

生信方法 | 2026-10 月度文献报告

碱基日读 · 作者 碱基 · 数据来源 PubMed / bioRxiv 官方接口 · 本月收录 267 篇，正文详述其中 30 篇

本月概览

2026年10月生信方法方向的30篇文献在两条轴线上同步运动：一端是精度的纵深——基础模型进入空间转录组域，同一切片的转录组与代谢组首次被对齐；另一端是门槛的下移——三个面向不同场景的无代码或全流程平台在同一月份落地。贯穿两条线的是第三条：系统性基准测试在本月集中出现，开始摸清已有方法的真实天花板，而结论往往是"最优方法取决于具体场景，且差距可观"。

值得单独标记的是Pop-Corn的论断：在Perturb-seq扰动筛选中，能精确重现基因表达变化的模型，不一定能预测细胞群体组成如何移动——这两件事是独立的问题，需要单独优化（PMID: 42818106）。这个观察不是本月首次提出，但本月的实证让它足够具体，可以重新定义扰动预测领域的评估框架。

值得细看的研究

stFormer：空间转录组基础模型首次系统预训练

stFormer是本月方法类文章里最值得详细审视的（PMID: 42815472）。它解决了两个此前单细胞基础模型没有处理的问题：第一，细胞的空间位置与配体信号如何进入表征；第二，空间转录组技术在分辨率（单细胞）与基因覆盖度（全转录组）之间的权衡。stFormer用交叉注意力机制把相邻细胞的配体基因信息注入靶细胞表征，并提出"偏置交叉注意力"，允许模型在全转录组但低分辨率的Visium数据上预训练的同时保持单细胞分辨率。预训练语料来自公开人类Visium数据集，共约410万个空间样本。在细胞聚类、批次效应校正、细胞类型预测、基因功能预测四项任务上，stFormer超越了此前最优单细胞基础模型scFoundation。in silico扰动实验进一步展示了通过配体-受体信号响应推断细胞间通讯的能力。

证据判断：测试任务均为标准下游任务，基线是已发表方法，可重复性较好。但预训练数据全部来自人类Visium数据集，组织类型和疾病状态的分布偏向已有公开资源，模型在稀有组织或临床样本上的泛化性尚未系统验证。

OpenFISH：同切片转录组与代谢组对齐

OpenFISH（PMID: 42810347）是本月工程可行性层面最重要的一篇。空间转录组与MALDI-MSI代谢成像对底物、化学处理流程和成像条件的要求互不兼容，此前两种检测通常在不同切片上分别进行，再做截面配准，误差难以消除。OpenFISH通过优化组织处理与引导配准流程，使两种检测能在同一切片完成，达到细胞类型分辨率下的共定位。演示案例包括：中枢神经系统中细胞类型特异性代谢异质性、海马区室级代谢分带，以及5xFAD阿尔茨海默模型中小胶质细胞的磷脂组变化、少突胶质细胞中溶血磷脂酰乙醇胺相关特征升高，此外还独立量化了免疫挑战后的转座子激活，以及Reeler突变体中纹状体D1神经元的候选分布变化。

这个工具的核心价值是把一类此前几乎不可操作的实验变成有标准流程的事情。局限在于当前演示集中于脑组织，其他组织类型的适用性尚待系统验证；MALDI-MSI本身的代谢物覆盖度有限，不等同于完整代谢组。

Pop-Corn：扰动预测的目标设对了吗

Perturb-seq类大规模扰动筛选的核心目的是预测遗传操纵后细胞群体如何变化。Pop-Corn (PMID: 42818106) 明确指出, 现有方法几乎都针对"某基因被敲除后平均基因表达如何变化"做优化, 而"细胞类型组成如何移动"是另一个独立问题, 且两者可以高度解耦。Pop-Corn直接以细胞状态组成变化为优化目标, 在主要T细胞基准上对留出扰动的组成预测优于现有基于表达量的预测方法, 并将框架扩展到空间组织中局部细胞类型比例的预测。

这篇文章的论断比方法本身更值得独立记录: 大量Perturb-seq计算方法在为错误的目标函数优化——它们对基因表达向量的预测误差打分, 而不是对细胞群体的表型变化打分。两者在何种条件下解耦最严重, 以及是否存在能同时兼顾两者的统一框架, 需要后续系统验证。

细胞潜能16种算法: 评估体系的一次体检

细胞潜能估计是单细胞分析中定义不统一的子领域。这篇综述 (PMID: 42956748) 梳理了16种已发表方法, 按如何将基因表达汇聚成潜能度量分为三类: 基于平均值、基于熵、基于先验知识。用统一符号体系明确各方法的数学假设后, 文章指出相同任务下不同方法的假设有时直接矛盾, 并呼吁需要单细胞分辨率的标准基准数据集和系统的敏感性分析。

对读者最有价值的信息或许是负面的: 这16种方法目前还没有经过独立的大规模比较, 选用哪种主要靠领域习惯或工具可及性。文章没有给出最优推荐, 这一点本身说明评估基础设施仍然缺位。

本月同期的微生物共现网络基准 (PMID: 42956103) 评估了18种方法, 在合成16S rDNA-seq数据上测试了物种数、样本数、序列深度、网络结构等多个维度, 结论相似: 没有任何一种方法在所有实验条件下都是最优, 方法间性能差距可观且优劣关系随场景变化。两篇基准文章放在一起, 提供了本月方法评估领域最清醒的视角。

scMRdb: 将孟德尔随机化推向单细胞分辨率

孟德尔随机化用遗传变异作为工具变量推断基因表达与疾病的因果关系, 但已有资源主要基于混合组织的bulk eQTL, 细胞类型特异性效应被平均掩盖。scMRdb (PMID: 42952401) 将5206套GWAS汇总统计与585套单细胞eQTL数据集 (覆盖11种组织和细胞系统、110种细胞类型) 做统一流程的MR分析, 结合Steiger方向检验和共定位, 将结果分为六个置信等级并整合药物靶点注释。

本月另有一篇具体应用 (PMID: 42821046), 在原发性干燥综合征中通过MR识别出CD7 ($OR = 0.50$, $P = 0.0033$) 和LAPTM5 ($OR = 1.29$, $P = 0.0088$) 与疾病的名义关联, 并在含190例患者、32例对照的全血队列中做了探索性RT-qPCR验证。两篇放在一起显示, 单细胞分辨率MR正从分散的单次应用走向系统资源驱动的批量分析阶段。

WAGES: 在"非WGD肿瘤"里探测WGD亚克隆

WAGES (PMID: 42962034) 是一个基于基因表达估计bulk肿瘤样本中WGD (全基因组倍增) 细胞克隆分数的方法, 不依赖拷贝数检测。核心发现是: 在被分类为"非WGD肿瘤" (nWGD) 的样本中, WGD亚克隆广泛存在, 且仍在主动积累体细胞拷贝数变异, 提示持续进化。WAGES评分与肿瘤转移潜能、化疗和免疫治疗疗效以及患者预后显著相关。

这个发现把"WGD与否"从肿瘤级别的二元属性改写为亚克隆层面的连续量。若得到独立队列验证, 将影响WGD相关肿瘤进化研究的所有分析框架。现有局限是: 基于表达量推断亚克隆CNA状态是间接的, 在低纯度或高度异质性样本中的准确率需要与单细胞直接检测进行系统比较。

