

生信方法 | 2026-09 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 329 篇，正文详述其中 30 篇

本月概览

2026年9月这批30篇文献以方法论创新为主轴，临床应用次之。最值得注意的进展集中在两个层面：其一，单细胞转录组学正在打破“静态快照”的根本局限——Kinetics-seq通过体内代谢标记直接测量RNA合成与降解速率，将单细胞分辨率的转录动力学从计算推断变为实验可测量的物理量（PMID: 42771508）；其二，空间多组学整合方法出现了方法论上的分叉，MultiSpaceNet用异质图统一配对空间转录组与蛋白质组，SpaHCC则专注于空间条件下的细胞间通信推断（PMID: 42788664、42804522）。人工智能在神经退行性疾病单细胞表型分析中的规模达到新高点：超过600万个细胞核、逾1000例个体（PMID: 42778763）。相对沉寂的是传统bulk RNA-seq方法创新，本月多数bulk分析论文属于应用驱动而非方法驱动。需要指出的是，本月清单中有若干文献（如乌干达Dinga病例调查、心肌组织钙波成像流程）与生信方法的核心主题关联较弱，系抓取策略的覆盖误差。

值得细看的研究

Kinetics-seq：将转录动力学从计算推断变为实验测量

这篇来自PNAS的研究将体内代谢标记策略与单细胞RNA测序整合，建立了一套可在组织内直接测量RNA丰度、更新速率、合成速率和降解速率的方法（PMID: 42771508）。此前RNA速率分析（如RNA velocity系列方法）依赖spliced/unspliced比例做计算推断，本质上是间接且假设驱动的。Kinetics-seq通过代谢标记绕开了这一间接推断链，使RNA动力学参数在单细胞水平上成为实验直接读出量。

关键发现：在肿瘤细胞群中，通过联合建模RNA合成与降解速率，揭示了基因特异性调控策略和肿瘤细胞之间显著的动力学异质性；利用RNA动力学作为筛选工具识别转录活跃基因子集，发现雌激素反应早期通路、PI3K-AKT-mTOR信号以及上皮间质转化通路与肿瘤进展的时间关联性强于单纯丰度分析。

证据强度：方法论进步在概念上是扎实的，但摘要未披露验证数据集的具体规模、组织类型数量及重复实验设计。代谢标记本身会对细胞生理产生扰动，标记效率的不均匀性如何影响动力学参数估计，摘要中未作说明。

对领域意义：若技术门槛足够低且标记扰动可控，Kinetics-seq将实质性地改变单细胞动态研究的证据标准，是本月方法创新中潜力最大、同时也亟需更严格独立验证的工作之一。

PASCode与PsychAD：超大规模数据推动AI表型发现

PsychAD项目利用来自超过1000例个体前额叶皮质的逾600万个细胞核单核RNA测序数据，构建了名为PASCode（表型关联单细胞编码器）的计算框架，用于量化单细胞表型关联得分（PMID: 42778763）。PASCode将多种统计方法集成进图神经网络，以提升关联得分的稳健性。

关键发现：在584例阿尔茨海默病相关表型捐赠者中识别出约150万个表型关联细胞（PAC）；在27个脑细胞亚类中比较PAC，识别出与AD病理相关的小胶质细胞亚群、可能赋予认知弹性的反应性星形胶质

细胞亚型（其神经保护与神经毒性基因表达均有改变）、认知障碍捐赠者中增强的兴奋性/抑制性失衡和线粒体功能障碍；并在阿尔茨海默病与抑郁症之间的星形胶质细胞群中识别出特定基因表达特征。

证据强度：数据集规模是迄今此类研究中最大的之一，多统计方法集成策略在一定程度上提升了稳健性。局限在于：所有样本均来自同一脑区（前额叶皮质），不代表全脑异质性；死后脑组织的RNA质量差异和死亡后间隔时间是潜在混杂因素；图神经网络模型的生物学可解释性相对于规模增益有所下降。

对领域意义：PASCode代表了将超大规模单细胞数据与复杂临床表型关联的方法论范式。600万细胞核这一规模将此类研究的数据基础提高了至少一个数量级，但计算资源门槛随之大幅上升，对多数实验室构成现实障碍。

MultiSpaceNet：配对空间转录组-蛋白质组的统一图框架

MultiSpaceNet针对同一组织切片上同时测量转录组和蛋白质组的配对空间数据，提出了基于异质图的联合表示学习框架（PMID: 42788664）。其核心设计是在共享节点集上构建单一细胞图，以不同类型的边承载空间、转录组和蛋白质组关系，两个模态分支保持独立直至每个细胞的注意力融合。

关键发现：在五个基准数据集上，MultiSpaceNet在空间域识别任务中平均调整兰德指数达0.472，优于已发表的9种方法；无泄漏RNA至蛋白质插补对信号丰富蛋白质的效果达到或超过现有专用方法；单个训练模型可同时输出空间域、蛋白质插补、跨切片联合嵌入和每细胞模态主导图。

证据强度：五个基准数据集的覆盖较同类工具有改善。"无泄漏"设计值得关注——此前不少整合方法存在训练时将预测目标纳入输入的隐患，MultiSpaceNet明确处理了这一问题。但基准数据集的选择和超参数调优过程不透明，仍存在选择性评估的可能。

对领域意义：配对空间多组学整合是当前方法论热点，MultiSpaceNet的异质图设计在架构层面比早期拼接或早期融合策略更灵活。单模型多任务的设计思路对实际使用者有吸引力。

crumblr：细胞组成分析的精度加权线性混合模型

crumblr专门解决大规模单细胞研究中细胞类型频率变化的统计检验问题，采用精度加权线性混合模型，并在细胞谱系层级的多个层次上进行多变量检验（PMID: 42778538）。

关键发现：在模拟中，crumblr增加了与现有方法相比的统计效能，同时控制假阳性率；支持随机效应以处理复杂研究设计；应用于衰老、结核病T细胞、前列腺癌骨转移和SARS-CoV-2感染的已发表数据集，均有可复现的演示。

证据强度：模拟验证加真实数据集复现是该类方法论文的标准路径，但模拟参数的设置直接影响效能比较的结论，而真实数据集的"正确答案"往往未知，使独立性有限。四个应用数据集的覆盖范围已属较好。

对领域意义：细胞组成变化分析是单细胞研究中常被轻视的统计问题——大多数流程直接对比细胞比例，忽略样本量和研究设计的复杂性。crumblr的精度加权和随机效应设计在方法上更完整，其多层次谱系检验能提升对稀有细胞亚群的统计效能，这对疾病研究尤其重要。

TOPAZ：将拓扑数据分析引入细胞动力学建模

TOPAZ将持续同调（persistent homology）与近似贝叶斯计算（ABC）及贝叶斯信息准则结合，用于从时空细胞数据中选择基于主体的模型并推断参数（PMID: 42789676）。

关键发现：利用成纤维细胞集体运动的模拟验证了参数恢复能力，并成功区分了基础ABM与加入对齐交互的扩展模型。拓扑描述符被用于量化细胞轨迹的空间特征，作为参数推断的低维摘要统计量。

证据强度：当前仅为模拟验证，无真实实验时空成像数据的独立验证案例。持续同调的计算成本较高，大规模数据集的可扩展性未经测试。目前属于概念验证阶段。

对领域意义：将拓扑数据分析引入细胞生物学建模是相对新颖的方向，持续同调为空间特征提取提供了不依赖坐标系的描述方式，适合细胞集体运动和组织形态等问题。然而ABM参数众多，贝叶斯推断对先验分布敏感，目前尚无法判断这条路径能走多远。

10X ExMSI：扩增策略突破MALDI质谱成像分辨率

10X ExMSI将膨胀显微镜技术与MALDI质谱成像结合，在标准商用仪器上实现了约500 nm的有效横向分辨率，使用5 μ m采集步长，不需要像素过采样（PMID: 42565645）。

关键发现：成功在小鼠脑组织中解析了树突树突化等亚细胞结构；在A549细胞上实现了亚细胞水平的脂质图谱；可检测甘油磷脂和鞘脂等主要脂质类别，但含伯胺的脂质因交联而减少。

证据强度：在两类样本（脑组织和培养细胞）上有实验演示，分辨率数据有具体指标。无SDS消化协议对脂质保留的系统评估，含伯胺脂质损失的程度和影响范围需要更完整的组学覆盖度数据来说明。

对领域意义：MALDI质谱成像的分辨率长期受光学聚焦和基质结晶限制，无标记单细胞分子成像是技术瓶颈。膨胀策略将有效分辨率提高约10倍而无需专用仪器，若脂质损失问题可控，将成为单细胞空间脂质组学的实用工具。

SpaHCC：空间细胞间通信的异质图推断框架

SpaHCC将单细胞转录组、空间转录组 and 先验配体-受体知识整合进异质图学习框架，针对点阵空间转录组数据推断单细胞分辨率的细胞间通信（PMID: 42804522）。基准和空间一致性分析显示，SpaHCC恢复了空间连贯的候选通信信号；在阿尔茨海默病数据中识别出与兴奋性神经元相关的重复模式，包括NRXN和FLRT2相关候选通信事件。

