



微生物学研究者的宏蛋白质组学指南

The Microbiologist's Guide to Metaproteomics

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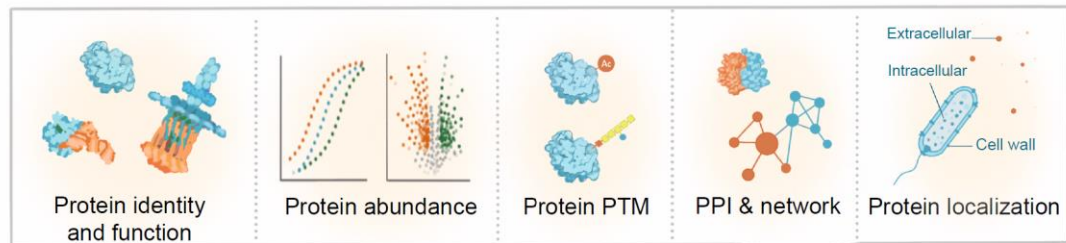
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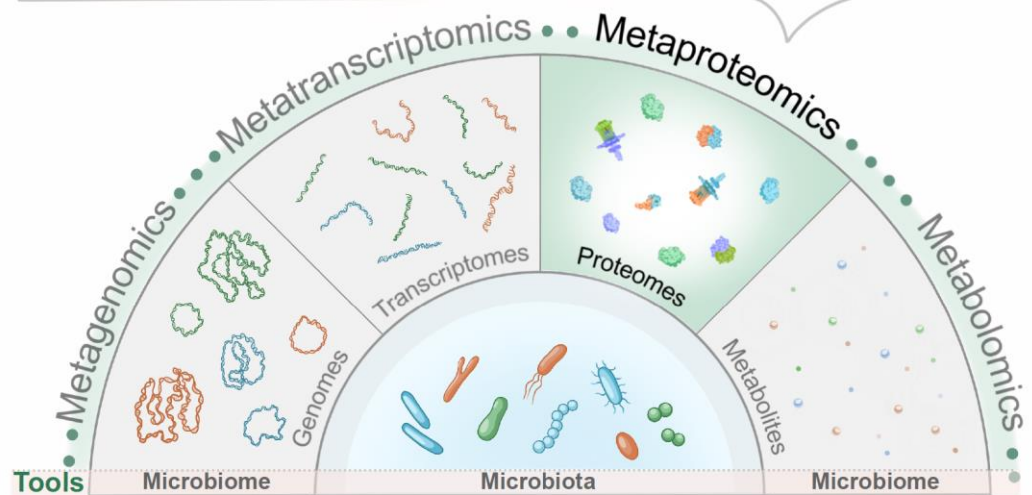


宏蛋白质组学是什么，它为何重要？



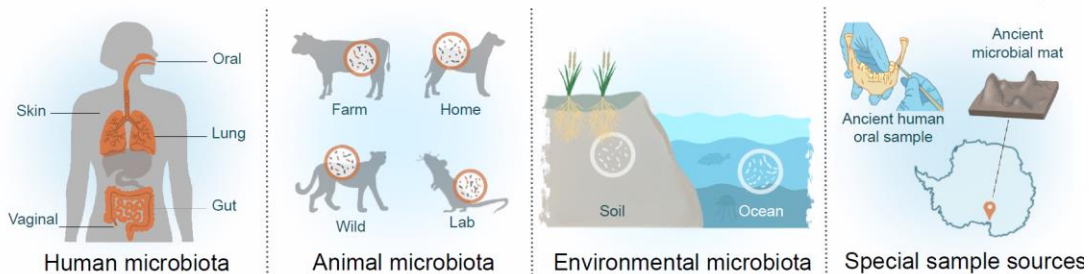
宏蛋白质组学能做什么？

- 识别蛋白质并定量其在微生物群落中的丰度
- 将蛋白质关联到分类学信息和功能注释
- 检测翻译后修饰 (PTMs)