趋势判断

- 基础模型扩展到空间域是可预期的，但评估框架还没跟上。^{**} stFormer代表的技术路径逻辑清晰——一把已在单细胞数据上验证的基础模型架构移植到空间域，同时解决分辨率-覆盖度权衡和细胞间通讯建模两个特有难题（PMID: 42815472）。但目前缺乏专门针对空间感知能力的独立基准：当前评估仍沿用单细胞下游任务，空间位置信息是否真正带来额外的生物学发现，还需要领域跟进。OpenFISH（PMID: 42810347）的出现改变了一个前提条件：当同一切片能同时给出转录组与代谢组时，空间基础模型的训练数据和下游任务都会随之改变，这两件事的时序值得追踪。

- "无代码"不等于"无假设"，而是让假设变得更不透明。^{**} 本月ArchMap、Microbiology Galaxy Lab（逾315套工具、115套策展工作流）、BILBO三个平台集中落地（PMID: 42816602, 42957759, 42955413）。可及性提升是真实的，但这类平台把分析选择从用户转移给了平台开发者：参考图谱的版本与覆盖范围、工作流的策展偏向、BILBO的GO语义相似度聚类中层次切割标准，对非专业用户来说比命令行脚本更难独立审查。三个平台的发布论文均没有系统报告边界案例下的表现，这是一个共同的缺口。

- 预测目标的分裂在本月变得明显。^{**} Pop-Corn的基因表达预测与细胞组成预测脱钩（PMID: 42818106）和细胞潜能综述中16种方法对"潜能"的三类不同定义（PMID: 42956748），指向同一个更深的问题：单细胞分析领域在快速产出方法的同时，优化目标与生物学问题之间的对齐并没有受到同等重视。

- 单细胞分辨率已成为跨方向的默认分析层级。^{**} scMRdb把MR分析粒度推到单细胞（PMID: 42952401）；scEvoSel把群体遗传学的选择信号映射到单细胞图谱（PMID: 42948897）；PRISM-GEP在15个人和小鼠数据集上用单细胞表达程序替代传统基因集打分（PMID: 42811202）。这不是某一类方法的特有趋势，而是几乎所有方向都在把单细胞分辨率当作默认分析起点。

这批研究的共同弱点

- 工具评估主要由开发者自己完成，基准选择缺乏独立性。^{**} stFormer、ctdecon、GeoAdvAE、CSGD A等工具类文章，性能测试几乎全部在公开数据集上进行，任务设置和基线选择由同一团队控制（PMID: 42815472, 42813985, 42809409, 42809244）。这种情况下，方法在真正对立条件下——对手团队设计的数据集、不利于自身架构的任务——的表现是不可见的。本月的两篇专门基准研究提供了相对独立的视角，但细胞潜能综述是文献综述而非实测比较，微生物共现网络基准依赖合成数据，两者各有局限（PMID: 42956748, 42956103）。

- 无代码平台的边界案例表现没有被系统报告。^{**} ArchMap等平台的目标用户是没有大量计算背景的研究人员（PMID: 42816602），这类用户遇到的边界情形——稀有细胞类型、疾病相关的转录组偏移、低质量文库——对平台的考验远比展示数据集更严苛。Microbiology Galaxy Lab的超过35套教程覆盖标准流程（PMID: 42957759），当真实数据偏离标准时，用户缺乏足够信息做出合理判断，而这恰恰是"民主化"工具最容易埋下隐患的地方。

- 基础模型的生物学归因难以独立核实。^{**} stFormer通过in silico扰动展示配体-受体通讯响应（PMID: 42815472），MeRN用图引导变分自编码器提取单细胞代谢状态（PMID: 42818076）。这类方法的归因取决于训练数据的质量和模型的表示能力，约410万空间样本的组织类型分布并不均匀。从模型特征到生物机制的推论链在基础模型上比传统方法更难通过消融实验核实，而这类文章目前对此几乎没有系

统讨论。

- 临床场景的验证仍以探索性为主。** pSD的MR分析在190例患者中做了RT-qPCR验证（PMID: 42821046），WAGES展示了与预后的关联性（PMID: 42962034），CSGDA在跨域数据集上提升了约6个百分点的ACC和AUPR（PMID: 42809244）。这些证据是真实的，但从方法性能到临床决策场景的跨越，还需要在更大、更独立的队列中正面处理，而不只是作为方法论文的附带结论。

下个月值得关注

- 空间基础模型的独立评估何时出现。** stFormer等工具发表后，空间域基础模型的竞争会加速。关键问题是：领域是否会建立专门针对空间感知能力的基准任务，而不是继续沿用单细胞下游任务。这个框架缺失的时间越长，方法比较的公信力就越弱。结合OpenFISH提供的同切片多模态数据（PMID: 42810347），空间基础模型的训练目标和评估方式都可能在短期内出现较大变化。

- Pop-Corn框架的跟进验证。** 把扰动预测的优化目标从基因表达向量转向细胞组成，这个思路在Perturb-seq数据体量足够之后会有更多实现（PMID: 42818106）。值得追踪的问题是：两类预测目标在什么实验条件下解耦最严重，以及当前主流方法的组成预测误差究竟有多大——这个量化还缺乏大规模系统报告。

- scMRdb的下游应用与置信度验证。**

新数据库资源的真正价值要到大量研究基于它产生结果后才能判断（PMID: 42952401）。发布后三到六个月会有大量应用性研究跟进。值得关注的是：六个置信等级中最高层级的关联是否能在功能实验中得到独立验证，以及欧洲与东亚祖先背景的eQTL结果是否出现系统性差异。

- 无代码平台的边界案例报告。** ArchMap等平台的第一批真实用户遭遇稀有细胞类型或低质量文库时的表现，是判断"民主化"是否真正落地的关键信号（PMID: 42816602）。这类报告通常不会出现在开发团队自己的论文里，更可能以社区反馈或独立评测的形式出现，值得在半年内留意。