方法的核心局限是：点阵空间转录组存在固有的细胞到点位映射不确定性，SpaHCC通过整合先验知识缓解但未消除这一问题。与MultiSpaceNet针对配对多组学数据不同，SpaHCC专注于通信推断，两者在应用场景上是互补而非竞争关系。

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趋势判断

- 动态化是单细胞方法的主轴，但技术路径尚未收敛**

本月最明确的方向性信号是单细胞转录组学从静态到动态的推进：Kinetics-seq（PMID: 42771508）直接测量动力学参数，零膨胀电报模型（PMID:

42789681）从统计建模层面引入转录爆发动力学，CRYSPER/CUREIPES（PMID: 42779099）则在RNA剪接和编辑层面提供单细胞分辨率读出。三条路径目标相近但切入点截然不同，且均处于早期验证阶段，尚看不出哪条会成为主流标准流程的组件。

- 空间多组学整合出现方法论趋同，但评估标准仍不统一**

MultiSpaceNet (PMID: 42788664) 和SpaHCC (PMID: 42804522) 都指向"在空间背景下整合多个信息层"这一目标，但两者的评估指标不重叠——调整兰德指数、空间一致性得分、通信事件生物验证率，没有统一的基准体系，使跨工具的独立比较非常困难。这是整个空间多组学领域的系统性问题，不是单一工具的问题。

- 大规模数据推动AI表型发现，可解释性成为代价**

PASCode (PMID: 42778763) 利用逾600万个细胞核训练图神经网络，在方法层面充分利用了数据规模，但集成多统计方法进图神经网络的设计使模型的生物学可解释性下降。这批研究总体上呈现出"规模换精度、模型换解释"的倾向，与更早期"机制清晰但数据稀少"的研究形成明显对立。这一取舍是否合适，取决于研究者希望得到预测工具还是机制理解。

- 组成型数据分析问题正被重新认真对待**

crumblr (PMID: 42778538) 和微生物组组成型数据方法综述 (PMID: 42805588) 从两个完全不同的角度指出同一类问题：相对丰度数据的统计处理长期存在根本缺陷。微生物组综述明确指出，目前对于哪种方法最能解决组成型问题没有共识，且低生物量样本中低水平微生物的检出意义被忽视 (PMID: 42805588)。集中出现说明领域内对这一基础问题的重视程度在上升，可能与单细胞和宏基因组数据集规模增大后偏差被放大有关。

- 被高估的方向：机器学习预后签名**

本月出现了若干基于公共数据集、利用机器学习构建预后签名的论文 (PMID: 42802232、42791187、42782481、42777131)。这类工作的共同模式是：整合多个GEO数据集、用LASSO或随机森林筛基因、验证集来自相同来源的不同队列。AUC=1的报告 (PMID: 42791187) 在医学预后研究中几乎可以直接指向训练集泄漏或数据集同质性过强，不代表生物学意义上的突破。免疫冷黑色素瘤的连接组学分析 (PMID: 42777131) 在富集分析中DNMT抑制剂的类富集在FDR校正后未达显著性 ($q=0.126$)，结论是探索性的。这类论文的数量与其实际方法贡献不成比例。

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这批研究的共同弱点

- 验证数据集的独立性存疑**

本月多篇论文的验证数据集来自公共数据库，且与训练集来自相同研究背景或相同测序平台。SLE诊断模型 (PMID: 42782481) 的"外部验证"数据集GSE112943与发现队列GSE318067的生物学背景高度相似，"外部"的程度有限。CIRI生物标志物 (PMID: 42791187) AUC=1横跨多个数据集，是数据集间过度同质性的典型信号。当发现和验证数据集都来自少数高引公共数据集时，"验证"实际上测量的是数据集间的相似性，而非方法的普适性。

- 样本量与统计效能的结构性不足**

Kinetics-seq (PMID: 42771508) 的摘要未披露验证样本量；TOPAZ (PMID: 42789676) 目前仅有模拟数据验证；10X ExMSI (PMID: 42565645) 的组织验证局限于小鼠脑和单一细胞系。这类方法论文的惯常路径是概念验证先发、广泛验证后补，但后补工作往往滞后数年，造成引

用传播与验证深度严重不匹配。

- 计算再现性缺乏统一标准**

MultiSpaceNet提供了源代码（PMID: 42788664），但多数论文对计算环境的描述粗略，超参数选择过程不透明。在空间多组学整合这类方法中，超参数对结果的影响往往大于架构选择本身，但本月论文普遍不报告超参数敏感性分析，使他人复现的起点不清晰。

- 临床验证几乎全部缺席**

本月方法论文中，能展示真实临床有效性的极少。儿科呼吸道病原体检测（PMID: 42782157）是例外，它在有独立临床诊断作为参考的真实患者样本上做了比较，BALF和咽拭子的Kappa系数分别为0.791（ $P < 0.001$ ）和0.757（ $P < 0.001$ ），tNGS与mNGS的一致性有实际意义。多数其他论文，特别是机器学习预后模型类，从未接触过前瞻性临床数据。

- 生物学机制验证与计算结论脱节**

PASCode（PMID: 42778763）识别出的约150万个表型关联细胞的功能，需要独立实验验证，但这类验证在方法论文的时间尺度内通常不会出现。Kinetics-seq揭示的动力学异质性是否具有临床可干预的靶点，同样没有实验链条。机器学习或图神经网络给出的"关联"在没有机制链条的情况下，转化价值有限。

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下个月值得关注

- Kinetics-seq的独立复现与扰动评估**

Kinetics-seq（PMID: 42771508）是本月方法创新中潜力最大的工作，但摘要对验证规模和技术局限的披露有限。值得跟踪：是否有独立实验室复现；代谢标记对细胞转录组本身的扰动是否被系统评估；方法是否可推广到非肿瘤或固定组织样本。

- 空间多组学整合的系统性基准比较**

MultiSpaceNet（PMID: 42788664）和SpaHCC（PMID: 42804522）在本月同时发表，但评估指标不重叠。若出现独立的系统性基准比较研究，将大幅提高这类工具的可信度，也有助于厘清"空间域识别"与"细胞间通信推断"这两类子问题各自的方法论前沿在哪里。

- 零膨胀模型在标准流程中的地位**

零膨胀电报模型（PMID: 42789681）在理论上正确区分了技术零值与生物学双峰分布，但零膨胀在单细胞数据中究竟是技术噪声还是生物学真零这一争论仍未有定论。下个月值得关注该模型是否进入主流单细胞分析包，或引发方法论反驳。

- 宏基因组平均基因组大小估计的方法论争议**

功能-分类缩放框架（PMID: 42801568）对16S宏条形码在极端环境下的AGS估计提出了系统性质疑，发现了土壤pH与AGS之间的U形关系，并对已发表研究关于盐梯度下生态进化权衡的结论提出了数据偏差质疑。若这一框架得到独立验证，将影响大量依赖16S估算基因组大小的存量研究的解读，是一个潜在的范式冲突点，值得持续观察。

- 废水宏基因组测序的规模化可行性**

混合捕获宏基因组测序应用于美国15个污水处理厂近450份周样本的研究（PMID: 42803564）显示中位病毒读段比例超过19%，与数字PCR定量结果相关。这一规模的多地点前瞻性部署是方法可行性的重要证明，下个月若有后续数据，值得看其在非呼吸道病原体或耐药基因检测中的表现。

附录：2026-09 全部收录文献（329 篇）

#	标题	期刊	日期	PMID
1	System-level synchronization and subtype-specific modules govern brain-wide serotonin axon innervation.	Proceedings of the National Academy of S	2026-Sep-2	42771501
2	Kinetics-seq enables comprehensive profiling of single-cell RNA kinetics in vivo to reveal dynamic tumor heterogeneity.	Proceedings of the National Academy of S	2026-Sep-2	42771508
3	Methods to Address Compositional Data Challenges in Clinical Studies for the Safety Assessment of Human Microbiome Perturbations.	Journal of food protection	2026-Sep-2	42805588
4	Air-Liquid interface midbrain organoids model the pathological features of Parkinson's disease.	Neuroscience	2026-Sep-2	42468771
5	Tenfold Expansion Submicrometer MALDI Mass Spectrometry Imaging of Tissues and Cultured Cells.	Angewandte Chemie (International ed. in	2026-Sep-2	42565645
6	Single-Cell Imaging of Site-Specific RNA-Protein Interactions.	Angewandte Chemie (International ed. in	2026-Sep-2	42615282
7	Prospective metagenomic sequencing of wastewater across the United States yields robust viral enrichment and concordance with digital PCR measurements.	Applied and environmental microbiology	2026-Sep-2	42803564
8	Spatial cell-cell communication inference based on cell-spot-ligand-receptor heterogeneous graphs.	PLoS computational biology	2026-Sep-2	42804522
9	Machine learning-driven M2 macrophage signature for precision prediction of survival and therapy response in acute myeloid leukemia.	Inflammation research : official journal	2026-Sep-2	42802232
10	PP4 deficiency drives airway epithelial senescence via the PERK-eIF2 α -ATF4-p21 axis in severe asthma.	Inflammation research : official journal	2026-Sep-2	42802286
11	Functional-Taxonomic Scaling Resolves Conflicting Average Genome Size Estimates Across Environmental Gradients.	Advanced science (Weinheim, Baden-Wurtte	2026-Sep-2	42801568
12	Single-Cell and Bulk RNA-Seq Profiling Identifies Cell Adhesion-Related Gene Signatures in Cerebral Ischemia-Reperfusion Injury.	eNeuro	2026-Sep-2	42791187
13	[Stability and viability optimization for filamentous microorganisms in droplet-based microfluidic screening].	Sheng wu gong cheng xue bao = Chinese jo	2026-Sep-2	42773672
14	MultiSpaceNet: Graph-based Joint Representation Learning for Paired Spatial Transcriptome-Proteome Data.	Bioinformatics (Oxford, England)	2026-Sep-2	42788664
15	Topologically-based parameter inference for agent-based model selection from spatiotemporal cellular data.	PLoS computational biology	2026-Sep-2	42789676
16	Integrating zero-inflation correction and transcriptional kinetics for single-cell transcriptomic analysis.	PLoS computational biology	2026-Sep-2	42789681
17	Xoublet: An Extreme-Scale Doublet Detection Algorithm for Cardiac Single-Cell Transcriptomics.	Journal of computational biology : a jou	2026-Sep-2	42781809
18	Resolution and automated analysis of single-cell Ca ²⁺ waves within living myocardial tissue slices.	The Journal of physiology	2026-Sep-2	42782096
19	A comparative study of mNGS and tNGS for pathogen detection in paired upper and lower respiratory tract specimens from pediatric pneumonia patients.	Microbiology spectrum	2026-Sep-2	42782157

