



Wekemo Bioincloud 2026: AI赋能的标准化多组学数据分析平台

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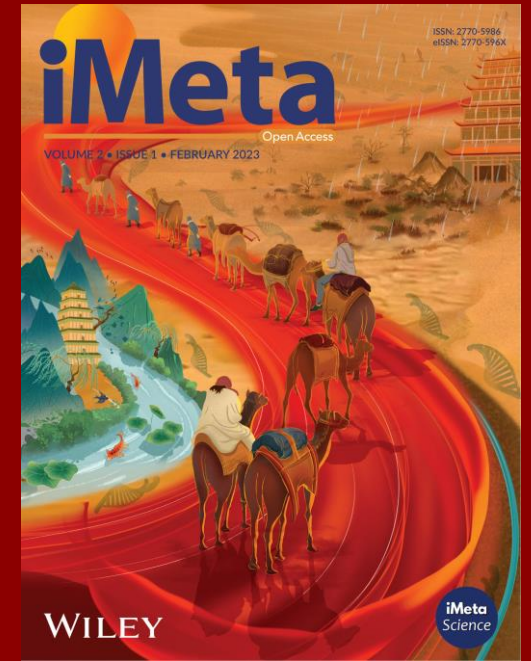
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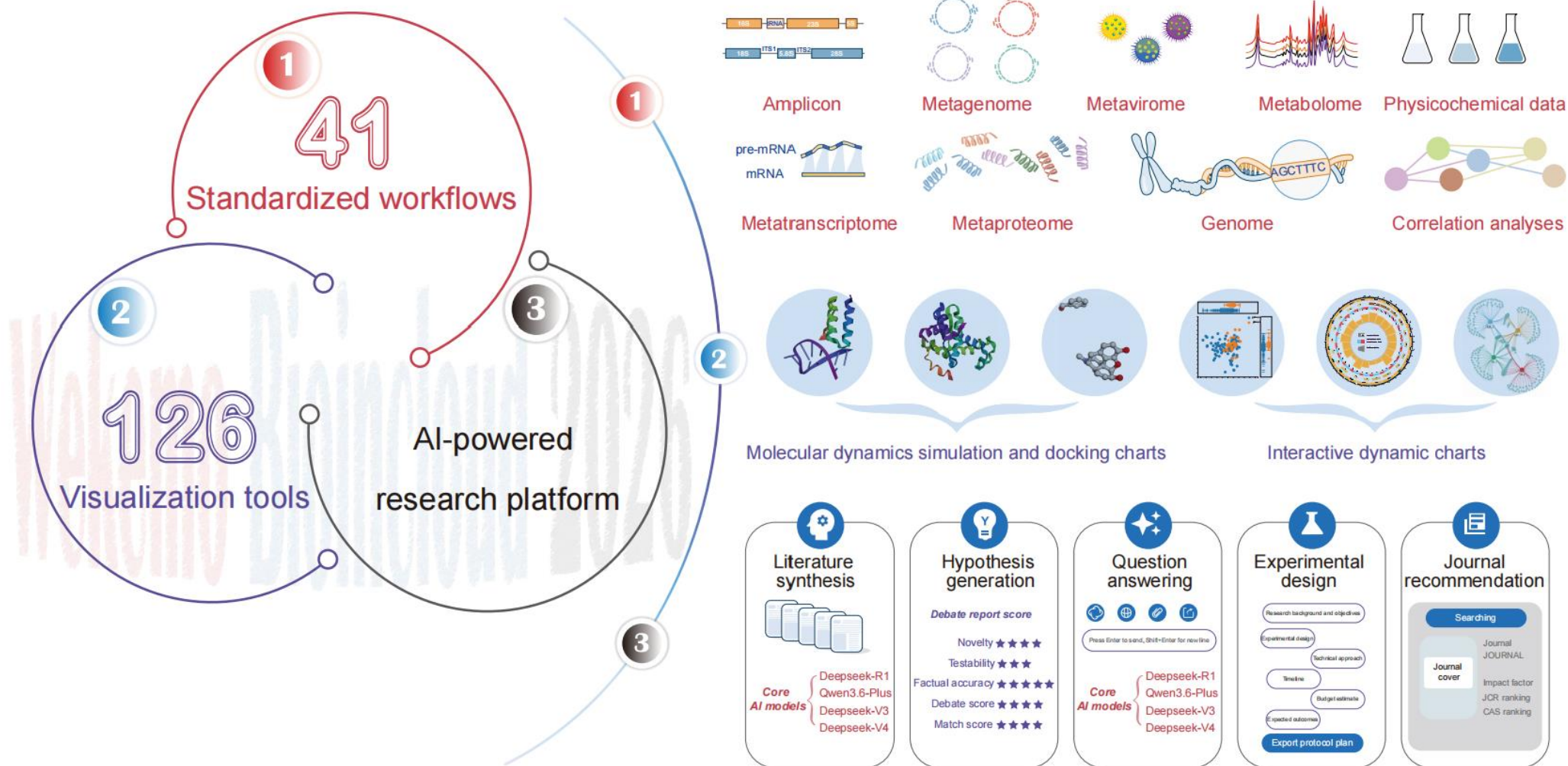
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简介

