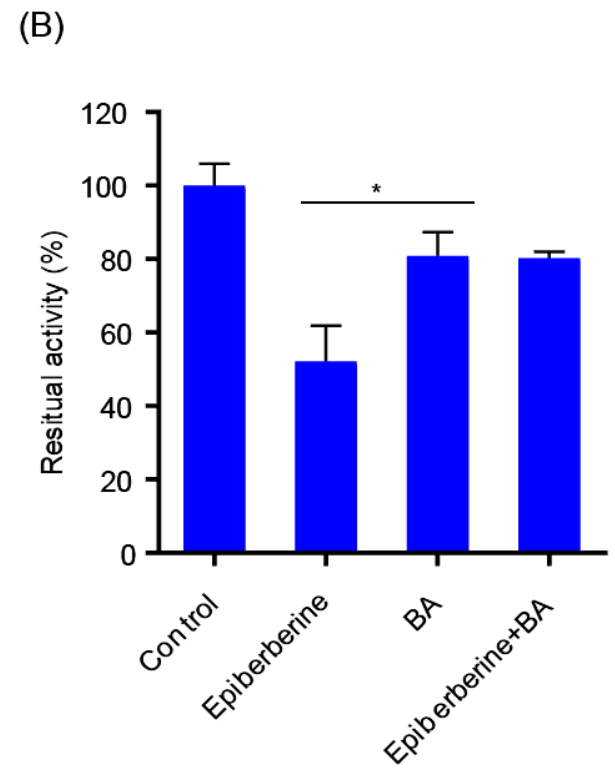
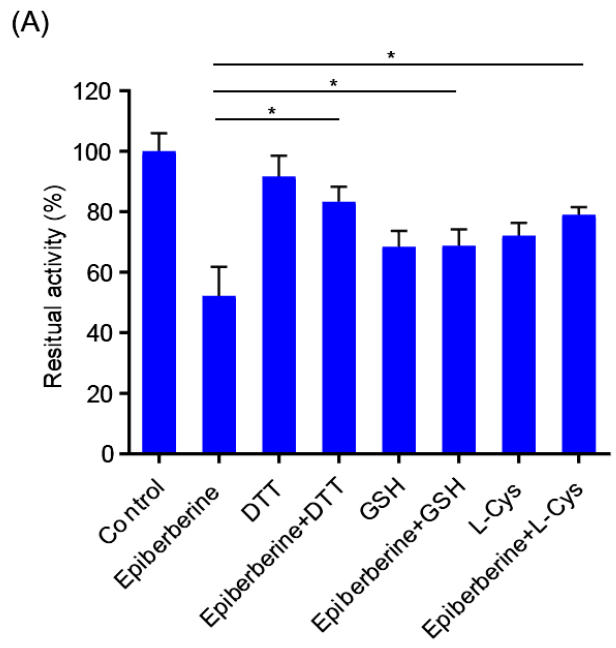
# 脲酶抑制剂的筛选与验证



人工瘤胃模拟系统



# 表小檗碱抑制脲酶的作用机制



### Interactions

- Coventional Hydrogen Bond
- Carbon Hydrogen Bond
- Pi-Sigma
- Pi-Alkyl
- Pi-Cation

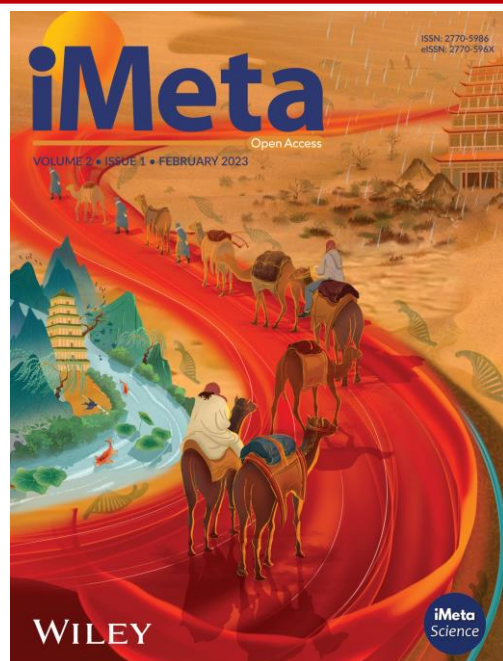


# 总结

- 开发并验证了一种调控微生物群落功能的新方法，该方法整合了优势功能蛋白鉴定、蛋白质结构分析、分子对接虚拟筛选和模拟模型功能验证。
- 成功鉴定了奶牛瘤胃微生物群中的优势脲酶，并发现天然化合物表小檗碱对瘤胃微生物脲酶活性具有强效抑制作用。
- 该方法为微生物组工程及其在动物生产、人类健康、环境改善和生物技术中的广泛应用提供了有前景的工具。

Shengguo Zhao, Huiyue Zhong, Yue He, Xiaojiao Li, Li Zhu, Zhanbo Xiong, Xiaoyin Zhang, et al. 2025. Leveraging core enzyme structures for microbiota targeted functional regulation: Urease as an example. *iMeta* 4: e70032.

<https://doi.org/10.1002/imt2.70032>



“**iMeta**” (影响因子**23.8**) 由威立、宏科学和千名华人科学家出版的期刊，主编刘双江和傅静远教授。  
收稿范围：任何领域高影响力的研究、方法和综述，重点关注生物技术、生物信息和微生物组等；  
影响力：[SCIE/WOS](#)、[PubMed](#)、[Google](#)、[Scopus](#)收录，**IF 23.8**位列**JCR**微生物学研究期刊全球第一；  
时效性：外审平均21天；投稿至发表中位数57天；  
“**iMetaOmics**” 主编赵方庆和于君教授，定位**IF>10**的高水平交叉学科综合期刊，欢迎投稿！



主页: <http://www.imeta.science>

出版社: <https://wileyonlinelibrary.com/journal/imeta>



[office@imeta.science](mailto:office@imeta.science)

[imetaomics@imeta.science](mailto:imetaomics@imeta.science)



投稿: <https://wiley.atyponrex.com/journal/IMT2>

<https://wiley.atyponrex.com/journal/IMO2>



宣传片



[iMeta](#)