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20	A mitoxyperiosis-associated gene signature correlates with immune disturbance and provides a potential diagnostic biomarker for systemic lupus erythematosus.	Clinical rheumatology	2026-Sep-2	42782481
21	Probing and Painting to Get the Full Picture of Macrophage Polarisation.	SLAS discovery : advancing life sciences	2026-Sep-2	42785586
22	A Multiscale Quantitative Systems Pharmacology Platform for Early Screening of MMAE-Based Antibody-Drug Conjugates.	European journal of pharmaceutical scien	2026-Sep-2	42785646
23	Transcriptomic immune subtyping and connectivity mapping nominate DNA methyltransferase inhibitors for immunodepleted melanoma.	Melanoma research	2026-Sep-2	42777131
24	Unraveling the dielectric heterogeneity response of cell lines under electroporation: a microfluidic single-cell on-chip system.	Microsystems & nanoengineering	2026-Sep-2	42778526
25	Fast, flexible analysis of differences in cellular composition with crumblr.	Nature communications	2026-Sep-2	42778538
26	AI-based characterization of Alzheimer's disease phenotypes from population-scale single-cell data.	Nature medicine	2026-Sep-2	42778763
27	Single-Bacterium Biosensing: A Rapid Electrochemical Strategy to Differentiate Antibacterial Efficacy and Mechanism.	ACS sensors	2026-Sep-2	42777140
28	Transcriptome-based postmortem interval prediction in the human dorsolateral prefrontal cortex using covariate-aware machine learning.	Forensic science international	2026-Sep-2	42777494
29	CRYSPEr and CUREIPES: two new molecular tools enabling analysis of RNA splicing and C-to-U RNA editing-inducible protein expression at single cell resolution.	Nucleic acids research	2026-Sep-2	42779099
30	Investigation of Dinga Dinga: A Cluster of Bilateral Lower-Extremity Tremors-Bundibugyo District, Uganda, 2023-2024.	The American journal of tropical medicin	2026-Sep-2	42772264
31	Large-scale organoid-derived cyst cultures as a drug discovery platform for polycystic kidney disease.	Kidney international	2026-Sep-2	42772449
32	Graph Masked Autoencoder With Multi-Head Latent Attention Mechanism for Gene Regulatory Link Prediction.	IEEE journal of biomedical and health in	2026-Sep-2	42776880
33	Uncovering heterogeneous effects via localized feature selection.	Proceedings of the National Academy of S	2026-Sep-2	42743276
34	Detection and sequencing of Ap2N-capped RNAs in human cells.	Proceedings of the National Academy of S	2026-Sep-2	42743287
35	Senescent Cell Heterogeneity: Tissue-Dependent Signatures and Age Dynamics Revealed by Human scRNA-Seq Data.	International journal of molecular scien	2026-Sep-2	42794841
36	Multi-omics integration and artificial intelligence for the conservation and utilization of local chicken genetic resources.	Poultry science	2026-Sep-2	42777373
37	Trajectory-informed gene feature selection in single-cell analysis with SEEK-VFI.	Cell reports methods	2026-Sep-2	42508407
38	Multi-omics integration identifies prognostic genes linked to adaptive immunity response and radiosensitivity in cervical cancer.	Translational oncology	2026-Sep-2	42767096
39	Sequential Chlorantraniliprole-Bacillus thuringiensis Application Enhances Transcriptomic Reprogramming and Disrupts Detoxification Pathways in Spodoptera frugiperda (Noctuidae: Le	Journal of applied toxicology : JAT	2026-Sep-2	42767978

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40	Trace-n-Seq combines retrograde fluorescent tracing with sorting and single-cell sequencing of innervating peripheral neurons.	Nature protocols	2026-Sep-2	42768210
41	Tissue expansion mass spectrometry imaging (TEMI) for high-spatial-resolution multiomics molecular mapping.	Nature protocols	2026-Sep-2	42768211
42	A scalable workflow for sensitive detection and genomic profiling of tumour cells in lymph nodes from FFPE tissue.	The Journal of pathology	2026-Sep-2	42768301
43	Code-multiplexed multi-frequency impedance cytometry with a unified deep-unfolding network.	Microsystems & nanoengineering	2026-Sep-2	42764344
44	Apollo-IRE1: A Genetically Encoded Sensor for Live Cell and Multiplexed Imaging of Endoplasmic Reticulum Stress.	ACS sensors	2026-Sep-2	42765999
45	Mapping a differentiation architecture for hard tissue mineralization with large-scale single-cell atlases.	PLoS computational biology	2026-Sep-2	42766664
46	STEAP2 Is a Candidate Marker of a 7q/CNA-Associated Iron-Handling Malignant Epithelial State in Lung Adenocarcinoma.	Cancers	2026-Sep-2	42795018
47	SMORE: joint dimension reduction and cell population discovery on single-cell methylome data.	bioRxiv : the preprint server for biolog	2026-Sep-2	42779705
48	A lifespan single-cell atlas of the human developing hippocampus benchmarks familial Alzheimer's disease brain organoids.	bioRxiv : the preprint server for biolog	2026-Sep-2	42779813
49	Proximity Labeling in Caenorhabditis elegans to Detect Neuronal Proteins During Memory Formation.	Bio-protocol	2026-Sep-2	42781333
50	Omics approaches in insect diapause research.	Journal of insect physiology	2026-Sep-2	42764118
51	Single-Cell Transcriptomic Profiling and Machine Learning Reveal Stage-Specific Gene Dynamics in Brucellosis.	Vector borne and zoonotic diseases (Larc	2026-Sep-2	42764522
52	Spatially resolved multimodal hallmarks of response to neoadjuvant immunotherapies in the melanoma ecosystem in 2D and 3D.	bioRxiv : the preprint server for biolog	2026-Sep-1	42779625
53	In vivo intercellular CRISPR screens using viral proximity barcoding reveal regulators of tumor-immune interactions.	bioRxiv : the preprint server for biolog	2026-Sep-1	42779810
54	Joint inference of paired dynamical gene regulatory networks reveals distinct cell-state landscapes of neutrophil reprogramming.	bioRxiv : the preprint server for biolog	2026-Sep-1	42780042
55	Isolation of Brain Microglia to Study Persistence of Human Immunodeficiency Virus-1.	Journal of visualized experiments : JoVE	2026-Sep-1	42762141
56	Rapid and accurate diagnosis of bloodstream infections: A multiplex real-time PCR assay with selective microbial enrichment for direct whole-blood detection and positive blood cult	Journal of microbiology, immunology, and	2026-Sep-1	42763279
57	Revealing therapeutic single-cell transcriptomic signatures using a simple classifier.	Cell reports methods	2026-Sep-1	42759521
58	ConvexGating infers gating strategies from clusters in single cell cytometry data.	Nature communications	2026-Sep-1	42760285
59	Community: Component based differential cell communication analysis in large multi-sample case-control scRNAseq datasets.	iScience	2026-Sep-1	42699773