Wekemo Bioincloud 2026:

An AI-enabled platform for standardized multi-omics data analyses



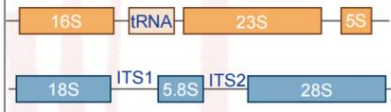


标准化分析流程全面升级

Overview of 41 analysis workflows in Wekemo Bioincloud 2026

I| Amplicon data analyses (2)

- Amplicon sequencing workflow
- Amplicon sequencing workflow (third-generation)



II| Metagenomic analyses (3)

- Metagenome workflow (reference-based)
- Metagenome workflow (de novo)
- Metagenome workflow (binning)



III| Metaviromic analysis (1)

- Metavirome workflow



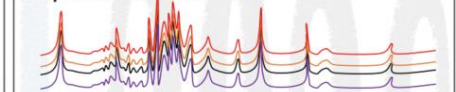
IV| Physicochemical analysis (1)

- Physicochemical properties workflow



V| Metabolomic analyses (4)

- Non-targeted metabolome workflow
- Targeted metabolome workflow (high-throughput)
- Targeted metabolome workflow
- Lipidomics Workflow



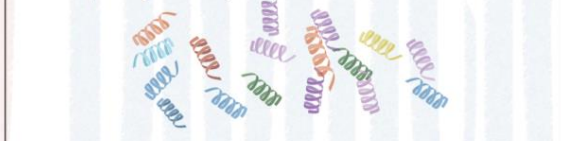
VI| Metatranscriptomic analyses (9)

- Metatranscriptome workflow
- miRNA transcriptome workflow ★
- lncRNA transcriptome workflow
- Eukaryotic transcriptome workflow (reference-based)
- Eukaryotic transcriptome workflow
- Eukaryotic transcriptome workflow 2.0 ★
- 10X single-cell transcriptome workflow
- Whole transcriptome workflow ★
- Prokaryotic transcriptome workflow (reference-based) ★



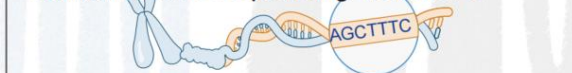
VII| Metaproteomic analyses (6)

- Metaproteome workflow (TMT-based)
- Metaproteome workflow (TMT-based) v2.0 ★
- Metaproteome workflow (label-free)
- Astral DIA proteomics workflow ★
- Astral DIA proteomics workflow (reference-free) ★
- Phosphorylation proteomics workflow ★



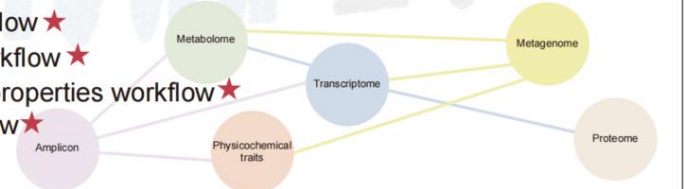
VIII| Genomic analyses (7)

- Bacterial genome workflow
- Bacterial genome workflow (PacBio+Illumina)
- Bacterial complete genome workflow (complete circular test) ★
- Fungal genome framework workflow
- Fungal genome workflow (PacBio+Illumina)
- Plant and animal genome resequencing and variant detection workflow ★
- Human-exome sequencing workflow ★



IX| Correlation analyses (8)

- Amplicon-Metabolome workflow ★
- Amplicon-Transcriptome workflow ★
- Amplicon-Physicochemical properties workflow ★
- Transcriptome-Metabolome workflow ★
- Metagenome-Metabolome workflow ★
- Metagenome-Transcriptome workflow ★
- Metagenome-Physicochemical properties workflow ★
- Transcriptome-Proteome workflow ★



