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Biological Repositories as Reproducibility Infrastructure: Enabling Reliable Science in the Biosciences

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Column Editor's Note: *For many of the articles in the Reinforcing Reproducibility and Replicability column, we have focused on social sciences, where reproducibility may be subject to concerns about data availability, computational tractability, or the accessibility of data and those computational resources. We may be concerned with data disappearing when governments take down websites or when a grant ends, or with how to assess reproducibility when the data are locked in secure rooms (see Pérignon, 2024). However, social scientists do not usually worry about what happens when a power outage affects the refrigerator holding thousands of biological samples, or how hot a furnace used to create a new alloy was. In this article, Chonnettia Jones introduces us to biological repositories, expanding this column into spaces (hot or cold) that have not been topics in the past.*

Keywords: biorepositories, reproducibility, research materials

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Introduction

Reproducibility is central to scientific progress. However, the physical materials that underpin experiments in the biological and biomedical sciences ('biosciences') often receive less scrutiny and priority than data or code. This oversight creates barriers to repeating, extending, or validating research findings. Reliable repetition and the extension of research findings depend on acquiring the original research materials and verified information about them.

Two concepts in scientific research are worth clarifying at the start (National Academies of Sciences, Engineering, and Medicine, 2019):

- **Reproducibility** refers to obtaining consistent results when a research study is repeated under the same documented conditions, including the use of the same or equivalent materials, methods, and protocols. It answers the question: *Can someone else achieve the same results if they follow the original procedures exactly*?
- **Replication** involves independent confirmation of a scientific claim using new data, material samples, or study designs. It asks: *Does the finding hold true when tested in a different context or with new materials?*

Different disciplines use these terms differently; here their definitions are foregrounded on the role of physical materials in the reproducibility of scientific research. While both are essential for scientific progress, this article focuses primarily on reproducibility—the ability to repeat and validate research findings using similar or equivalent research materials and experimental conditions—while not discounting the complementary role of replication in advancing scientific knowledge.

With this distinction in mind, this article explains how biological repositories, which are defined later more precisely, address the practical challenges of reproducibility in the biosciences, and why robust infrastructure for research materials is essential for reliable science. While this article draws primarily on examples from the biosciences, the underlying challenges and the practices that biological repositories demonstrate could extend to any field where experimental tools or interventions shape outcomes.

The Essential Role of Research Materials in Reproducibility

The biosciences have made meaningful progress in sharing data sets and code, but biological conclusions often rest on physical research objects (materials) that are harder to describe, preserve, and reacquire. A computational workflow can be perfectly documented, but the experimental workflow is difficult to reproduce if the research materials are ambiguous, unavailable, or variable from one lab to the next.

The FAIR principles (Findable, Accessible, Interoperable, Reusable; Wilkinson et al., 2016) are a useful framework for the reproducibility of digital objects such as data sets and code, but their fit for research materials is limited for multiple reasons. First, biological materials introduce variables (genetic drift, physical handling conditions, and accidental contamination) that digital objects do not. Second, an identifier for a biological material refers to a *record* about the material (not the material itself) and its behavior under specific conditions. Third, interoperability provides no assurance that a material will behave exactly the same across experiments, or across labs. For these reasons, biological materials used in follow-on experiments are considered to be *similar* or *equivalent*, but often not identical.

The unifying principle, however, is that biological research materials should be findable, well-characterized, and well-documented to support their use from lab to lab, and from experiment to experiment. Biological repositories are integral in this process by strengthening the findability and reuse of materials in research, bridging the gap between published research and the reproducibility of its results. The same is true for other repositories that hold physical materials, such as the national archives that store, manage, and preserve nonbiological, inorganic, and synthetic materials for planetary, industrial, and archaeological research.

Challenges to Reproducibility in the Biosciences

Achieving reproducibility in the biosciences is uniquely challenging because many experiments involve complex biological materials. Examples include cell lines, plasmids, and multicellular organisms whose characteristics can vary with their source of origin, handling, and experimental conditions. The difficulty of reproducing research findings is well documented, with many studies reporting substantial barriers to repeating and confirming the validity of published results (Errington et al., 2021).

One major obstacle to reproducibility is insufficient description and standardization of research materials. The methods sections in publications often lack the necessary detail to uniquely identify or reliably recreate a biological material. This omission creates ambiguity about what was used in an experiment, making it difficult for others to repeat the work with confidence. Adopting standardized practices for transparency and openness, such as those outlined in the TOP Guidelines (Transparency and Openness Promotion Guidelines; policy framework for increasing the verifiability of research claims), is essential for improving reproducibility and enabling others to reliably repeat experiments or extend previous research findings (Nosek et al., 2015).

Operational barriers also pose significant challenges. The process of sharing materials can be slow, costly, and complicated by administrative or regulatory requirements and logistical challenges. Moreover, informal or ad hoc transfer of materials between labs frequently breaks down when staff turnover occurs or labs close, further hindering the accessibility of research materials.

Without independent checks, mistakes such as incorrect genetic sequences, contamination, or mislabeled materials can spread from lab to lab and become embedded in the scientific literature, undermining the reliability of future research (Kahn et al., 2024; Liu et al., 2019; Souren et al., 2022). HeLa cells, one of the most commonly used cell lines in biomedical research, exhibit significant genomic variability across labs (Liu et al., 2019). Contamination by bacteria called mycoplasma is a persistent problem in laboratory settings that confounds experimental results if undetected.

Inadequate provenance tracking of where a material came from and how it was handled exacerbates these problems. When materials are shared informally, proper documentation of their origin and changes over time is often neglected. This lack of traceability makes it challenging to monitor material drift, experimental manipulations, and version history, all of which are vital for verification or validation required for reproducibility.