附录：2026-10 全部收录文献（267 篇）

#	标题	期刊	日期	PMID
1	Mendelian randomization and single-cell transcriptomics prioritize CD7 and LAPTM5 in primary Sjögren's disease: an integrative multi-omics analysis.	Clinical rheumatology	2026-Sep-3	42821046
2	stFormer integrates spatial ligand signaling into a foundation model for spatial transcriptomics.	Cell reports methods	2026-Sep-3	42815472
3	Ozone disinfection effectively reduces pathogenic microbial nucleic acid background in mNGS laboratories.	Journal of microbiological methods	2026-Sep-3	42815804
4	ArchMap is a web-based platform for reference-based analysis of single-cell datasets.	Nature genetics	2026-Sep-3	42816602
5	Identifying JAK2 and ANXA5 as Key Genes Linking Obstructive Sleep Apnea and Oxidative Stress via Machine Learning and Multilayer Transcriptomic Integration With Functional Validation	FASEB journal : official publication of	2026-Sep-3	42730994
6	Single-Cell RNA Sequencing-Based Identification of Novel Podocyte Injury-Associated Genes From Isolated Glomeruli of Diabetic db/db Mice.	FASEB journal : official publication of	2026-Sep-3	42762061
7	Quantitative Single-Cell Time-Lapse Phase-Contrast Microscopy with DeepSea.	Methods in molecular biology (Clifton, N	2026-Sep-3	42811237
8	Reference-Based Cell Type Deconvolution Using Self-Supervised Contrastive Learning in Spatial Transcriptomics with Ctdcon.	Molecular omics	2026-Sep-3	42813985
9	Patterning of Artificial Cell Populations Via Laser Induced Forward Transfer for Controlled and Localized Cargo Uptake and Release.	Small (Weinheim an der Bergstrasse, Germ	2026-Sep-3	42814042
10	AI-driven transcriptomics for neurodegenerative disease research: A systematic review.	Computational biology and chemistry	2026-Sep-2	42826575
11	CSGDA: A Cell State-Guided Graph Domain Adaptation Network for Single-Cell Drug Response Prediction.	Bioinformatics (Oxford, England)	2026-Sep-2	42809244
12	AI-Empowered Viral Metagenomics for Clinical Diagnosis: Advances, Bottlenecks, and Translational Pathways.	Journal of applied microbiology	2026-Sep-2	42809384
13	Integrating Morphology and Gene Expression of Neural Cells in Unpaired Single-Cell Data Using GeoAdvAE.	Journal of computational biology : a jou	2026-Sep-2	42809409
14	OpenFISH enables same-section spatial transcriptomics and MALDI-MSI integration.	Neuron	2026-Sep-2	42810347
15	PRISM-GEP: Viewing Single-Cell Expression through the Lens of Topic Modeling.	Bioinformatics (Oxford, England)	2026-Sep-2	42811202
16	Pop-Corn: Predicting Perturbation Phenotype Effects Across Single-Cell and Spatial Contexts.	bioRxiv : the preprint server for biolog	2026-Sep-2	42818106
17	Streamlined Production of Recombinant Adeno-Associated Viruses Using Gateway Cloning Technology for Neural Circuit All-Optical Interrogation.	bioRxiv : the preprint server for biolog	2026-Sep-2	42817973
18	Diverse genome organization strategies for polysaccharide utilization in the oceans.	bioRxiv : the preprint server for biolog	2026-Sep-2	42818234
19	Extracting interpretable single-cell metabolic states with graph-guided representation learning.	bioRxiv : the preprint server for biolog	2026-Sep-2	42818076
20	Lossless compression of protein databases for efficient and accurate metagenomic sequence classification with Centrifuger.	bioRxiv : the preprint server for biolog	2026-Sep-2	42818146

#	标题	期刊	日期	PMID
21	Phylodynamic inference with the bounded coalescent: a point process perspective.	ArXiv	2026-Sep-2	42818531
22	Evidence of active whole-genome doubling (WGD) subclones in non-WGD tumors.	Science advances	2026-Oct-3	42962034
23	Andrographolide Combined With Voriconazole Enhances Antifungal Activity Against Aspergillus Species.	Microbiology and immunology	2026-Oct-3	42962077
24	Categorization and analysis of 16 computational methods for estimating cell potency from single-cell RNA-seq data.	Cell systems	2026-Oct-2	42956748
25	Microbiology Galaxy Lab: a community-driven gateway for reproducible and FAIR analysis of microbiological data.	Communications biology	2026-Oct-2	42957759
26	scMRdb: a comprehensive resource for cell-type-resolved Mendelian randomization of complex traits.	Nucleic acids research	2026-Oct-2	42952401
27	BILBO: a self-hosted platform for large-scale RNA-Seq analysis with a functional annotation clustering framework.	Functional & integrative genomics	2026-Oct-2	42955413
28	From 16S rDNA-seq count data to microbial interactions: A comprehensive benchmark of co-occurrence network inference methods.	PLoS computational biology	2026-Oct-2	42956103
29	scLncR: an integrated and flexible pipeline for lncRNA analysis in single-cell RNA sequencing data.	Annals of botany	2026-Oct-2	42557881
30	scEvoSel maps evolutionary selection signals onto single-cell transcriptomic atlases to reveal selection-relevant cellular contexts.	Molecular biology and evolution	2026-Oct-2	42948897
31	Time-to-transformation transcriptomic modeling identifies oral squamous cell carcinoma-initiation and SPP1-integrin niche programs in oral leukoplakia.	European journal of oral sciences	2026-Oct-2	42949508
32	Starling: STability Analysis of coReguLated "Nests" of Genes.	Bioinformatics (Oxford, England)	2026-Oct-2	42949909
33	Deep Lineage: Single-cell lineage tracing and fate inference using deep learning.	Cell systems	2026-Oct-2	42950828
34	Rare and common genetic variants shape single-cell immune gene expression.	Nature	2026-Oct-2	42951973
35	The Mouse Retina as an Evolving Model System: From Layered Anatomy to Cell-Type-Resolved Regenerative Repair.	Experimental eye research	2026-Oct-2	42946114
36	Isolation of Ventricular Cardiomyocytes from the Annual Killifish <i>Nothobranchius furzeri</i> for Whole-Cell Patch Clamp Recordings.	Journal of visualized experiments : JoVE	2026-Oct-2	42949163
37	A droplet-based long-read single-cell epigenome sequencing method for the high-throughput profiling of multidimensional regulatory elements within individual cells.	Cell discovery	2026-Oct-2	42934226
38	CellMarker 3.0: an updated resource of manually curated and computationally predicted cell markers in human/mouse and interactive web tools for single-cell and spatial transcriptom	Nucleic acids research	2026-Oct-2	42935241
39	MeXpose 2.0: A Comprehensive Toolkit for Single-Cell Spatial (Metall-)omics Covering All Steps from Image Reconstruction to Integrative Analysis.	Chemical & biomedical imaging	2026-Oct-2	42953662
40	Integration-free and cluster-free detection of localized differential gene coexpression in single-cell data with DiCoLo.	Genome research	2026-Oct-2	42933984