★ Workflows newly introduced in Wekemo Bioincloud 2026

Wekemo Bioincloud 2026共提供41个多组学数据标准化分析流程。



可视化工具全面升级

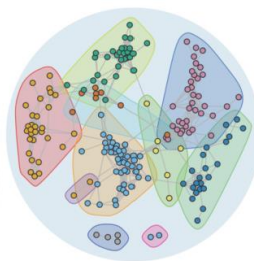
Enhanced visualization tools in Wekemo Bioincloud 2026



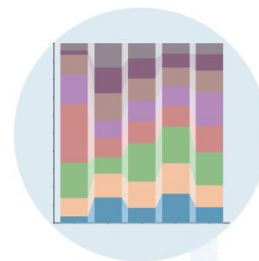
Mantel test-based correlation heatmap



Circular heatmap



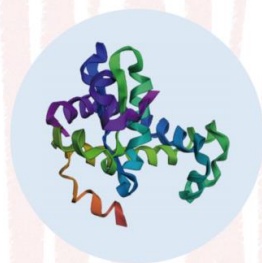
Co-occurrence network analysis



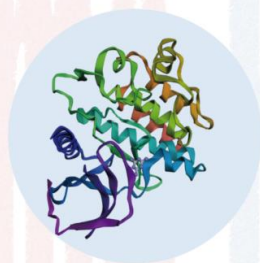
Connected stacked chart



Dynamic species abundance sankey chart



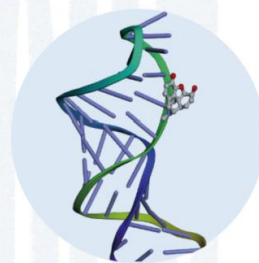
Protein-protein docking



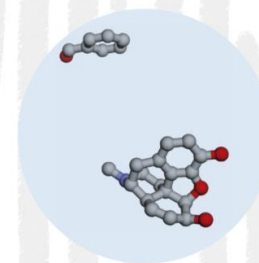
Protein-small molecule docking



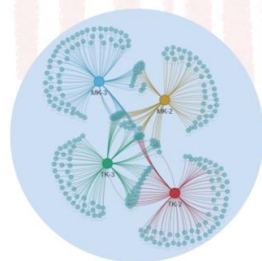