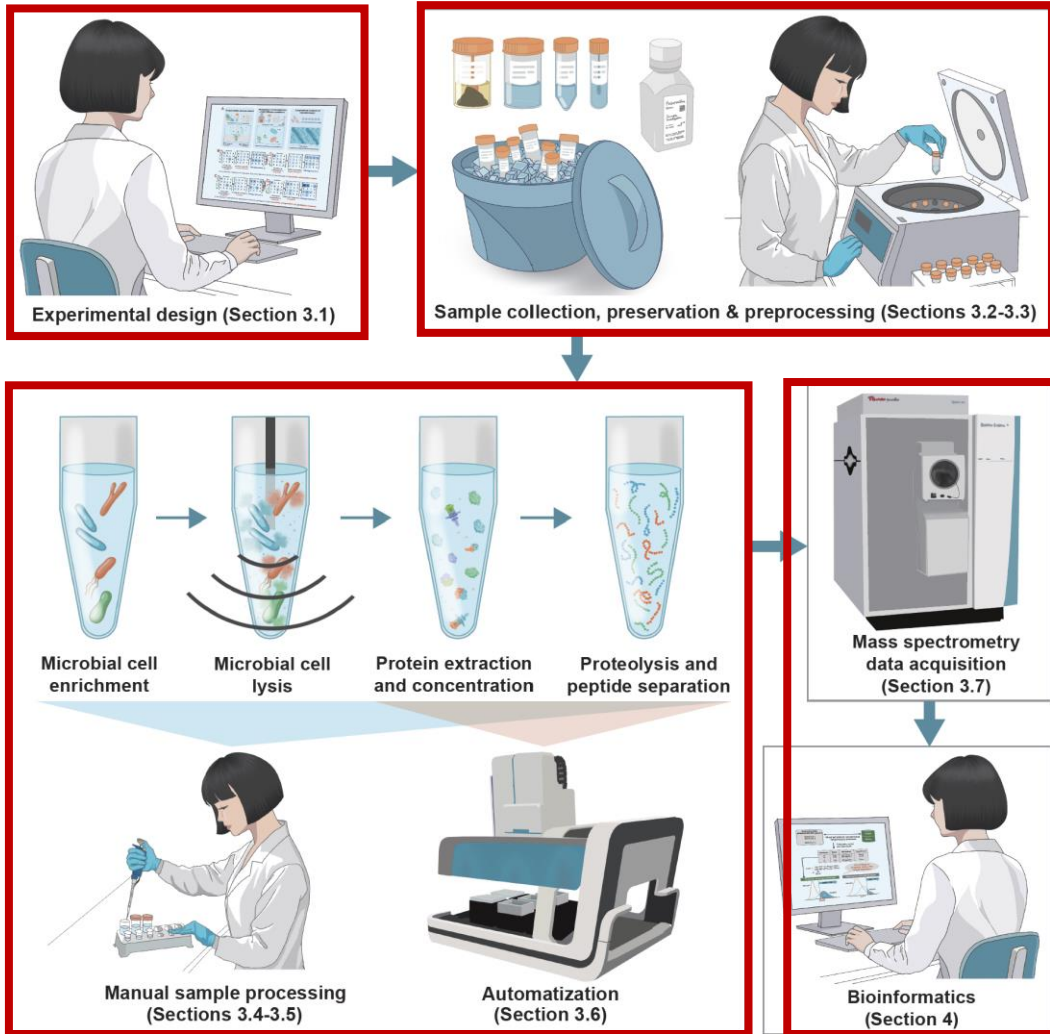


为什么要做宏蛋白质组学？

- 能够捕捉微生物群落中的真实活性功能
- 作为宏基因组、宏转录组和代谢组研究的补充

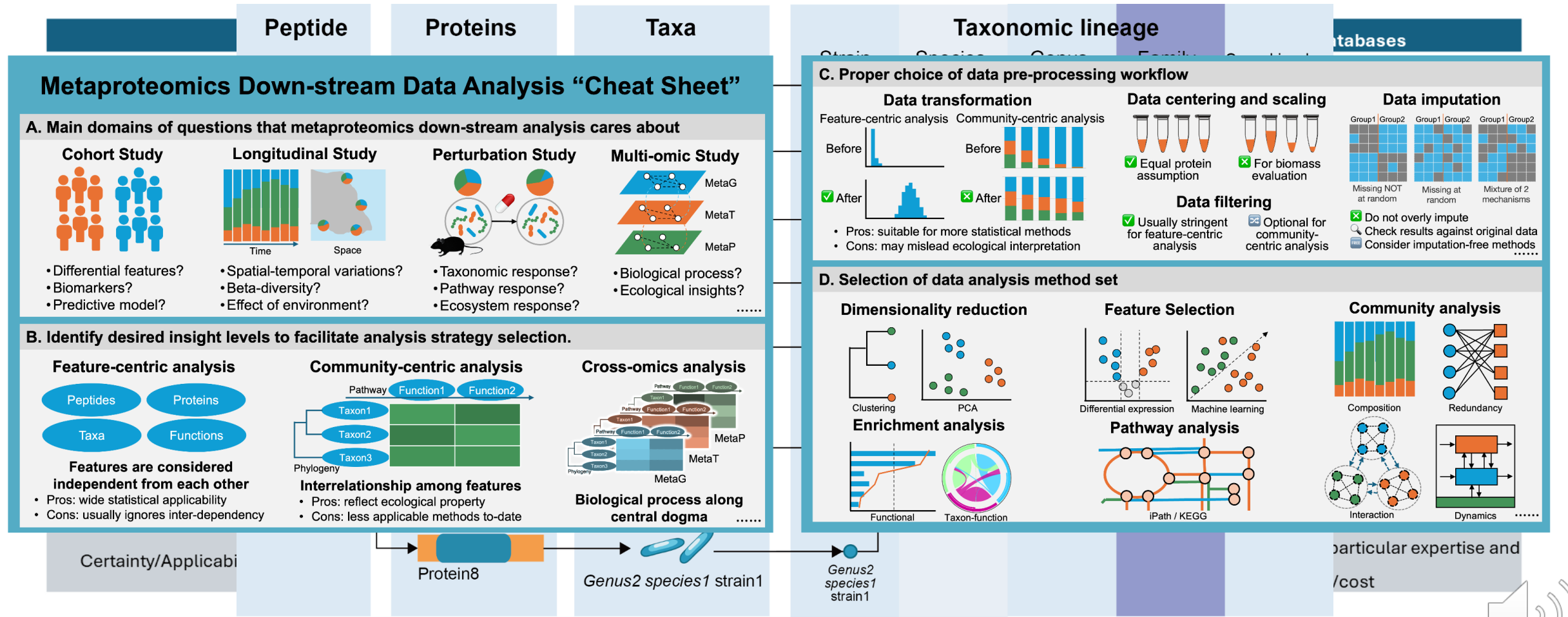


综述全面覆盖了从实验设计到生物信息分析的各个环节



Method	Description	Advantages	Disadvantages
Chemical Lysis	Disrupts cell membranes with chemicals like urea or guanidine hydrochloride.	Can unfold complex proteins.	If not removed or sufficiently diluted, it can interfere with protease activity. Risk of urea-induced carbamylation.
Detergent Lysis	Uses detergents (e.g., SDS, Triton X-100) to solubilize cell membranes.	Mild, preserves protein function, ideal for membrane proteins.	If a detergent is not removed or sufficiently diluted, it can interfere with protease activity.
Freeze-Thaw Cycles	Repeatedly freezes and thaws the sample to rupture cell membranes.	Simple, no special equipment needed.	Time-consuming, may not fully lyse cells, risk of protein degradation.
Bead beating	Physical force such as using bead beating to break cell walls.	Effective for bacterial cell lysis.	Requires specific instrument, sample loss due to contact with beads, can generate heat, risk of protein degradation.