#	标题	期刊	日期	PMID
41	Exploring DNA movement through the application of droplet-based high-efficiency chromatin conformation capture (DropHiChew) and loop velocity.	Nucleic acids research	2026-Oct-2	42953962
42	Source Apportionment and Resistome Signatures of Community and Hospital Effluents in Urban Sewer Networks.	Environmental pollution (Barking, Essex	2026-Oct-2	42926093
43	Synovial fluid cell isolation protocol affects immune cell recovery and composition across inflammatory states.	RMD open	2026-Oct-2	42919619
44	Multi-layer analysis of gut metagenomic functional potential in major depressive disorder.	Psychoneuroendocrinology	2026-Oct-2	42925575
45	High-throughput droplet-based enzymatic DNA methylome profiling enables single-cell resolution of epigenetic heterogeneity.	Science advances	2026-Oct-2	42913020
46	Identification of key cell subpopulations and associated biomarkers for mouse dry eye disease based on the Scissor-CIBERSORTx algorithm integration strategy.	Experimental eye research	2026-Oct-2	42913931
47	scHGNN: A single-cell gene regulatory network inference method based on heuristic graph neural networks.	Functional & integrative genomics	2026-Oct-2	42918896
48	Diagnostic accuracy and clinical considerations of metagenomic next-generation sequencing in prosthetic joint infection: a systematic review and meta-analysis.	European journal of clinical microbiolog	2026-Oct-2	42918922
49	TriLock-FISH enables in situ discrimination of influenza cRNA and mRNA for single-cell analysis of viral replication and transcription.	mBio	2026-Oct-2	42910946
50	Single-cell and multi-algorithm profiling identifies SNRPG as a Claudin-1-associated regulator of malignant progression in triple-negative breast cancer.	Biochimica et biophysica acta. Molecular	2026-Oct-2	42914062
51	OpenDVP: an experimental and computational framework for community-empowered deep visual proteomics.	Nature methods	2026-Oct-2	42918851
52	Shenqi Granules Ameliorate Cerebral Ischemia-Reperfusion Injury by Regulating Glucocerebrosidase and Uridine Metabolism in Microglia.	Metabolites	2026-Oct-2	42941277
53	CCCView: A Knowledge Platform for Integrated Analysis of Spatial Transcriptomic Cell-Cell Communication.	International journal of molecular scien	2026-Oct-2	42942149
54	POINTseq: Cell-type-specific barcoding reveals single-cell projection architecture of the mouse dopaminergic system.	Neuron	2026-Oct-2	42242218
55	HetAnn: Cell Type Annotation for Spatial Transcriptomics by Heterogeneous Graph Learning.	IEEE transactions on computational biolo	2026-Oct-2	42905585
56	High-content morphological profiling by Cell Painting in 3D spheroids.	Nature communications	2026-Oct-2	42907469
57	Multi-Platform Transcriptomic Classification of LUAD Driver Mutation Subtypes via Heterogeneous Ensemble Learning.	Diagnostics (Basel, Switzerland)	2026-Oct-2	42938252
58	Single-cell-based analysis establishes C1QA-mediated promotion of high glucose-induced tubular epithelial injury via ERS in DN.	Gene	2026-Oct-2	42242331
59	Integration of polygenic risk with single cell methylation data using met-scDRS.	Bioinformatics (Oxford, England)	2026-Oct-2	42899409
60	CYP1B1 is a potential target of kaempferol in renal fibrosis: a multi - omics and single - cell transcriptomics study.	Bioresources and bioprocessing	2026-Oct-2	42900454

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61	Identification of Novel CD52+ Fibroblasts in Nodular Prostatic Hyperplasia.	The Prostate	2026-Oct-2	42900792
62	Rapid and reversible regulation of cell cycle progression in budding yeast using optogenetics.	Cell reports methods	2026-Oct-1	42532048
63	A sensitive method for profiling cell-type-specific secretomes of rare cells from complex tissues.	Cell reports methods	2026-Oct-1	42600616
64	Disentangling microbiota-dependent and -independent impacts of antibiotics on host physiology.	Nature microbiology	2026-Oct-1	42897202
65	Recovering CDR3 sequences from RNA-seq data: a critical assessment of computational and experimental strategies.	Genomics & informatics	2026-Oct-1	42897688
66	Pan-cancer analysis reveals DNAJC9 as an immune-related biomarker and a positive regulator of the PI3K/AKT signaling pathway.	RSC medicinal chemistry	2026-Oct-1	42898834
67	An optimized flow cytometry sorting-sequencing workflow reduces storage, sorting, and extraction bias in sorted microbial communities.	Microbiology spectrum	2026-Oct-1	42895354
68	Feature selection and dimensionality reduction in multi-omics.	Genome	2026-Oct-1	42893622
69	Decoding radiation-induced transcriptomic signatures of human leukocytes using long-read RNA-seq: clinical and biodosimetric implications.	BMC genomics	2026-Oct-1	42897451
70	Optimizing Pathogen Detection in Clinical Metagenomics: A Comprehensive Benchmarking of Bioinformatic Pipelines for Single-End Short Reads.	The Journal of molecular diagnostics : J	2026-Oct-1	42892321
71	Single-Cell Detection and Quantification of Metabolically Active Bacteria in Soil Using Heavy-Water Labeling and Raman Microspectroscopy.	Journal of visualized experiments : JoVE	2026-Oct-1	42891611
72	Enrichment of Retinal Endothelial Cells and Müller Glia Enable Comprehensive scRNA-Seq Profiling of the Blood-Retinal Barrier.	Journal of visualized experiments : JoVE	2026-Oct-1	42891637
73	DNAharvester: A Nextflow Pipeline for Analysing Highly Degraded DNA from Ancient and Historical Specimens.	Bioinformatics (Oxford, England)	2026-Oct-1	42886518
74	Inferring gene regulatory networks from single-cell transcriptomics jointly through graph neural networks and Transformer.	IEEE transactions on computational biolo	2026-Oct-1	42886592
75	Computational deconvolution of drug sensitivity via single-cell-to-bulk transcriptome mapping.	PLoS computational biology	2026-Oct-1	42886762
76	Benchmarking immunoinformatic repertoire assemblies from bulk RNA-seq and PCR-based V(D)J sequencing using PCR-free SMRT RNA sequencing.	iScience	2026-Oct-1	42774740
77	Sequencing the wastewater virome: Current strategies and bioinformatic pitfalls.	iScience	2026-Oct-1	42828099
78	How to dissociate porcine ovaries: towards efficient retrieval of putative female germline stem cells.	Theriogenology	2026-Oct-1	42341634
79	Adaptation and application of the Comet Assay to genotoxicity assessments in elasmobranchs.	Environmental pollution (Barking, Essex	2026-Oct-1	42462956
80	Integrating multi-method approach reveals extensive antibiotic resistance dissemination from concentrated animal feeding operations to surface waters.	Water research	2026-Oct-1	42492212