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60	iPscDB: a comprehensive platform for plant single-cell transcriptomic data integration and analysis.	Nucleic acids research	2026-Sep-1	42755294
61	In vitro induction of human germinal center B cells.	Science immunology	2026-Sep-1	42758797
62	Integration of cell-specific gene expression and chromatin accessibility facilitates localization of neurodegenerative risk in microglia.	bioRxiv : the preprint server for biolog	2026-Sep-1	42780032
63	Whole-transcriptome-scale isoform-resolved spatial imaging of single cells in tissues.	Cell	2026-Sep-1	42462710
64	CoSAG-nf: A Scalable Nextflow Pipeline for Co-assembly, Optimization, and Interactive Visualization of High-Throughput Single-Cell Genomes.	Bioinformatics (Oxford, England)	2026-Sep-1	42752543
65	Novel insight into diversity of active tetracycline-resistant bacteria and genes in sludge by in situ microcapsule-entrapped cultivation.	Bioresource technology	2026-Sep-1	42754122
66	A Real-Data-Driven Framework for Evaluating Differential Transcript Usage Methods Across Long-Read Bulk, Single-Cell, and Spatial Transcriptomics.	Advanced science (Weinheim, Baden-Wurtte	2026-Sep-1	42755034
67	Key genes identified in ammonia-induced cell death during pediatric sepsis: Machine learning, single-cell, and virtual gene knockout approaches.	Biochemical and biophysical research com	2026-Sep-1	42520338
68	STAT1: a central hub linking ferroptosis and inflammation in hepatic ischemia-reperfusion injury.	Inflammation research : official journal	2026-Sep-1	42752934
69	A systematic evaluation of the sources of nonuniform coverage in RNA-seq and limitations of current practices.	RNA (New York, N.Y.)	2026-Sep-1	42527318
70	Identification of broadly tumour-reactive $\gamma \delta$ TCRs from multiple myeloma.	Nature	2026-Sep-1	42749802
71	A dual-mode nano-microelectrode for PTH detection at the single-cell level.	The Analyst	2026-Sep-1	42598968
72	Synthesis of Pt-Pd bimetallic nanorods and nanoparticles supported on single-walled carbon nanotubes via a solvothermal approach.	Chemical communications (Cambridge, Engl	2026-Sep-1	42745609
73	Intracellular gelation technology: frontier exploration in biomaterials and biomedical applications.	Journal of materials chemistry. B	2026-Sep-1	42746902
74	Benchmarking reference-based cellular deconvolution algorithms to predict cell proportions.	Computational biology and chemistry	2026-Sep-1	42762696
75	TopClust: Topological-based analysis of scRNA-seq data for data-driven identification of clusters and core cluster cells.	Biophysical journal	2026-Sep-1	41981916
76	Quantitative imaging of dynamic processes in intestinal organoids.	Nature protocols	2026-Sep-1	42744928
77	Multimodal AI and single-cell transcriptomics integrate to construct a histopathological prognostic model for bladder cancer, revealing the RTN3-glycolysis axis in chemoresistance.	Experimental hematology & oncology	2026-Sep-1	42745263
78	Integrated Visualization of Neutrophil Recruitment and Inflammatory Cytokine Profiling in Bronchoalveolar Lavage Fluid.	Journal of visualized experiments : JoVE	2026-Sep-1	42747099
79	Paean: A Unified and Efficient Transcriptome Quantification System Using Heterogeneous Computing.	Journal of molecular biology	2026-Sep-1	41887362

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80	ShapeME: A Tool and Web Front-end for De Novo Discovery of Structural Motifs Underpinning Protein-DNA Interactions.	Journal of molecular biology	2026-Sep-1	41997213
81	Deepptosis: A Deep Learning-Based Platform for Label-Free Discrimination of Apoptosis and Pyroptosis from Brightfield Microscopy.	Journal of molecular biology	2026-Sep-1	41999938
82	A surface enhanced Raman scattering nanotag library based on cucurbit[7]uril controlled nanoparticle aggregates for fast cell imaging.	Journal of colloid and interface science	2026-Sep-1	42013531
83	Fast fourteen-frequency impedance spectroscopy of single erythrocytes and yeast cells in flow.	Biosensors & bioelectronics	2026-Sep-1	42127674
84	Function-driven analytical strategies for identifying contaminants of emerging concern-degrading bacteria: From enrichment cultures to single-cell technologies.	Environmental research	2026-Sep-1	42476392
85	Unlocking the Full Potential of Spatial Omics in Plants: Practical Challenges, Solutions, and a Path Forward.	The Plant cell	2026-Sep-1	42740657
86	Unique Molecular Identifiers Don't Need to be Unique: A Collision-Aware Estimator for RNA-Seq Quantification.	Journal of computational biology : a jou	2026-Sep-1	42741932
87	BrIS: Visualizing Internal Standards at the MS1 Level via Bromine Fingerprint for Sensitive and Robust Proteomics Quality Control.	Angewandte Chemie (International ed. in	2026-Sep-1	42742076
88	The Spatiotemporal Evolution of Radiation Resistance in Glioblastoma.	Neuro-oncology	2026-Sep-1	42742387
89	Domain Elastic Transform: Bayesian Function Registration for High-Dimensional Scientific Data.	IEEE transactions on pattern analysis an	2026-Sep-1	42743026
90	Cell-type-specific circadian and light-responsive transcriptional dynamics in adult Drosophila neurons.	Proceedings of the National Academy of S	2026-Sep-1	42709819
91	Revalidating KCrPDTA for aqueous redox flow batteries.	EES batteries	2026-Sep-1	42756771
92	Machine learning-based identification of core regulatory targets in 1-nitropyrene-induced placental trophoblast dysfunction and FGR.	Ecotoxicology and environmental safety	2026-Sep-1	42735479
93	An immune related cell death index for prognostic stratification and immunotherapy response prediction in oral cancer.	Translational oncology	2026-Sep-1	42735562
94	Elucidating how calcium inhibits anammox systems and a novel recovery strategy using cation exchange resin: Performance and mechanisms.	Bioresource technology	2026-Sep-1	42735857
95	k-mer-based Upstream Preprocessing of long reads for Isoform Discovery.	Genome research	2026-Sep-1	42736018
96	Cell cycle-dependent protein dynamics in budding yeast resolved by deconvolution of bulk proteomics.	Molecular systems biology	2026-Sep-1	42736370
97	ScLRR Identified From BSR-seq Inhibits Sugarcane Yellow Leaf Virus Accumulation by Interacting With Its Coat Protein in the Nucleus.	Plant, cell & environment	2026-Sep-1	42740305
98	Steady Cone-Jet Mode of Electrospray for Single-Cell Deposition.	ACS biomaterials science & engineeri	2026-Sep-1	42561109
99	Library strategies differentially shape microbial, functional, and host signals in clinical metagenomic sequencing.	mSystems	2026-Sep-1	42734361
100	Using Mapping-Profiles to Refine Strain-Level Metagenomic Classification.	Journal of computational biology : a jou	2026-Sep-1	42730546

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101	Detection of antibiotic heteroresistance in clinical microbiology: current and emerging methodologies.	Clinical microbiology and infection : th	2026-Sep-1	42731626
102	Associations between brain phenotypes and temporomandibular disorders: An integrative multi-omics investigation.	Cranio : the journal of craniomandibular	2026-Sep-1	42731980
103	OscillomeR infers ultradian oscillations and targets of the Hes family.	Patterns (New York, N.Y.)	2026-Sep-1	42746303
104	Disentangling covariate effects on single-cell-resolved epigenomes with DeepDive.	Patterns (New York, N.Y.)	2026-Sep-1	42746519
105	Genetic Deletion of Cis-Regulatory Elements to Dissect the Function of the Non-coding Genome in human Preimplantation Models.	Journal of visualized experiments : JoVE	2026-Sep-1	42730668
106	Distinct cochlear cell types associated with genetic susceptibility to sensory and metabolic hearing loss in older adults.	American journal of human genetics	2026-Sep-1	42727577
107	Disagreement-Informed Arbitration for Gene Regulatory Network Inference: A Score-Level Meta-Classifer and a Diagnostic Typology of Inter-Method Conflict.	Bio Systems	2026-Sep-1	42727749
108	Evaluating and comparing the signalling and functional landscape of hiPSC-CMs derived from patients with dilated cardiomyopathy.	npj biomedical innovations	2026-Sep-1	42728314
109	Estimating cis and trans contributions to differences in gene regulation.	Genetics	2026-Sep-1	42725652
110	VISTA: a classifier for metagenomic subspecies and community state typing of the vaginal microbiome.	Microbiology resource announcements	2026-Sep-1	42725726
111	Obesity-Related Tendon Pathology: Cardiometabolic Mechanisms, Clinical Implications, and Management.	Current obesity reports	2026-Sep-1	42726433
112	Multiview Transformer-Based Hierarchical Fusion Model for Cell Type Identification.	IEEE journal of biomedical and health in	2026-Sep-1	42726615
113	A systematic comparison of single-cell perturbation response prediction models.	Science advances	2026-Sep-1	42715312
114	Single-cell vector copy number analysis of phenotypically defined long-term hematopoietic stem cells for gene therapy safety assessment.	Molecular therapy. Advances	2026-Sep-1	42733658
115	Photonic fingerprint barcodes mediated by microsphere WGM lasing.	Nanoscale	2026-Sep-1	42584226
116	Velociraptor Machine Learning Quantifies Similarity to Known Cell Types and Matches Cells Across Flow and Imaging Cytometry Platforms.	Cytometry. Part A : the journal of the I	2026-Sep-1	42720181
117	Partaker: deep-learning-based single-cell-resolution analysis of multi-dimensional, long-term, microfluidic-based time-lapse microscopy data.	Bioinformatics (Oxford, England)	2026-Sep-1	42720611
118	DMGRN: Enhancing Diffusion Models for Gene Regulatory Network Inference.	IEEE transactions on computational biolo	2026-Sep-1	42721176
119	Clinical translation of senescence-related pan-cancer multi-omics: tools for assessment and immunotherapy prediction.	Cancer gene therapy	2026-Sep-1	42722723
120	DNA/RNA Hybrid Hairpin Gold Nanobeacons Targeting miR-31 Reprogram Invasion in Lung Cancer and Remodel Tumor Histo-Architecture In Vivo.	ACS materials Au	2026-Sep-0	42729941