Protein-nucleic acid docking



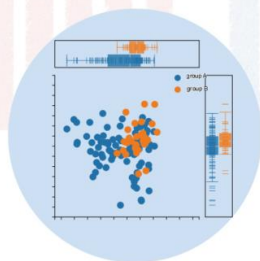
Nucleic acid-small molecule docking



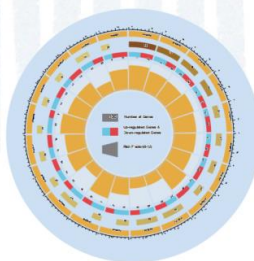
Small molecule-small molecule docking



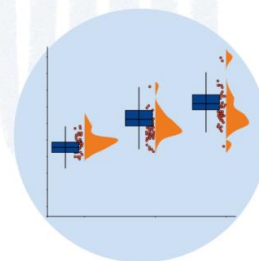
Network venn chart



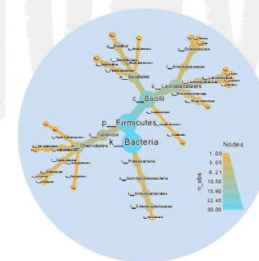
Scatter chart with boxplots



Gene enrichment circle chart



Raincloud plot



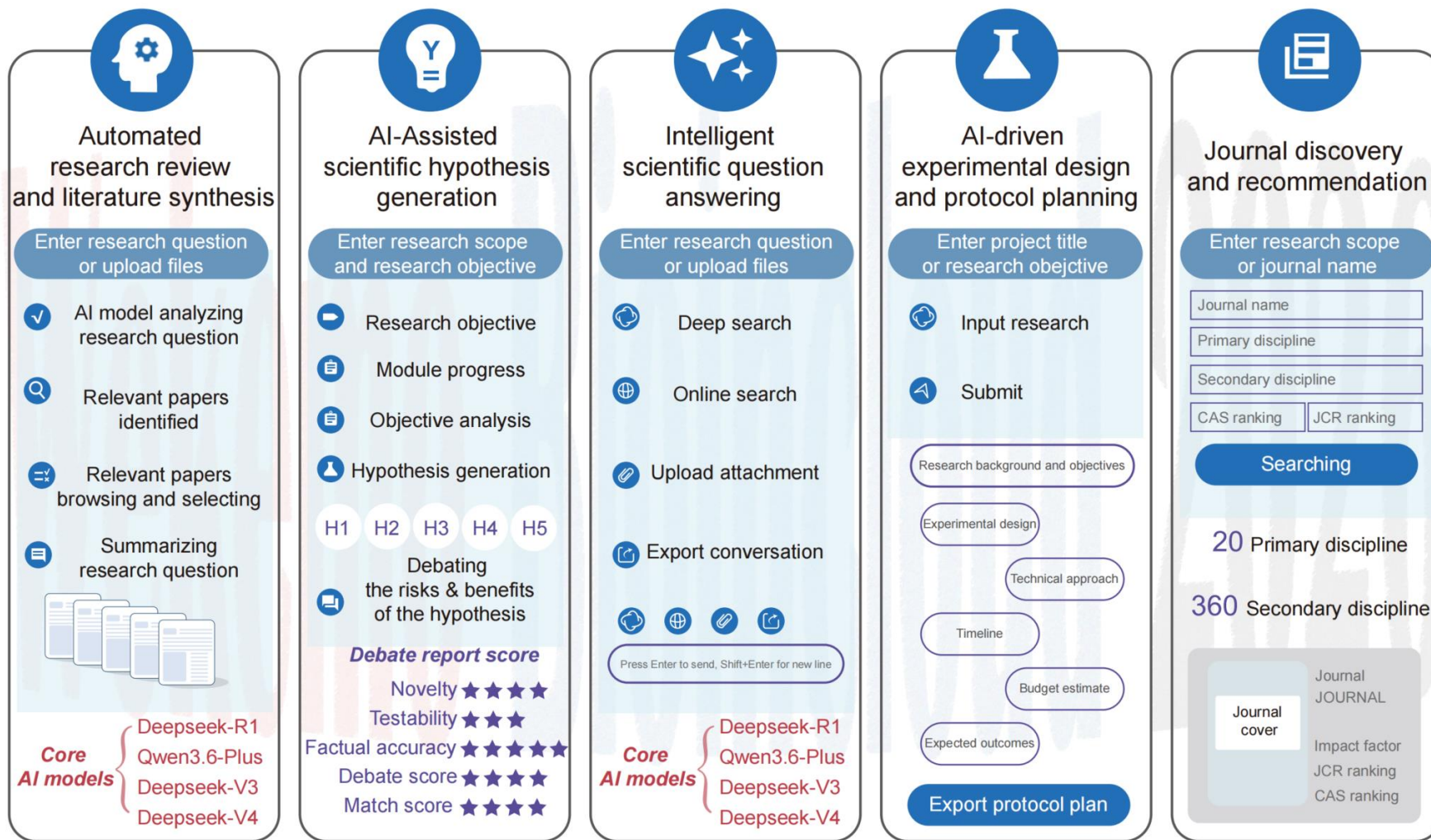
Taxonomic heat tree

Wekemo Bioincloud 2026平台可视化模块共集成126种分析与可视化工具。



AI科研平台实现科研全过程智能辅助

New AI-powered research platform in Wekemo Bioincloud 2026

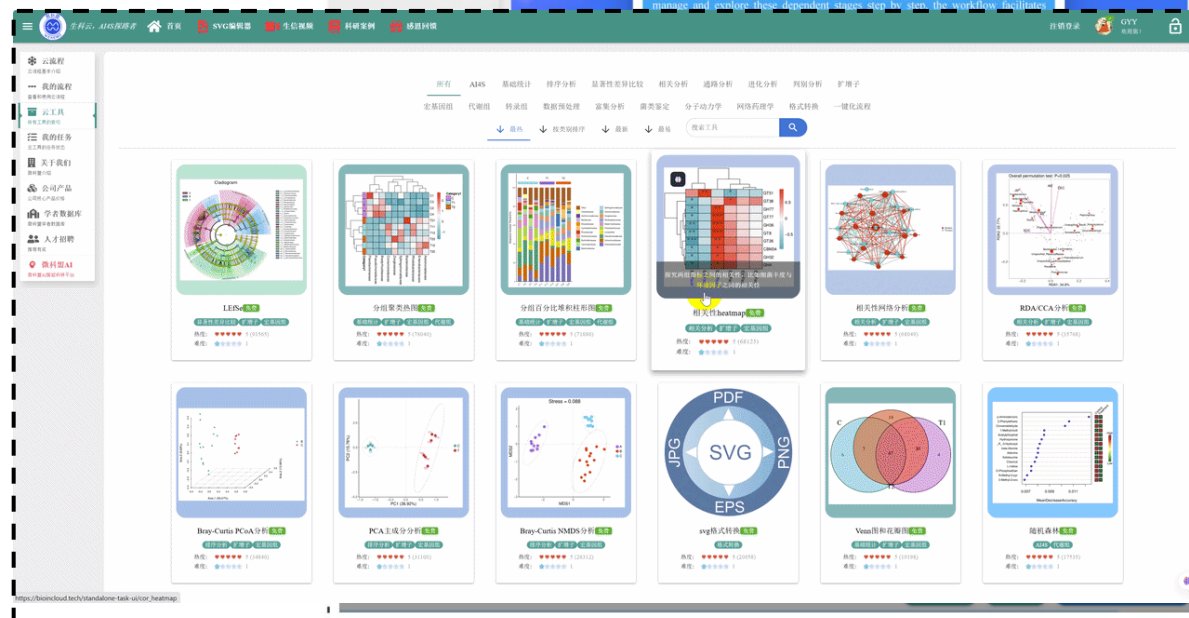


AI科研平台整体架构示意图。平台包含五大核心功能模块：文献自动综述与研究进展总结、AI辅助科学假设生成、智能科研问答、AI驱动实验设计与方案规划，以及目标期刊发现与推荐。