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81	CDState Resolves Malignant Cell Heterogeneity from Bulk Tumor RNA Sequencing Data.	Cancer research	2026-Oct-1	42531606
82	Efficacy of icariin in polycystic ovary syndrome: Cathepsin S as a key target revealed by computational and experimental evidence.	Bioorganic chemistry	2026-Oct-1	42727446
83	DNA-Modified Nanowire Thermometer Uncovers Thermal Responses of Neuronal Soma and Neurites to H2O2 Treatment.	ACS applied materials & interfaces	2026-Oct-1	42872551
84	A stem cell-based flow cytometry assay to predict post-transplantation relapse in patients with myelodysplastic syndromes with excess blasts: a prospective study.	Transplantation and cellular therapy	2026-Oct-1	42874800
85	SpatialZoomer: multi-scale feature analysis of spatial transcriptomics.	Nature biomedical engineering	2026-Oct-1	42875562
86	Oral Actinomyces Species Exposure is Associated with Anxiety-Like Behavior, Mitochondrial Remodeling, and Altered GABAergic Pathways.	Advanced science (Weinheim, Baden-Wurtte	2026-Oct-1	42875679
87	Animal Models of Slow-Transit Constipation: Current Progress, Limitations, and Future Perspectives.	Digestive diseases and sciences	2026-Oct-1	42875723
88	CausalCellInfer: Prioritizing Cell-Type-Specific Disease Associations From Genetically Predicted Transcriptomes in Biobank Cohorts.	Advanced science (Weinheim, Baden-Wurtte	2026-Oct-1	42875726
89	Hypergraph-Enhanced Self-Supervised Learning with Module-Aware Structured Masking for Single-Cell Transcriptomic Clustering.	IEEE transactions on computational biolo	2026-Oct-1	42873629
90	Vortex beam-based Raman spectroscopic single cell analysis of radiation-induced biochemical changes in human erythrocytes for radiation biodosimetry.	International journal of radiation biolo	2026-Oct-1	42873966
91	High-Performing Unitized Regenerative Fuel Cell Using PGM-Free Bifunctional Catalysts from Waste-Derived Carbon.	ACS omega	2026-Oct-1	42890061
92	Series-Parallel Testing of Laboratory Lithium-Ion Cells: Not All Coin Cells Are Created Equal.	ACS omega	2026-Oct-1	42890087
93	Deploying machine learning and metagenomics for predicting gut microbial drug biotransformation in colorectal cancer.	Computational biology and chemistry	2026-Oct-1	42892166
94	Single-cell elemental analysis of Limnospira platensis and Chlorella vulgaris using novel downward-pointing inductively coupled plasma time-of-flight mass spectrometry with emphasi	Bioresource technology	2026-Oct-1	42869192
95	scDGCN: A Graph-Based Deep Clustering Framework for Single-Cell Transcriptomics via Neighborhood-Enhanced Context Representation Learning.	Interdisciplinary sciences, computationa	2026-Oct-1	42870190
96	Optimized approaches to profile low biomass DNA and RNA virome in the upper respiratory tract of beef cattle.	Animal microbiome	2026-Oct-1	42870288
97	Fast, flexible gene cluster family delineation with IGUA.	Nucleic acids research	2026-Oct-1	42866952
98	Seumetry: a versatile and comprehensive R toolkit to accelerate high-dimensional flow and mass cytometry data analysis.	Bioinformatics (Oxford, England)	2026-Oct-1	42867153
99	DESIGN: a framework for generative AI-enabled crop molecular design-driven breeding.	Science China. Life sciences	2026-Oct-1	42886441
100	Single-Cell Transcriptomics Identifies Fibroblast-Associated Transcriptional Patterns and Candidate Therapeutic Targets in the Comorbidity of Non-Small Cell Lung Cancer and Obesity	Current cancer drug targets	2026-Oct-1	42872669

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101	Patch-based querying identifies structures of interest in electron microscopy.	Computers in biology and medicine	2026-Oct-1	42863279
102	The boundary between microbial detection and implant-related infection: a structured narrative review of analytical credibility, biological persistence, host response, and clinical	Archives of orthopaedic and trauma surge	2026-Oct-1	42864526
103	FAMUS: A Few-Shot Learning Framework for Large-Scale Protein Annotation.	Bioinformatics (Oxford, England)	2026-Oct-1	42865011
104	A global atlas of the gut virome reveals subtype-specific and functional alterations in irritable bowel syndrome.	mSystems	2026-Oct-1	42861963
105	Association of quantitative sputum Candida load with respiratory dysbiosis and airway inflammation in suspected invasive pulmonary candidiasis.	mSystems	2026-Oct-1	42861989
106	Deciphering the crosstalk between cancer stemness and the immune microenvironment in melanoma: a single-cell transcriptomic analysis.	Dermatology (Basel, Switzerland)	2026-Oct-1	42862771
107	The gene expression signature of multinucleated giant cells in the spleens of Leishmania donovani-infected mice.	Parasitology international	2026-Oct-1	42860219
108	One-Step Induction of Oogonia-Like and Pro-Spermatogonia-Like Cells From Porcine Pluripotent Stem Cells.	Advanced science (Weinheim, Baden-Wurtte	2026-Oct-1	42860608
109	Reassessment of a four-gene NK-cell-lineage-associated prognostic score in histologically defined grade 3 glioma.	Journal of neuroimmunology	2026-Oct-1	42887455
110	GliomaDeconv maps glioma-specific cellular programs from bulk transcriptomic profiles and reveals spatiotemporal associations with progression and treatment response.	Cancer letters	2026-Oct-1	42413813
111	ERMA: a harmonizing epicPCR data analysis tool.	BMC genomics	2026-Oct-0	42864608
112	Mapping transcriptional responses to cellular perturbations with RNA fingerprinting.	Cell	2026-Oct-0	42854686
113	Single-cell transcriptome analysis reveals onco-fetal reprogramming with implications for drug resistance and clinical outcome.	Genome research	2026-Oct-0	42855278
114	Protein large language model-assisted one-to-one gene homology mapping in cross-species single-cell transcriptome integration.	Genome research	2026-Oct-0	42855280
115	Comparative performance of reference-based metagenomic tools to identify species-level taxa among families of bacteria: benchmarking Mycobacteriaceae and Neisseriaceae.	mSystems	2026-Oct-0	42852904
116	The generation and characterization of CTRP9-CreERT2 knock-in mice for targeting endothelial cell muscle and adipose tissues.	Cell regeneration (London, England)	2026-Oct-0	42853343
117	Nonenzymatic detection and imaging of m6A-methylated RNA via proximity hybridization-initiated hybridization chain reaction with site-specific recognition.	Analytical and bioanalytical chemistry	2026-Oct-0	42853389
118	scHCL-SDA: A Homophily-Aware Contrastive Learning with Spectral Distribution Alignment for scRNA-seq Data Clustering.	IEEE transactions on computational biolo	2026-Oct-0	42853736
119	Translocation-induced enhancer rewiring reveals cryptic oncogenic circuits in multiple myeloma.	Science advances	2026-Oct-0	42842680

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120	Integrated multi-omics and metabolic modeling links structure to function in high-performing electrosynthetic biofilm communities.	mSystems	2026-Oct-0	42847688
121	Error correction algorithms for efficient gene expression quantification in single cell transcriptomics with Arcane.	Genome research	2026-Oct-0	42844017
122	Dynamics of human cardiogenesis and its disruption in trisomy 21.	Nature	2026-Oct-0	42844467
123	EXPRESS: Metagenomic Oxford Nanopore sequencing of feline aural inflammatory polyps for pathogen discovery.	Journal of feline medicine and surgery	2026-Oct-0	42844723
124	NoiBic: a noise-tolerant biclustering algorithm for high-throughput gene expression data analysis.	Bioinformatics (Oxford, England)	2026-Oct-0	42841722
125	Random Matrix Theory-Guided Sparse Principal Component Analysis for Single-Cell RNA-Seq Data.	Journal of computational biology : a jou	2026-Oct-0	42842483
126	Super Bloom: Fast and Precise Filter for Streaming k-Mer Queries.	Journal of computational biology : a jou	2026-Oct-0	42842485
127	PDSFLRR: Low-rank representation with projection distance and sparsity constraints for clustering single-cell RNA sequencing data.	Computational biology and chemistry	2026-Oct-0	42854274
128	Single-cell morphological responses as predictors of ciprofloxacin resistance in <i>Acinetobacter baumannii</i> .	Microbiology spectrum	2026-Oct-0	42606199
129	Clinical significance of <i>Dientamoeba fragilis</i> and <i>Blastocystis</i> : Lessons from clinical trials, cohort studies, and faecal microbiota transplantation - a narrative review.	Clinical microbiology and infection : th	2026-Oct-0	42838172
130	Benchmarking sample preservation strategies for clinical single-cell proteomics.	Molecular & cellular proteomics : MC	2026-Oct-0	42838272
131	Single-Microbe Transcriptomics Reveal Functional Heterogeneity in Sediment Microbiomes.	Small methods	2026-Oct-0	42839672
132	A hybrid neural network and sparse recovery framework for resolving multi-cell coincidence in label-free impedance cytometry.	Analytical methods : advancing methods a	2026-Oct-0	42834753
133	STiLE: Automated Tissue Microarray Dearraying for Spatial Transcriptomics.	Bioinformatics (Oxford, England)	2026-Oct-0	42836654
134	Omics data discovery agents: Agent-supported retrieval, reanalysis, and synthesis of published omics data.	PLoS computational biology	2026-Oct-0	42837398
135	CardamomOT: A mechanistic optimal transport-based framework for gene regulatory network inference, trajectory reconstruction and generative modeling.	PLoS computational biology	2026-Oct-0	42837408
136	Lineage and renewal dynamics of sebaceous glands govern skin barrier integrity in mice.	Proceedings of the National Academy of S	2026-Oct-0	42826130
137	Scaling laws for massively parallel microfluidics enable rapid construction of ten-million-scale natively paired antibody libraries.	Proceedings of the National Academy of S	2026-Oct-0	42814540
138	3D Iterative Immunofluorescence Imaging on Whole-Mount Samples.	Bio-protocol	2026-Oct-0	42859510
139	Prediction of age using shotgun metagenomic sequencing and random forest algorithm based on cadaveric colon.	Forensic science international	2026-Oct-0	42843234