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121	Causal assessment of Bayesian gene regulatory networks from single-cell transcriptomics.	Cell reports methods	2026-Sep-0	42716018
122	Plasma membrane order maps functional diversity in immune cells.	Nature chemical biology	2026-Sep-0	42717051
123	Circular RNAs orchestrate integrated post-transcriptional responses to combined heat and drought stress in rice.	Molecular genetics and genomics : MGG	2026-Sep-0	42711459
124	Multimodal discovery of a pathogenic B cell-dependent T cell state in multiple sclerosis.	Brain : a journal of neurology	2026-Sep-0	42714077
125	MADCAP: isolation of novel nAb-na ï ve AAV capsids from metagenomic data.	Journal of virology	2026-Sep-0	42714164
126	A Protoplast-based method to visualize early cell biological events in plant cellular reprogramming and regeneration.	Development (Cambridge, England)	2026-Sep-0	42714221
127	STRATUM-Structured Framework for Reporting, Assessment, and Translational Utility of Metagenomics.	Journal of AOAC International	2026-Sep-0	42714244
128	Spatiotemporal Sequential Fluorescence and Electrochemistry Bimodal Quantitation of Enzyme Activity in a Living Cell.	Nano letters	2026-Sep-0	42715043
129	Development of a novel universal primer set with high sensitivity and specificity for detection of diatom.	Legal medicine (Tokyo, Japan)	2026-Sep-0	42721651
130	Development and validation of a long-term co-maturation protocol for human stem cell-derived microglia and neuronal networks.	Stem cell reports	2026-Sep-0	42624101
131	LINC01871-Mediated Sensitivity to Cyclin-Dependent Kinase 4/6 Inhibitors in Human Breast Cancer.	Journal of visualized experiments : JoVE	2026-Sep-0	42714000
132	Divergent avian strains drive an off-season influenza A peak in municipal wastewater.	Microbiology spectrum	2026-Sep-0	42708591
133	An Instrumental Optimization of a Label-Free Proteomic Method for Trace Protein Input.	Analytical chemistry	2026-Sep-0	42708762
134	scCGC2T: Curriculum-Guided Contrastive Co-Training Framework for scRNA-Seq Data Clustering.	IEEE transactions on computational biolo	2026-Sep-0	42709526
135	Not every gene is special: Modelling scale controls the false discovery rate when analysing high-throughput sequencing data.	PLoS computational biology	2026-Sep-0	42709908
136	Single-cell profiling of mitochondrial phenotyping-coupled mtDNA genotyping.	Proceedings of the National Academy of S	2026-Sep-0	42673453
137	Integrated single-cell and bulk transcriptomic analysis reveals an epithelial cell-derived prognostic and immunotherapeutic signature with ADAM12 as a key functional regulator in n	Translational oncology	2026-Sep-0	42705211
138	ON-Time enables rapid microbiome sequencing and analysis for precision medicine.	Cell reports methods	2026-Sep-0	42705234
139	Site-specific gene integration by recombinase-mediated cassette exchange in anhydrobiotic Pv11 cells.	In vitro cellular & developmental bi	2026-Sep-0	42706481
140	NFS1 activates PI3K/AKT/mTOR signaling to upregulate GPX4 expression and enhance ferroptosis resistance in osteosarcoma.	Functional & integrative genomics	2026-Sep-0	42704489
141	DECANT: Decoupling mechanism from context in single-cell drug perturbation representation.	Bioinformatics (Oxford, England)	2026-Sep-0	42704667
142	Automated Sperm Tracking Using Deep Learning for High-Resolution Analysis of Motility.	Reproduction (Cambridge, England)	2026-Sep-0	42704692

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143	Graph-Attentional Deep Sparse Subspace Clustering for Single-Cell Transcriptomics.	IEEE transactions on computational biolo	2026-Sep-0	42704804
144	Single-cell transcriptomics on FFPE placenta: A novel method for comprehensive exploration of an entire placental section.	Placenta	2026-Sep-0	42727380
145	When light colour matters: Spectral quality is associated with distinct small RNA candidates in Arabidopsis thaliana.	Journal of photochemistry and photobiolo	2026-Sep-0	42715797
146	Determining the Age of Every Cell Within Each Budding Yeast Microcolony Combining Single-Cell Microencapsulation With Confocal Microscopy.	Bio-protocol	2026-Sep-0	42725359
147	Cable Bacteria Accelerate Nitrogen Removal in Freshwater Sediments by Mitigating Diffusion Limitation via Long-Distance Electron Transport.	Environmental research	2026-Sep-0	42700855
148	A chemoresistance-associated proliferation gene signature identified by single-cell and machine learning analysis predicts prognosis in high-grade serous ovarian carcinoma.	Translational oncology	2026-Sep-0	42696959
149	Comparative Analysis of Primary and Liver Fibroblasts Reveals MET as a Potent Target in Pancreatic Cancer Metastasis.	Cellular and molecular gastroenterology	2026-Sep-0	42697413
150	Exploratory study on blood and urine transcriptomes for identifying miRNA biomarkers in pediatric febrile bacterial and viral infections.	Scientific reports	2026-Sep-0	42697918
151	Dynamic Supervised Prelabel Diffusion for Single-Cell Clustering.	Journal of computational biology : a jou	2026-Sep-0	42695374
152	Meta-CD: a metagenomic sequencing coverage and depth calculator for target species.	Microbiology resource announcements	2026-Sep-0	42695693
153	Identification of Glioblastoma Cell Surface Proteins and Assessment of Their Expression Across Patient-Derived Stem-Like Cell Cultures.	Journal of proteome research	2026-Sep-0	42695909
154	Morphogen-guided neocortical organoids with anteroposterior areal identity.	Cell stem cell	2026-Sep-0	42624107
155	Proteomic analysis of pancreatic endocrine cells by mechanistic single-cell isolation identifies membrane pathways.	Experimental & molecular medicine	2026-Sep-0	42693238
156	A who's who of cell types in skeletal muscle.	Communications biology	2026-Sep-0	42693270
157	Machine learning identifies ac4C-related prognostic signature and TUBA1C as therapeutic target in COAD.	Mammalian genome : official journal of t	2026-Sep-0	42693326
158	Redirected T-cell cytotoxicity identifies BRD9-PTGES axis as an immune-sensitising vulnerability in ovarian cancer.	Biochemical and biophysical research com	2026-Sep-0	42349121
159	Optimizing a culture-enriched hybrid metagenomics pipeline to assess the AMR footprint of livestock manure in anaerobic digestate.	Microbiology spectrum	2026-Sep-0	42690060
160	Time heals all wounds: Identification of RNA biomarkers for forensic wound age estimation in human skin tissue samples.	Forensic science international. Genetics	2026-Sep-0	42710152
161	Evaluating sampling strategies for the detection of avian influenza viruses in the environment.	Virology	2026-Sep-0	42704958
162	FusionX: Automated, Standardized quantification of cell-to-cell fusion across diverse systems.	Molecular biology of the cell	2026-Sep-0	42684847
163	Grass Expression Atlas: an RNA-seq-based expression resource for grass species.	Plant & cell physiology	2026-Sep-0	42685250

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164	Three-Dimensional Gelatin-Based Hydrogel Degradation and Cell Control by Two-Photon Excitation.	ACS biomaterials science & engineeri	2026-Sep-0	42690902
165	COBRA: Cell-type-specific Orthogonal Batch effect Removal Algorithm in single cell RNA-sequencing data.	Bioinformatics (Oxford, England)	2026-Sep-0	42684056
166	DPAS-Graph: adaptive spatial-feature relation learning for spatial RNA-to-protein prediction and virtual protein profiling.	Briefings in bioinformatics	2026-Sep-0	42709957
167	Interpretable deep neural network identifies robust biomarkers for diseases with mechanistic insights from omics data.	Briefings in bioinformatics	2026-Sep-0	42704266
168	Gene-Chronos: parameter-efficient developmental time inference using a pretrained single-cell foundation model.	Briefings in bioinformatics	2026-Sep-0	42696754
169	Mapping ovarian cellular and molecular landscape across the lifespan of women: a scoping review.	Human reproduction update	2026-Sep-0	42467724
170	EpiCure (Epithelial Curation): a versatile and handy tool for curation of epithelial segmentation.	Development (Cambridge, England)	2026-Sep-0	42554056
171	Benchmarking methods for extracting microbial signal from host-dominated metatranscriptomes.	Briefings in bioinformatics	2026-Sep-0	42685266
172	Microfluidic platform for nanoliter qPCR of several retinal pigment epithelial (RPE) cells.	Journal of micromechanics and microengin	2026-Sep-0	42687870
173	Pattern-Filter structural validation of single-cell RNA-seq reads reduces artifactual barcodes and improves biological resolution.	Genome research	2026-Sep-0	42586759
174	A human epithelial cell cycle dataset.	Scientific data	2026-Sep-0	42680767
175	A single-cell atlas of multiple myeloma defines malignant archetypes and proliferative states.	Nature genetics	2026-Sep-0	42680839
176	MetaCAT enables reconstruction of high-quality microbial genomes and their association with host traits from metagenomic data.	Nature microbiology	2026-Sep-0	42680886
177	MethyAnno: An Interpretable Automated Annotation Method Leveraging Multi-Scale Information and Metric Learning Framework for scDNAm Data.	Advanced science (Weinheim, Baden-Wurtte	2026-Sep-0	42681808
178	A Cost-Effective Workflow for Mono- and Multiplex Immunofluorescence in Adherent Two-Dimensional Cell Cultures on Glass Coverslips.	Journal of visualized experiments : JoVE	2026-Sep-0	42683913
179	A label-free impedance cytometry platform for multi-functional and high-precision bacterial characterization.	Talanta	2026-Sep-0	42068934
180	FLIMExplorer: interactive GUI for object-based visualization and analysis of fluorescence lifetime images.	JPhys photonics	2026-Sep-0	42416368
181	DINCH exposure contributes to osteoarthritis pathogenesis via TSPO-mediated chondrotoxicity: Evidence from in silico prediction to experimental validation.	Chemico-biological interactions	2026-Sep-0	42501774
182	High-content imaging driven algal phenotypes enable precise multilevel discrimination of heavy metal stress.	Journal of hazardous materials	2026-Sep-0	42531928
183	Single-cell transcriptomic atlas of Alzheimer's disease middle temporal gyrus reveals region, cell type, and sex specificity of gene expression with novel genetic risk for MERTK in	Journal of Alzheimer's disease : JAD	2026-Sep-0	42678676
184	VicMAG, an open-source tool for visualizing circular metagenome-assembled genomes highlighting bacterial virulence and antimicrobial resistance.	NAR genomics and bioinformatics	2026-Sep	42712876