Ultrasonication	Uses ultrasound waves to break cell membranes/walls and release proteins.	Fast, effective and can be non-contact for small samples, no need for harsh chemicals.	Can denature proteins if overused, heat generation requires sample cooling.

生物信息学部分介绍数据库构建、FDR计算、蛋白质分组、LCA分类法及下游统计分析等核心概念



国际宏蛋白质组学倡议：一个由宏蛋白质组学研究者发起、服务于该领域研究者的国际性学术社群

来自23个国家、95个实验室的350多位成员

三大核心支柱：

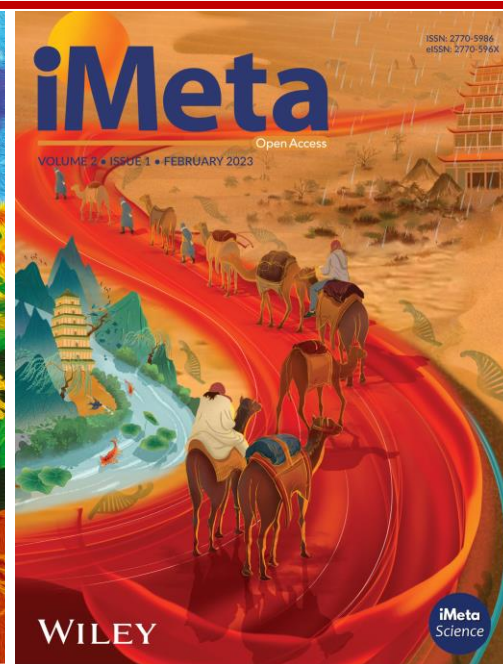
- **交流与合作**（如 CAMPI 项目、国际宏蛋白质组学研讨会等）
- **教育与推广**（包括本次 *iMeta* 旗舰综述、组织专题工作坊等）

• **标志** Article | [Open access](#) | Published: 15 December 2021
Critical Assessment of MetaProteome Investigation prot





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“***iMetaOmics***” is a sister journal of “***iMeta***” launched in 2024, with a **target IF>10, and its scope is similar to *Nature Communications, Microbiome, ISME J, Nucleic Acids Research, Briefings in Bioinformatics, etc.*** All contributes are welcome!

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