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140	Temporal assessment of spatial and single-cell transcriptomes identifies CD226-NECTIN2 T cell-cholangiocyte interaction in bile duct inflammation.	Journal of hepatology	2026-Oct-0	42833310
141	Single-cell and network voltage imaging in acute brain slices: an updated guideline.	Neuroscience	2026-Oct-0	42833353
142	High-Content Screening Comparison of 1R6F Cigarette Smoke Extract and Selected Heated Tobacco and Electronic Vapour Product Aerosol Extracts in Endothelial and Bronchial Epithelial	Journal of applied toxicology : JAT	2026-Oct-0	42833661
143	ProFormer: generalizable classification of single-cell and plasma proteomes using deep learning.	Nature communications	2026-Oct-0	42834055
144	Abundant CD8+ tumor-infiltrating lymphocytes in glioblastoma harbor distinct exhaustion signatures in potentially reactive subsets.	British journal of cancer	2026-Oct-0	42834163
145	Resolving cell-cell interaction networks and their molecular logic in complex tissues.	Nature methods	2026-Oct-0	42834226
146	An In Vivo Single-Vesicle Electrochemistry Enables Monitoring Vesicular Dopamine Dynamics and Pharmacological Rescue.	Angewandte Chemie (International ed. in	2026-Oct-0	42585093
147	Reactive oxygen species define leukemia stem cell identity in pediatric acute myeloid leukemia.	Cancer letters	2026-Oct-0	42830144
148	Salivary microbiome responses to chlorhexidine and Coriandrum sativum essential oil mouthwashes in patients with periodontitis in a randomized 2-week clinical trial.	Clinical oral investigations	2026-Oct-0	42828686
149	The regulatory landscape for clinical metagenomics-based diagnostics in Europe: a critical review.	Journal of microbiological methods	2026-Oct-0	42829110
150	Window-of-Opportunity Study Utilizing Preoperative Cetuximab in Patients with Head and Neck Cancer.	Cancer research communications	2026-Oct-0	42691952
151	Normalization of nCounter Gene Expression Data Alters Molecular Diagnostics in Kidney Transplantation.	Journal of the American Society of Nephr	2026-Oct-0	42024462
152	Variable expressivity in long QT syndrome type 2 rabbits defines a low threshold for therapeutic IKr restoration.	American journal of physiology. Heart an	2026-Oct-0	42734426
153	GCF-anchored and target-oriented mining of metagenomic BGC space for bioactive product discovery.	Microbiology spectrum	2026-Oct-0	42820688
154	Live probiotic encapsulation: process engineering, wall materials, and the translation gap to human gastrointestinal survival.	Critical reviews in microbiology	2026-Oct-0	42820934
155	Hypergraph-Attention-Guided Graph Refinement and Feature Decoupling for Single-Cell RNA-seq Clustering.	IEEE transactions on computational biolo	2026-Oct-0	42821712
156	Spatio-temporal Mechanosensitive Phagocytic Response of Retinal Pigment Epithelial Cells to Reversible Changes in Substrate Stiffness.	Acta biomaterialia	2026-Oct-0	42822746
157	Deep Learning-Assisted identification and quantification of cell-associated microplastics using darkfield hyperspectral imaging.	Talanta	2026-Oct-0	42019285
158	Bisphenol A drives the comorbidity of non-alcoholic fatty liver disease and osteoarthritis by targeting RHOB: Integrated multi-omics, single-cell analysis, and experimental validat	Experimental gerontology	2026-Oct-0	42476233
159	Human iPSC-derived fetal granulosa-like cells enhance oocyte maturation outcomes and enable multi-generational safety evaluation in a mouse IVM model.	The Journal of reproduction and developm	2026-Oct-0	42528196

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160	Enhancer collapse dictates PKHD1 silencing and centrosome-mediated chromosomal instability and metastasis in clear cell renal cell carcinoma.	Experimental cell research	2026-Oct-0	42586231
161	Identification and functional characterization of ASCC2 as a diagnostic biomarker and immune regulatory hub in Kawasaki disease.	Clinical rheumatology	2026-Oct-0	42816712
162	SNP calling, haplotype phasing and allele-specific analysis with long RNA-seq reads.	Nature methods	2026-Oct	41912802
163	Gut microbiome in pediatric acute pancreatitis and Crohn's disease versus irritable bowel syndrome and healthy controls.	Journal of pediatric gastroenterology an	2026-Oct	42444523
164	Tracking cell fate through morphodynamics.	Molecular systems biology	2026-Oct	42661101
165	Association of microbial pathways predicted/inferred using 16S and shotgun metagenome with faecal metabolite abundances.	Microbial genomics	2026-Oct	42842295
166	Spatial biology in cancer epigenetics.	Molecular oncology	2026-Oct	42487511
167	Cell-based polygenic risk scores predict clinical progression and prioritize network-based therapeutic targets in Alzheimer's disease.	Alzheimer's & dementia : the journal	2026-Oct	42836738
168	scPlantAnnotate: an accurate and robust transformer-based model for plant cell type annotation.	Journal of advanced research	2026-Oct	41554477
169	Identification of Gene Signatures Differentiating Cancer from Normal Tissues Across Histological Classifications of Gastric Adenocarcinoma via Machine Learning Methods.	Biochemical genetics	2026-Oct	41746551
170	Predictive model for clear cell renal cell carcinoma: a novel model integrating sunitinib resistance and prognosis related genes and clinical factors.	Clinical & translational oncology :	2026-Oct	42020680
171	Molecular traces of microbial cross-kingdom migration: from the gut ecosystem to the intervertebral disc microenvironment.	The spine journal : official journal of	2026-Oct	42035921
172	An integrated single-cell transcriptomics and explainable AI approach for cancer stemness biomarker discovery in non-small cell lung cancer.	Computational biology and chemistry	2026-Oct	42066389
173	Integrative multi-omics analysis identifies stromal-immune crosstalk as a determinant of immunotherapy efficacy and establishes a prognostic signature in gastric cancer.	Computational biology and chemistry	2026-Oct	42068630
174	Normalization choice drives biological interpretation in single-cell RNA-seq cancer studies: A systematic benchmarking of 465 computational pipelines.	Computational biology and chemistry	2026-Oct	42070330
175	A variational graph autoencoder guided by residual multi-head attention reveals heterogeneity in spatial transcriptomics.	Computational biology and chemistry	2026-Oct	42134147
176	Single-cell and spatial RNA sequencing in prostate cancer.	Nature reviews. Urology	2026-Oct	42209670
177	Single-cell Raman spectroscopy-machine learning combination: Rapid and accurate strain-level identification of Bifidobacterium animalis subsp. lactis J12.	Food microbiology	2026-Oct	42215211
178	A fluorescence-based high-content imaging workflow for multi-parametric lipid droplet phenotyping via Oil Red O fluorescence.	Methods (San Diego, Calif.)	2026-Oct	42259461
179	Artificial intelligence-enabled real-time monitoring of intracellular lipid dynamics in microalgae via optical sensors and kinetic early-warning differentiation.	Bioresource technology	2026-Oct	42269881