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185	Prognosis of Patients Infected With <i>Talaromyces marneffei</i> Across Various Risk Factors.	Journal of general and family medicine	2026-Sep	42707924
186	Expanded detection of canine enteric viruses in UK dogs with diarrhoea.	Microbial genomics	2026-Sep	42709036
187	Identifying fate-determining transcription factors with single-cell omics.	Trends in genetics : TIG	2026-Sep	42242982
188	The establishment of prostate-specific, SKP2 humanized mice by CRISPR knock-in method reveals neoplastic initiation and microenvironmental reprogramming.	Oncogene	2026-Sep	42538409
189	Single-nucleotide transcription start sites profiling via Nascent Strand-Specific RNA sequencing uncovers IFN- γ -induced promoter dynamics.	Journal of genetics and genomics = Yi ch	2026-Sep	41866111
190	Volumetric DNA microscopy for mapping spatial transcriptomes in three dimensions.	Nature protocols	2026-Sep	41735501
191	Alignment-free integration of single-nucleus ATAC-seq across species with sPYce.	Nature ecology & evolution	2026-Sep	42231007
192	Full-length single-cell spatial transcriptomics reveals spatial and cell-type-specific transcript isoforms in the primate brain.	Nature methods	2026-Sep	42498883
193	Scalable joint non-negative matrix factorization for paired single cell gene expression and chromatin accessibility data.	NAR genomics and bioinformatics	2026-Sep	42694579
194	A Step-by-Step Guide to Successful Multiparametric Microbiota Flow Cytometry.	Current protocols	2026-Sep	42696306
195	Label-free, single-cell-precise, and monomeric-unit-resolved monitoring of biopolymer fermentation by ramanomics.	Trends in biotechnology	2026-Sep	41966920
196	TissuStamp: a novel high-throughput tissue transfer workflow for FFPE spatial biology assays.	Journal of histotechnology	2026-Sep	42011599
197	Interpretable multi-omics integration across mixed-order tensors with MANTRA.	Molecular systems biology	2026-Sep	42315933
198	An open-source pipeline for longitudinal single-cell tracking and cell-cycle/migration coupling analysis for neurotherapeutic screening.	Neuroprotection (Chichester, England)	2026-Sep	42499344
199	Clinical impact of metagenomic next-generation sequencing for pathogen identification and guided therapy in pediatric intensive care unit patients with severe pulmonary infections.	Microbiology spectrum	2026-Sep	42474199
200	Comparative metagenomic assessment of Illumina-compatible library preparation methods, short-read lengths, and PacBio HiFi sequencing reveals differences in microbial and functiona	Microbiology spectrum	2026-Sep	42505127
201	Metaviromic profiling of mosquito excreta using superhydrophobic collection devices expands the known RNA virome of North America.	Microbiology spectrum	2026-Sep	42517626
202	Metagenomic next-generation sequencing for tuberculosis diagnosis: enhanced performance and cost-effectiveness.	Microbiology spectrum	2026-Sep	42523101
203	Developing mouse inhibitory neuron single-cell transcriptomes reveal distinct modes of cell-type diversification.	Nature neuroscience	2026-Sep	42547805
204	Comparative evaluation of probe-capture and conventional metagenomic sequencing across multiple clinical sample types, with analysis of paired bronchoalveolar lavage fluid and bloo	Microbiology spectrum	2026-Sep	42549916

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205	SANNO: A Graph-Transformer Enhanced Optimal Transport Tool for Spatial Transcriptomic Annotation.	Interdisciplinary sciences, computaciona	2026-Sep	40789829
206	DEAPLOG: Differential Expression Analysis and Pseudo-Temporal Locating and Ordering of Genes in Single-Cell Transcriptomic Data.	Interdisciplinary sciences, computaciona	2026-Sep	41118050
207	DiTSim: A Diffusion-Transformers Based Single-Cell ATAC-seq Data Simulator.	Interdisciplinary sciences, computaciona	2026-Sep	41120648
208	A Sparse Constrained Optimization Method for Resolving Coincident Single-Cell Events in Microfluidic-Based Impedance Sensing.	IEEE transactions on bio-medical enginee	2026-Sep	41385424
209	Whole-genome sequencing identifies genetic diversity and adaptive signatures of hypoxia and ultraviolet radiation in Chinese chickens.	Journal of advanced research	2026-Sep	41443473
210	Mechanobiological Ultrasound Simulation Reveals Suppression of Epithelial-to-Mesenchymal Transition and Stemness Programs in Colorectal Cancer.	Cancer biotherapy & radiopharmaceuti	2026-Sep	41742663
211	Transcriptomic signatures reveal systemic adaptations and immune modulation in response to training and competitive racing in horses.	Equine veterinary journal	2026-Sep	41793277
212	Genome-wide association study reveals two novel genetic loci associated with chronic lung allograft dysfunction.	The Journal of heart and lung transplant	2026-Sep	41864285
213	Precise capture of heterogeneous microscale targets using an integrated spherical vortex acoustic tweezer.	Ultrasonics	2026-Sep	41932047
214	A novel classification system based on cheese microbial profiles for the assessment of cheese typicity.	Food microbiology	2026-Sep	41963033
215	The impact of clinical metagenomic testing on patient management: facts versus fantasy.	The Lancet. Infectious diseases	2026-Sep	42030968
216	Rapid species-level discrimination of pulmonary TB and NTM by metagenomic next-generation sequencing with concurrent respiratory microbiome profiling.	Diagnostic microbiology and infectious d	2026-Sep	42066541
217	From culture to metagenomics: A paradigm shift in diagnosing infective endocarditis.	Diagnostic microbiology and infectious d	2026-Sep	42085838
218	A novel method to sort and enrich sensory neurons.	Journal of neuroscience methods	2026-Sep	42097460
219	TEAMSTER: End-to-end pipeline for generation, processing, and automated quantitative image analysis of 3D tumour spheroids for nanobiology.	Methods (San Diego, Calif.)	2026-Sep	42102983
220	Late-window oxygen pulsing unlocks lignin-carbohydrate shielding and enhances fiber deconstruction during maize stover fermentation.	Bioresource technology	2026-Sep	42119744
221	The zone of calcified cartilage: A human explant culture model and a proof-of-concept transcriptomic study of 3D laser-cut interface tissue.	Osteoarthritis and cartilage	2026-Sep	42128199
222	Bisphenol A induces osteoporosis by targeting LAMA4 and OLR1: Novel insights into environmental bone toxicity.	Toxicology	2026-Sep	42128337
223	Macrophage reprogramming nodes for bone repair identified by single-cell and spatial omics.	Bone	2026-Sep	42142794
224	Antimicrobial Activity of Eugenol Against NDM-Producing Escherichia coli: An In Vitro and In Vivo Study.	Microbial drug resistance (Larchmont, N.	2026-Sep	42165803