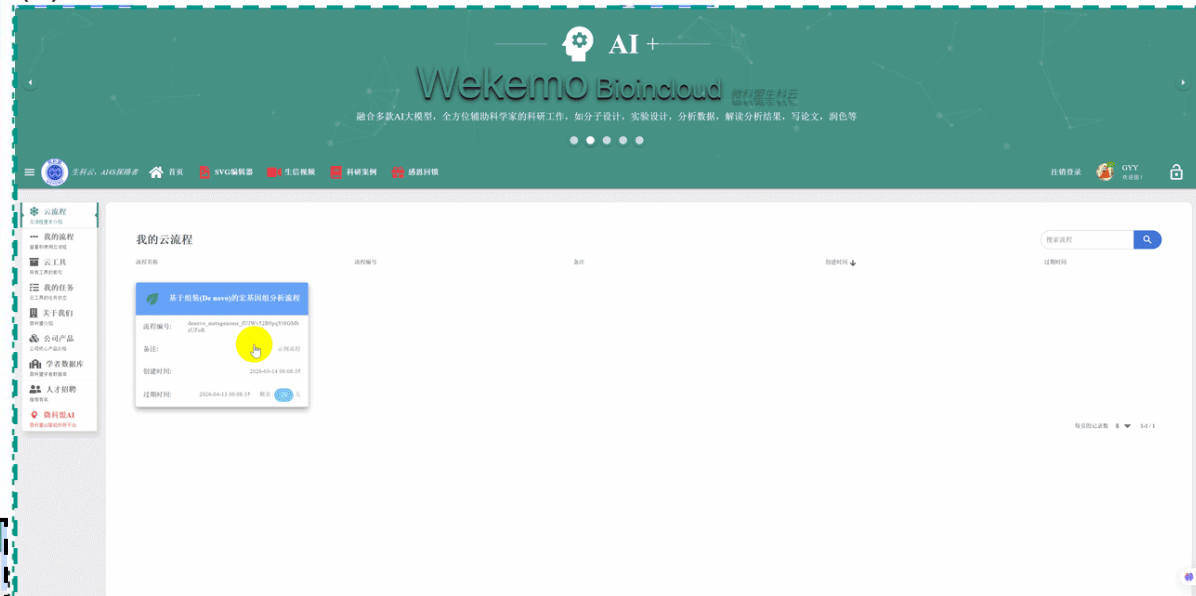


AI辅助分析结果智能解读

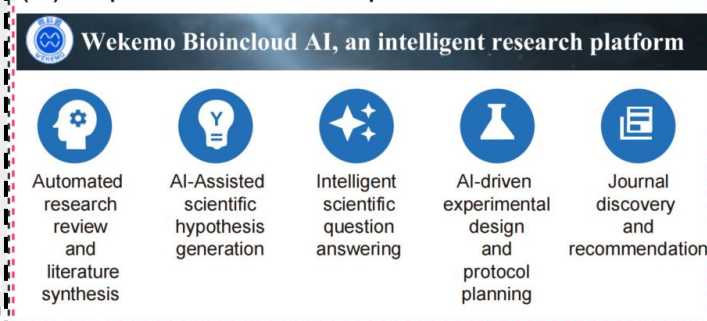
(B) Visualization tools



(A) Workflows



(C) AI-powered research platform



Wekemo Bioincloud 2026平台AI辅助功能的典型应用示例



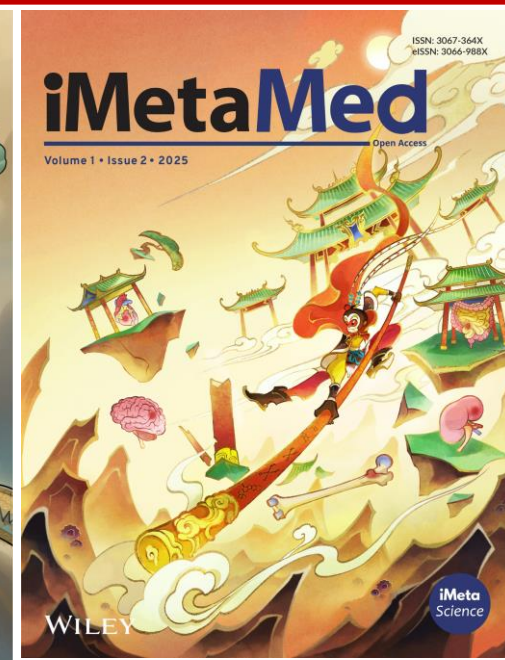
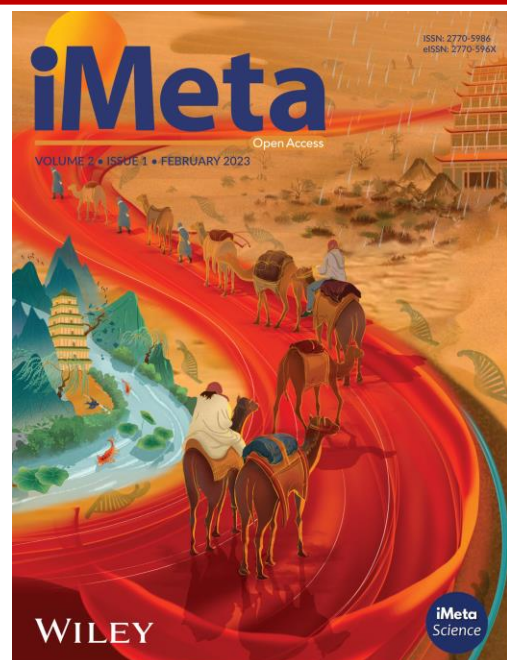
总结

- ❑ 构建覆盖九大分析领域的41条标准化分析流程，新增跨组学相关性分析模块，为多组学综合分析提供更加完善的标准化解决方案；
- ❑ 可视化工具扩展至126个，集成AI辅助数据预处理、参数推荐及图形自动解读功能，进一步提升数据分析效率和结果可解释性；
- ❑ 创新推出AI科研平台，支持文献综述、科学假设生成、实验设计、智能科研问答及期刊推荐，为科研全过程提供智能化辅助支持；
- ❑ 平台网址：<https://www.bioincloud.tech/>。

Yunyun Gao, Guoxing Zhang, Chengrui Wang, Hao Xu, Zhanhui Yu, Shunyao Jiang, and Yong-Xin Liu. 2026. Wekemo Bioincloud 2026: An AI-Enabled Platform for Standardized Multi-Omics Data Analyses. *iMeta* 5: e70149. <https://doi.org/10.1002/imt2.70149>

iMeta(宏): 生物和医学顶级成果发表平台

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iMeta(宏)期刊由宏科学创办，对标**Cell**的生物/医学综合期刊，**SCIE**、**PubMed**收录，影响因子(IF)44.4，位列全球第47，中国第4，**分区表生物学1区Top**，外审平均21天，投稿至发表中位数87天(比同水平期刊快3倍)，欢迎高影响力的研究、方法和综述投稿，CNS外审稿件可带意见和回复转投。

iMetaOmics (宏组学)，定位IF>15对标**NC/SA**的生物/医学综合期刊，已被**ESCI**、**PubMed**等收录。

iMetaMed (宏医学)定位IF>15的医学综合期刊，欢迎投稿！



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