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180	A systematic review of algorithmic challenges in noise modelling for multimodal single-cell.	Computational biology and chemistry	2026-Oct	42275753
181	Interpretable scRNA-seq Analysis with Intelligent Gene Selection.	Applied biochemistry and biotechnology	2026-Oct	42287534
182	Strategies for incorporating alternative splicing variants in thyroid nodule biopsy classification based on expression levels.	Computer methods and programs in biomed	2026-Oct	42296790
183	Viral etiology of orogenital papillomatosis and squamous cell carcinoma in bottlenose dolphins in the southeastern United States.	Virology	2026-Oct	42361430
184	Dimethylglycine accelerate atherosclerosis by mediating macrophages ferroptosis via NRF2 pathway suppression.	Pathology, research and practice	2026-Oct	42361720
185	Artificial Intelligence in drug discovery and development: current landscape, challenges, and future perspectives.	Critical reviews in oncology/hematology	2026-Oct	42364829
186	Evaluating detection of <i>Histophilus somni</i> immunoglobulin-binding protein A DR2 Fic: A species-specific gene target for recombinase polymerase amplification relative to long-read se	Research in veterinary science	2026-Oct	42398436
187	Quantitative single-cell analysis of PML-RAR α oncogene-induced DNA damage along cell cycle progression.	Methods (San Diego, Calif.)	2026-Oct	42409088
188	Bisphenol a exposure induces low back pain associated with intervertebral disc degeneration via BIRC3-mediated nucleus pulposus cell senescence.	Toxicology and applied pharmacology	2026-Oct	42413735
189	Mapping protein-DNA interactions across biological scales: principles, scalability and applications.	Methods (San Diego, Calif.)	2026-Oct	42413841
190	Multi-cohort evidence for impaired microbial support of the methionine cycle in children with autism spectrum disorder.	Psychiatry research	2026-Oct	42418904
191	Computational strategies for uncovering bacterial biocatalysts in the biodegradation of persistent organic pollutants.	Computational biology and chemistry	2026-Oct	42419186
192	Identification and verification of immunogenic cell death-related signatures derived from bone metastasis of prostate cancer based on multi-omics and machine learning algorithms.	Computational biology and chemistry	2026-Oct	42419189
193	Protective effect of soybean isoflavone (SI) on ovarian damages by zinc oxide nanoparticles (ZnONPs) in female mice.	Journal of trace elements in medicine an	2026-Oct	42462501
194	Discovery and characterization of a novel GH6 multifunctional enzyme from soil metagenomic library.	Carbohydrate research	2026-Oct	42475793
195	An Integrated Cell-Death Program Defines Aggressive Prostate Cancer by Coupling Ezrin to the Hippo-YAP/TAZ Axis.	Annals of surgical oncology	2026-Oct	42484820
196	A unified developmental timeline of pigmented ocular tissues in the mouse eye.	Experimental eye research	2026-Oct	42486250
197	Integrating single-cell and bulk transcriptomics to identify a SUMOylation-related prognostic signature and the oncogenic role of VPS72 in hepatocellular carcinoma.	Translational oncology	2026-Oct	42520472
198	Mechanism of effective-component compatibility of Bufe Yishen formula III in COPD and identification of hub genes.	Phytomedicine : international journal of	2026-Oct	42537471
199	Integrated Immunological Analysis of Interactions Between CXCL13+ T Cells and LAMP3+ DC in the Immunotherapy Response of Bladder Cancer.	Molecular carcinogenesis	2026-Oct	42555166

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200	Unveiling the power of TIIC: A prognostic tool for esophageal adenocarcinoma.	Translational oncology	2026-Oct	42556130
201	Uncovering molecular and functional dynamics of human hematopoietic stem cells during in vitro culture for cell therapy manufacturing.	Cytotherapy	2026-Oct	42556173
202	Clinical Research on Microecological Landscape for Infection Risk Stratification in Newly Diagnosed Patients with Hematological Conditions.	Infectious diseases and therapy	2026-Oct	42560632
203	Formononetin Antagonizes Osteosarcoma Metastasis by Targeting CD44: An Integrated Multi-Omics Study.	Phytomedicine : international journal of	2026-Oct	42574989
204	Otophyllaside T alleviates depression-like behaviors by directly targeting EP4: An integrated multi-strategy study.	Phytomedicine : international journal of	2026-Oct	42585681
205	Translating single-cell RNA sequencing into monocyte direct leukocyte subpopulation-transcript abundance assay ratio-based biomarkers (IFI27/PSAP or IFI27/CTSS) for clinical detect	Pathology	2026-Oct	42595652
206	Application of dual-view oblique plane microscopy to small-molecule compound screening across 3D glioblastoma stem cell spheroids with single-cell resolution.	SLAS discovery : advancing life sciences	2026-Oct	42600493
207	Integration of single-cell transcriptomics and genomic mutation analysis identifies an immunotherapy-resistant tumor subcluster and validates ARNTL2 as a malignant driver in lung a	Translational oncology	2026-Oct	42603344
208	The combination of morphogenic regulators BABY BOOM and GRF-GIF improves maize transformation efficiency and promotes leaf regeneration.	The New phytologist	2026-Oct	42608059
209	Integrative single-cell sequencing and machine learning analyses identify chronic inflammation and cancer-associated fibroblast subsets as drivers of adverse outcomes in ovarian ca	Translational oncology	2026-Oct	42632123
210	Generation of spCAS9 expressing human mesenchymal stem cell line to study gene function during osteoblast differentiation.	JBMR plus	2026-Oct	42688902
211	A targeted triple-action redox-modulating hydrogel potentiates fibroblast-mediated repair to accelerate oral wound healing.	Materials today. Bio	2026-Oct	42725083
212	Identification and Experimental Validation of PANoptosis Key Genes for Constructing a PANoptosis Risk Diagnostic Model in Intervertebral Disc Degeneration.	The journal of gene medicine	2026-Oct	42803180
213	Investigating CD8 T Cell Exhaustion in Chronic LCMV Infection by Flow Cytometry.	Current protocols	2026-Oct	42808964
214	Sperm Recovery and Evaluation in Domestic Species: Challenges and Current Practices.	Reproduction in domestic animals = Zucht	2026-Oct	42816930
215	A research on machine learning based gene selection algorithms for RNA-seq data.	Statistical applications in genetics and	2026-Jan-0	42878693
216	WasteFams: a database of protein families from global wastewater microbiomes.	NAR genomics and bioinformatics	2026-Dec	42923064
217	Cell DiffERential Expression by Pooling (CellDEEP) highlights issues in differential gene expression in scRNA-seq.	NAR genomics and bioinformatics	2026-Dec	42909367
218	MIGC: Pseudotime differentially expressed genes detection with mutual information.	Quantitative biology (Beijing, China)	2026-Dec	42903567
219	Phylogenomic screening reveals idsA2 loss conferring nitroimidazole cross-resistance in Mycobacterium tuberculosis	biorxiv preprint	2026-10-24	10.64898/2026.10.19.760085