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225	Insights From Spatiality: Accelerating Pharmaceutical Research Using Mass Spectrometry Imaging.	Medicinal research reviews	2026-Sep	42179332
226	TFRC-mediated immune exclusion as a therapeutic vulnerability in cervical cancer: A comprehensive analysis based on the cancer immunoediting process.	Cancer genetics	2026-Sep	42202548
227	Cell Type Prediction for Single-Cell RNA Sequencing Utilizing Unsupervised Domain Adaptation and Semi-Supervised Learning.	Journal of computational biology : a jou	2026-Sep	42267961
228	Cas9-PALB2 fusion protein enhances CRISPR/Cas9 mediated gene knock-in efficiency.	Journal of bioscience and bioengineering	2026-Sep	42276945
229	Diagnostic performance and clinical impact of metagenomic next-generation sequencing in 841 patients with suspected lower respiratory tract infections: A 4-year retrospective study	International journal of infectious dise	2026-Sep	42288243
230	Automated method for determining the zeta potential of red blood cells via motion tracking in microelectrophoresis.	Biochemistry and biophysics reports	2026-Sep	42292695
231	GeneSEA Explorer: An R Shiny Tool for Differential Gene Expression Analysis With Shannon's Entropy Aggregation.	Biotechnology and bioengineering	2026-Sep	42296430
232	Touching the cell without contact: a comprehensive review of scanning ion conductance microscopy methodologies for advanced subcellular mechanical imaging.	Micron (Oxford, England : 1993)	2026-Sep	42308801
233	Identifying breast cancer subtypes and exploring spatial expression patterns of the key subtype-specific gene based on pathological images, single-cell sequencing, and spatial tran	Breast cancer (Tokyo, Japan)	2026-Sep	42310259
234	A blood transcriptomic signature anchored to central nervous system pathology enables noninvasive detection of multiple sclerosis.	Neurobiology of disease	2026-Sep	42331233
235	Diagnostic Performance and Cost-Effectiveness of BALF mNGS in Older Adults with Pulmonary Infections.	Infectious diseases and therapy	2026-Sep	42360629
236	Application value and challenges associated with plasma cell-free DNA metagenomic sequencing technology in the diagnosis of infections in patients with hematological disorders.	Blood science (Baltimore, Md.)	2026-Sep	42367641
237	Democratized single-cell proteomics resolves cell state heterogeneity in skin tumors.	Life science alliance	2026-Sep	42373542
238	Sleep Deprivation and Neuronal Hyperexcitation Share Transcriptomic Signatures.	Neuropsychopharmacology reports	2026-Sep	42380019
239	Single-cell and machine learning-based neural regulation signature for prognosis prediction and immunotherapy response in lung adenocarcinoma.	Translational oncology	2026-Sep	42391672
240	scCLIP: A contrastive masked-reconstruction framework for paired single-cell multi-omics integration.	Journal of biomedical informatics	2026-Sep	42419494
241	Molecular characterization of cell dynamics during osteosarcoma progression.	Translational oncology	2026-Sep	42424801
242	Integrated machine learning framework identifies EPSTI1 as a key diagnostic biomarker for Sjögren's disease: multi-cohort transcriptomic validation and single-cell characterization	Clinical rheumatology	2026-Sep	42429909
243	A hybrid machine learning framework with two-step feature selection for identifying key biomarkers and drug targets in monkeypox.	Biochemistry and biophysics reports	2026-Sep	42434339

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244	Chromatin accessibility of the jejunum in two high-yielding laying hen strains under divergent mineral phosphorus supply during the transition to egg laying.	Animal nutrition (Zhongguo xu mu shou yi	2026-Sep	42438676
245	A systematic benchmark of bioinformatics methods for single-cell and spatial RNA-seq nanopore long reads data.	NAR genomics and bioinformatics	2026-Sep	42441075
246	Multi-omics analysis of arginine metabolism in ovarian cancer: A prognostic signature and GTF2F2-driven stromal remodeling.	Translational oncology	2026-Sep	42442222
247	Navigating Human Astrocyte Differentiation: Direct and Rapid One-Step Differentiation of Induced Pluripotent Stem Cells to Functional Astrocytes Supporting Neuronal Network Develop	Glia	2026-Sep	42452972
248	Sarand: exploring antimicrobial resistance gene neighbourhoods in complex metagenomic assembly graphs.	NAR genomics and bioinformatics	2026-Sep	42454225
249	Chronic prosthetic joint infection caused by Coxiella burnetii diagnosed by metagenomic next-generation sequencing: A case report and literature review.	Journal of infection and public health	2026-Sep	42456224
250	Establishment of a new germ-free Spodoptera frugiperda model to explore the gut microbiota on larval, pupal development and adult reproduction.	Journal of insect physiology	2026-Sep	42462808
251	Single-cell transcriptomics decodes the immunological landscape of thyroid cancer: Implications for immunotherapeutic targeting and precision oncology.	Critical reviews in oncology/hematology	2026-Sep	42463025
252	scDFVA: Single-Cell Deep Clustering by Fusing Variational Graph Attention Autoencoder and ZINB-Based Autoencoder.	Journal of computational biology : a jou	2026-Sep	42478602
253	Identification and functional validation of lipid droplet-associated prognostic biomarkers in breast cancer via integrative multi-omics and machine learning approaches.	International journal of clinical oncolo	2026-Sep	42484744
254	metaWEPP: leveraging biobank-scale intra-species phylogenies for near-haplotype resolution in metagenomic analysis.	NAR genomics and bioinformatics	2026-Sep	42488460
255	Multimodal features and prognostic risk assessment in locally advanced gastric cancer patients following neoadjuvant therapy based on machine learning algorithms: a multicenter stu	Gastric cancer : official journal of the	2026-Sep	42490033
256	Integrative single-cell and machine learning analysis identifies a tumor doubling time-related prognostic signature and therapeutic targets in head and neck squamous cell carcinoma	Translational oncology	2026-Sep	42492364
257	RNA-seq Molecular Risk Classification Refines Prognostic Stratification in Childhood B-Cell Acute Lymphoblastic Leukemia Treated With the CCG-ALL-2020 Protocol: A Real-World Cohor	Pediatric blood & cancer	2026-Sep	42496614
258	Gene-Based Clustering Identifies QSOX1 and IL1RAP as Biomarkers of Metabolic Dysfunction-Associated Steatotic Liver Disease.	Liver international : official journal o	2026-Sep	42522643
259	SuSha: A multi-model ensemble learning framework for predicting microbial salinity adaptation.	Engineering microbiology	2026-Sep	42597889
260	LivAge: An Online Aging Clock for Murine Transcriptomic Age Estimation.	Aging cell	2026-Sep	42629583
261	Network Model to Predict Age-Related Transcriptional Reprogramming.	Aging cell	2026-Sep	42631664
262	From Single Cells to Diagnosis: Proteomics Technologies in the Multi-Omics Landscape of Rare and Mitochondrial Diseases.	Journal of inherited metabolic disease	2026-Sep	42638396

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263	Unraveling the pathogenic mechanisms of osteoarthritis and obesity: An integration of GWAS, cellular specificity, and spatial transcriptomics.	Osteoarthritis and cartilage open	2026-Sep	42656980
264	Massively Parallel Profiling of Single-Cell RNA Dynamics Using Well-TEMP-seq.	Current protocols	2026-Sep	42671929
265	Feto-Maternal Microchimerism and the Brain: Mechanisms, Neurological Implications, and Translational Perspectives.	American journal of reproductive immunol	2026-Sep	42672076
266	From rules to foundation models: a comprehensive review of machine learning approaches for siRNA design.	NAR genomics and bioinformatics	2026-Sep	42676509
267	Stratifying lung adenocarcinoma: a novel prognostic model based on mitochondrial outer membrane permeabilization activity.	3 Biotech	2026-Oct	42745950
268	Diagnostic value of metagenomic next-generation sequencing for bacterial and fungal detection and its role in antimicrobial therapy adjustment in critically ill patients with non-r	Annals of medicine	2026-Dec	42806854
269	MERTK-related engulfment of norepinephrine neuronal presynaptic membrane by astrocytes following acute TBI and potentiation effect of peripheral nerve modulation.	Annals of medicine	2026-Dec	42802576
270	Circadian reprogramming of inflammation and metabolism in chronic kidney disease.	Renal failure	2026-Dec	42703061
271	Construction of molecular signatures based on the co-expression network of NECSO-related gene TRPM4 and its prognostic value in hepatocellular carcinoma.	Journal of gastrointestinal oncology	2026-Aug-3	42703320
272	GAMclust: identification of regulated metabolic modules in bulk, single cell and spatial gene expression data.	Bioinformatics (Oxford, England)	2026-Aug-3	42633560
273	Pesci: fast and user-friendly software to compare single-cell gene expression across species.	Bioinformatics (Oxford, England)	2026-Aug-3	42616853
274	Modtector: ultra-fast modification signal mining on mapped sequencing reads.	Bioinformatics (Oxford, England)	2026-Aug-3	42625378
275	Integration of artificial intelligence and multi-omics for precision medicine.	Functional & integrative genomics	2026-Aug-3	42669717
276	Integrated pan-cancer analysis reveals a cancer-associated fibroblast oxidative stress response signature predicting immunotherapy response and prognosis.	Apoptosis : an international journal on	2026-Aug-3	42671485
277	Identification of iron and zinc responsive TonB-dependent transporters in Pseudomonas aeruginosa.	Biometals : an international journal on	2026-Aug-3	42671697
278	An integrated reference atlas of human skeletal muscle.	EBioMedicine	2026-Aug-3	42673766
279	The multifaceted role of atomic force microscopy in bacteriology.	Trends in microbiology	2026-Aug-3	42674874
280	Sulfonated cobalt phthalocyanine coupled with poly(dopamine-co-sulfobetaine methacrylate) for single-cell electrochemical monitoring of glutathione.	Biosensors & bioelectronics	2026-Aug-2	42679777
281	A Protocol for Multivariate Data Visualization and Pseudotime Modeling for Analysis of Disease Trajectories Detected by Mass Spectrometry Imaging.	Journal of the American Society for Mass	2026-Aug-2	42683911
282	Placental transcriptomics identifies a candidate HLA-DQA2-FGL2 immune signature in gestational diabetes mellitus.	Placenta	2026-Aug-2	42673706

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283	Benchmarking cell type annotation in spatial transcriptomics: resolving cellular hierarchies, biological fidelity, and dynamic cell states.	Research square	2026-Aug-2	42687963
284	An <i>Aspergillus luchuensis</i> isolated from a patient with hemoptysis insights from a comprehensive genome-based analysis: Case report.	Medicine	2026-Aug-2	42675750
285	High-Dimensional SERS Mapping of Single Circulating Tumor Cells Deciphers the Phenotypic Landscape and Stratifies Metastatic Risk in Pancreatic Cancer.	ACS sensors	2026-Aug-2	42676027
286	Maternal immune gene expression trajectories and dynamic genetic regulation throughout pregnancy	medrxiv preprint	2026-09-25	10.64898/2026.09.22.26363644
287	Direct Pan-Cancer Multi-Omic Analysis of Radiotherapy Response Reveals Coding and Regulatory Genomic Variation, and Extracellular Adaptive Programs Underlying Radioresistance	medrxiv preprint	2026-09-25	10.64898/2026.09.23.26363823
288	Methylation-driven Cancer Genes and Methylation Profiling in Glioma: A Comparative Study between East Asian and non-Hispanic White Populations	medrxiv preprint	2026-09-25	10.64898/2026.08.14.26360452
289	A Community-Driven Single-Cell PBMC Reference Integrating Landmark Datasets Spanning Health and Disease	biorxiv preprint	2026-09-25	10.64898/2026.09.21.749940
290	Spatially resolved contrastive analysis of perturbation-driven microenvironmental heterogeneity across tissues and conditions	biorxiv preprint	2026-09-25	10.64898/2025.12.08.693051
291	Pruning the Search, Not the Signal: Adaptive-Banding Needleman-Wunsch Sequence Alignment via Protein Language Model Confidence	biorxiv preprint	2026-09-25	10.64898/2026.08.26.747234
292	Disruption of a Structural Niche for Otoconia Maintenance May Underlie Common Vestibular Disorders	biorxiv preprint	2026-09-25	10.64898/2026.09.16.752180
293	Wastewater metagenomic sequencing enables broad pathogen and resistome monitoring in Lagos, Nigeria	medrxiv preprint	2026-09-23	10.64898/2026.09.22.26363641
294	A Computational Pipeline for Retinal Capillary Blood Flow Measurement using Adaptive Optics Line Confocal Ophthalmoscopy	biorxiv preprint	2026-09-23	10.64898/2026.09.21.753337
295	ChromBPNet: bias factorized, base-resolution deep learning models of chromatin accessibility reveal cis-regulatory sequence syntax, transcription factor footprints and regulatory v	biorxiv preprint	2026-09-23	10.1101/2024.12.25.630221
296	An NR2F1-dependent retinoic acid network controls retinal specialization in mice and reveals foveal hypoplasia in patients with BBSOAS	biorxiv preprint	2026-09-23	10.64898/2026.09.22.753406
297	Speciesformer learns conserved cellular states for cross-species generative virtual cell modeling	biorxiv preprint	2026-09-23	10.64898/2026.09.22.752128
298	Stromal innervation is prognostic in non-muscle-invasive bladder cancer and predicted by a distinct microenvironmental transcriptomic signature	biorxiv preprint	2026-09-23	10.64898/2026.09.21.751588
299	Lineage-informed factor analysis reveals heritable programs of single-cell gene expression	biorxiv preprint	2026-09-23	10.64898/2026.09.21.753290
300	A gut microbiome-derived risk score is associated with future cancer development	medrxiv preprint	2026-09-15	10.64898/2026.09.09.26362619
301	platpy: A spatial-first framework for multi-layer spatial transcriptomic analysis	biorxiv preprint	2026-09-05	10.64898/2026.05.26.727917

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302	A chromosome-scale genome assembly of the Swiss Lolium multiflorum ecotype Tremona reveals a scalable method to purge spurious duplications	biorxiv preprint	2026-09-05	10.64898/2026.08.18.745395
303	Minimizing time in culture: A prototypic autologous manufacturing workflow for monoclonal iPSC lines within seven weeks	biorxiv preprint	2026-09-05	10.64898/2026.08.04.741960
304	Timing of metabolomics-driven supplementation strategies affects protein expression in E. coli-based cell-free expression systems	biorxiv preprint	2026-08-27	10.64898/2026.08.26.746766
305	Fusion-derived phospho-neoepitopes define a prioritized candidate neoantigen repertoire in MASLD-HCC	biorxiv preprint	2026-08-27	10.64898/2026.08.26.747243
306	GABAergic Circuit Activation Induces a Therapeutically Responsive State for anti-PD-L1 Immunotherapy in Glioblastoma	biorxiv preprint	2026-08-27	10.64898/2026.08.26.747200
307	Glutamatergic Neuron-Meningioma Synapse Interaction Promotes Brain-Invasive Tumor Growth	biorxiv preprint	2026-08-27	10.64898/2026.08.26.747240
308	The Neural Impact Score benchmarks drugs in Multi-Region Brain Organoids	biorxiv preprint	2026-08-27	10.64898/2026.08.26.746777
309	Diagnostic Performance of Bronchoalveolar Lavage Fluid Metagenomic Next - generation Sequencing versus Conventional Microbiological Tests in Immunocompromised and Immunocompetent Pat	Infection and drug resistance	2026	42801158
310	scLTF: A self-training clustering framework for large-scale single-cell RNA-Seq data.	PloS one	2026	42784630
311	Integrative transcriptomic analysis of peripheral blood identifies NETosis-associated programs and a stratified adaptive immune suppression pattern in severe acute pancreatitis.	PloS one	2026	42789536
312	Integrative computational analysis of public fecal lipidomics and transcriptomics datasets suggests a candidate association between the COX-2 pathway and CE(20:4) in colorectal ade	PloS one	2026	42789583
313	Cytotoxic T-cell exhaustion analyses by in situ single-cell immunofluorescence in relation to colorectal cancer patient age, tissue bacteria and mortality.	BMJ oncology	2026	42781492
314	Identification of key molecular targets in nicotine-induced spontaneous abortion through network toxicology and multi-omics integration.	Tobacco induced diseases	2026	42774927
315	Deciphering the Immune Landscape of Abdominal Aortic Aneurysm: A Machine Learning and Cross-Species Validated Multi-Omics Approach.	Journal of inflammation research	2026	42769759
316	Current Concepts in Periprosthetic Joint Infection: Modern Biomarkers, Microbiome Insights, Molecular Diagnostics, and Emerging Prevention Strategies.	Orthopedic research and reviews	2026	42746583
317	From in silico prediction to experimental validation: Identification of drugs and novel synergistic combinations that inhibit growth of inflammatory breast cancer cells.	PloS one	2026	42748134
318	Identification and Validation of a Two-Gene NK Cell-Related Risk Model for COPD: Integration of Single-Cell and Bulk RNA-Seq Analysis.	International journal of chronic obstructive pulmonary disease	2026	42741419
319	The dental pulp as a high-resolution model for neurovascular niche biology.	Journal of tissue engineering	2026	42718951

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320	Fedflow: cloud orchestration for federated learning with the FeatureCloud platform.	Bioinformatics advances	2026	42725323
321	Multi-omics mapping of PSC genetic risk to a high TWAS-active JAML+ lipid-associated macrophage program: bridging single-cell heterogeneity, spatial fibrotic niches, and machine le	Frontiers in cell and developmental biol	2026	42707798
322	Diagnostic and Therapeutic Impact of Metagenomic Next-Generation Sequencing in Tuberculous Osteoarticular Infections with Negative or Confounding Conventional Cultures.	Infection and drug resistance	2026	42699249
323	Immune-Like Malignant Epithelial Programs Shape Tumor-Immune Interactions and Inform Prognostic Stratification in Lung Adenocarcinoma.	BioFactors (Oxford, England)	2026	42702944
324	Potentially Deleterious Nonsynonymous Single Nucleotide Polymorphisms (nsSNPs) in the Human MCPH1 Gene: Systematic In Silico Predictions and Implications for Structure and Function	Human mutation	2026	42694451
325	Selenium-Doped Calcium Hydroxide Nanoparticles Inhibit Osteoclasts and Promote Osteogenesis for Osteoporosis Treatment.	International journal of nanomedicine	2026	42689238
326	High AUROC can mask decision failure in sepsis transcriptomic classifiers: Preprocessing stability outweighs post hoc calibration across cohorts.	PloS one	2026	42691061
327	PRKCB Mediates Ferroptosis-Immune Crosstalk in Acute Lung Injury: Insights from Integrated Single-Cell Transcriptomics.	Journal of inflammation research	2026	42683062
328	Constitutional Ring Chromosomes in Greek Pediatric Patients: A 50-year Single-center Cytogenetic Study.	In vivo (Athens, Greece)	2026	42665402
329	Multicohort Construction, Immune Landscape Analysis, and PCOLCE2 Functional Validation of an Inflammation-Related Prognostic Model in Colorectal Cancer.	BioFactors (Oxford, England)	2026	42666044

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