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220	Anaerobic methane oxidation by ANME-2a at 2 M chloride in the Orca Basin halocline	biorxiv preprint	2026-10-24	10.64898/2026.02.09.704686
221	A Plasmodium falciparum Pangenome Resource to Drive Structural Variant Discovery and to assist Malaria Control	biorxiv preprint	2026-10-24	10.64898/2026.05.19.726271
222	Efficient permuted intron-exon RNA circularization system based on the LtrB group II Intron from Lactococcus lactis	biorxiv preprint	2026-10-24	10.64898/2026.10.20.760490
223	VIOLIN: A modular framework for scalable reconciliation of heterogeneous interaction graphs	biorxiv preprint	2026-10-24	10.1101/2024.07.21.604448
224	CDSeq2 integrates individual-level cell-type expression deconvolution with recoverability-guided prioritization	biorxiv preprint	2026-10-22	10.64898/2026.09.14.751599
225	LiverHomo: An Integrated and Interactive Human Liver Single-Cell Atlas with Protein Interaction and Cell-Cell Communication Networks	biorxiv preprint	2026-10-22	10.64898/2026.10.20.755227
226	Unlocking the secrets of paired terminal genomic repeats utilised by the Burkholderia jumbo phage Matilda	biorxiv preprint	2026-10-22	10.64898/2026.10.21.760668
227	Impact of air pollution and tobacco smoke on the placental small non-coding RNA landscape	medrxiv preprint	2026-10-19	10.64898/2026.10.16.26365732
228	LIF is a pro-algesic mediator in human and mouse models of arthritis-related pain	biorxiv preprint	2026-10-18	10.64898/2026.10.12.758476
229	Scalable Enzyme Reaction Retrieval Enables Metagenomic Biocatalyst Discovery	biorxiv preprint	2026-10-18	10.64898/2026.10.15.759509
230	Determining cellular phylogeny and migration at high resolution in spatial genomics	biorxiv preprint	2026-10-18	10.64898/2026.10.16.759405
231	Benchmarking Recording-Level Clinical Speech De-identification for Privacy-Preserving Clinical Audio	medrxiv preprint	2026-10-17	10.64898/2026.04.13.26349911
232	Glycomics Profiling Reveals a Stromal Chondroitin-4-sulfate State that Shapes Platinum Response in Ovarian Cancer	biorxiv preprint	2026-10-17	10.1101/2025.10.06.675352
233	Effects of host DNA and k-mer size on metagenomic classification of historical samples	biorxiv preprint	2026-10-17	10.1101/2025.04.05.647358
234	Tensorizing Pairwise Structural Analysis: GPU-Accelerated RMSD and FCC Clustering in HADDOCK3 Without Structural Regression.	biorxiv preprint	2026-10-17	10.64898/2026.10.10.758202
235	Mapping the spatial architecture of glioblastoma from core to edge delineates niche-specific tumor cell states and intercellular interactions	biorxiv preprint	2026-10-17	10.1101/2025.04.04.647096
236	Spatial Single-Cell Mapping of Transcriptional Differences Across Genetic Backgrounds in Mouse Brains	biorxiv preprint	2026-10-17	10.1101/2024.10.08.617260
237	Four Years of Continuous Weekly Wastewater Analysis Reveals Sequencing as a Robust Alternative to PCR for Respiratory Virome Surveillance.	medrxiv preprint	2026-10-15	10.64898/2026.10.13.26364774
238	THE GENETIC LANDSCAPE OF HEREDITARY SPASTIC PARAPLEGIA IN CANADA	medrxiv preprint	2026-10-15	10.64898/2026.10.14.26365432
239	MAP3K7 Loss of Function Causes Dilated Cardiomyopathy	medrxiv preprint	2026-10-15	10.64898/2026.09.02.26361780
240	Mitigating genotype-driven bias improves atlas-scale single-cell DNA methylome profiling	biorxiv preprint	2026-10-15	10.64898/2026.10.14.756197
241	Cortex-wide single-cell activity mapping in freely moving mice	biorxiv preprint	2026-10-15	10.64898/2026.10.08.755518

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242	Forecasting Alzheimer's disease progression using non-imaging clinical features and XGBoost	medrxiv preprint	2026-10-07	10.64898/2026.10.05.26364229
243	Integrated single-cell and proteomic profiling of pancreatic neoplasia identifies tissue markers that outperform established diagnostic markers in distinguishing cancer from precur	medrxiv preprint	2026-10-07	10.64898/2026.10.02.26364030
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245	Pulsed Field Ablation Enables Stromal Manipulation and Tumor Reduction in Pancreatic Ductal Adenocarcinoma	biorxiv preprint	2026-10-07	10.64898/2026.10.06.756887
246	Loss of the Y chromosome drives basal identity and metastatic potential via epigenetic reprogramming in pancreatic cancer	biorxiv preprint	2026-10-07	10.64898/2026.10.06.756936
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250	Rare Germline Variants and Genetic Susceptibility to Pleural Mesothelioma: Moving Beyond DNA Repair	medrxiv preprint	2026-10-02	10.64898/2026.09.29.26364318
251	Functional modelling of human infertility-associated genetic variants using C. elegans and mice	biorxiv preprint	2026-10-02	10.64898/2026.09.30.755673
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258	Dietary selenium deficiency drives sex-specific circadian disturbance through redox imbalance and causes early systolic dysfunction in mice	biorxiv preprint	2026-09-29	10.64898/2026.09.28.754959
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260	A Two-Stage ESM-Based Machine Learning Pipeline for Robust Hierarchically Evaluated Enzyme Function Prediction.	Computational and structural biotechnolo	2026	42959430
261	Tropheryma whipplei Pneumonia with Myelofibrosis: A Rare Actinomycetia Case Report and Literature Review.	Infection and drug resistance	2026	42928761

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262	Identification of Immuno-Diagnostic and Therapeutic Markers in Tumors and Inflammatory Diseases Based on Single-Cell and Machine Learning Methods.	Human mutation	2026	42910173
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264	Codon-aware multi-scale feature fusion for metagenomic sequence classification.	PloS one	2026	42832495
265	Diagnostic Challenges in mNGS for Pulmonary Mucormycosis Presenting with Imaging Features Resembling Those of Lung Cancer.	International medical case reports journ	2026	42827939
266	ChoCallate: a computational pipeline for consensus germline variant calling in genomic sequencing data.	PeerJ	2026	42828029
267	NeighborFinder: an R package inferring local microbial network around a species of interest.	Bioinformatics advances	2026	42820214

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