Biorepositories exist to reduce these failure modes at scale by making identification, verification, preservation, and access part of the default research workflow rather than an afterthought.

How Biorepositories Address Reproducibility Challenges in the Biosciences

Biorepositories are organizations that collect, verify, store, and distribute research materials. In practice, they function as a reliability layer for the biosciences: they preserve (or archive) materials over time, curate essential metadata, and provide stable identifiers that link a material to its publication.

Useful examples of these practices are held by long-standing biorepositories such as the American Type Culture Collection (ATCC), a nonprofit that maintains and distributes authenticated cell lines and microbial strains to researchers worldwide. Cheng and Bradford (2025) explain that ATCC's impact goes well beyond shipping materials: they support reproducibility by ensuring global access to well-characterized reference materials and by advancing standardized best practices for authentication, cryopreservation, maintenance, and use of cell lines.

Different biorepositories specialize in different material classes such as those listed in Table 1, but the reproducibility principles are the same: make materials findable, identifiable, accessible, and reliably reusable.

Table 1. Representative biorepositories and the material types they specialize in.

Material Type	Representative Repositories
Cell lines	American Type Culture Collection (ATCC), Coriell Institute for Medical Research, Yeast Genetic Stock Center
Plasmids	Addgene, DNASU Plasmid Repository at Arizona State University
Organisms	Mutant Mouse Resource & Research Centers, Bloomington Drosophila Stock Center, Arabidopsis Biological Resource Center
Antibodies	Developmental Studies Hybridoma Bank
Clinical samples	NIH NeuroBioBank, UK Biobank
Multiple types	RIKEN BioResource Research Center, CancerTools.org

Reproducibility Mechanisms That Biorepositories Make Routine

Biorepositories improve reproducibility by turning materials into first-class research objects with a durable provenance trail. While the application of broader reproducibility guidance across disciplines (Vilhuber et al., 2023) improves the reliability of downstream work, it does not, on its own, prove that a biological research claim is correct.

Biorepositories deploy five mechanisms to support reproducibility in scientific research. First, they capture structured provenance and metadata—genetic or protein sequence data, strain background, depositor identity, and experimental conditions—that would otherwise remain informal lab knowledge. Second, they standardize quality checks for common failure modes (mislabeled samples, incorrect sequences, contamination) and make the results of those checks visible to users. Third, by supporting deposit of the material prior to publication, they enable earlier error detection, before discrepancies become embedded in the literature. Fourth, stable identifiers such as accession numbers and Research Resource Identifiers (RRIDs) create a practical bridge between a paper and the material used, making materials findable and citable (Bandrowski et al., 2016). Fifth, even with centralized checks, responsible reuse requires independent verification; good biorepositories provide guidance on what users should confirm in their own experimental context.

What does a biorepository provide?

- A stable identifier that can be cited (biorepository ID and/or Research Resource Identifier (RRID))
- Structured metadata and provenance (what it is, where it came from, key features)
- A visible quality signal (for example, sequence verification or authentication)
- Clear reuse guidance (recommended citation text and core handling/verification steps)

Addgene: An Exemplary Biorepository for Reproducibility

Addgene was founded in response to persistent, widely recognized barriers researchers faced in accessing DNA reagents called plasmids. Today, its mission remains to enable the scientific community to acquire high-quality, curated, and authenticated plasmids and materials derived from plasmids. Addgene provides robust material identity verification and tracking (Figures 1 and 2), comprehensive documentation, and durable records accessible across laboratories and over time (Abitua & Kamens, 2019; Kamens, 2014). Quality control ensures genetic sequences of these materials are rigorously verified and discrepancies transparently communicated. Systematic quality control is indispensable for biorepositories like Addgene to function effectively.

Persistent identifiers, such as Addgene accession numbers and RRIDs, help researchers locate the exact material referenced in a publication. Identifier adoption increases when these are integrated directly into biorepository ordering and citation workflows, rather than left to journal policies alone (Piekniewska et al., 2025).

Addgene also aggregates essential metadata, sequence maps, depositor notes, and links to relevant publications into a single material record. This allows researchers to navigate from a paper to the original material, view the verified sequence, and reuse the material, reducing troubleshooting and enabling reproducibility supported by well-annotated resources.

Biorepository practices can support reproducibility earlier in the research lifecycle. Authentication, provenance documentation, and standardized metadata should be integrated when materials are first sourced and incorporated into experimental design and not treated as tasks at the publication stage. Supporting this, biorepositories like Addgene provide depositor checklists and pre-submission authentication protocols. Pre-publication deposition and standardized citation language allows authors to reference stable material identifiers in methods sections of papers to accelerate independent validation.

Experiment-specific validation remains essential even where biorepositories minimize avoidable errors. Biorepositories help to ensure that observed differences in results reflect biological variables or methodological choices, not material inconsistencies. Addgene's Data Hub extends this further by inviting independent scientists to share additional experimental data on materials used in their labs, supporting reproducibility by other scientists.



Figure 1. Each barcoded vial contains bacteria carrying a unique DNA sample called a plasmid, precisely tracked through standardized verification, storage, and distribution workflows. Processes like this help researchers around the world work with well-characterized and documented materials, supporting reproducible science. Credit: Matt McKee Photography for Addgene.



Figure 2. Barcoded samples are stored frozen in organized racks inside −80 °C freezers. Redundant storage and careful tracking ensure that each biological material remains secure, findable, and accessible for researchers worldwide. Credit: Matt McKee Photography for Addgene.

Lessons From Open-Source Antibodies

Addgene illustrates how biorepository principles work for sequence-defined DNA reagents, but some material classes pose even more difficult reproducibility challenges. For example, the issue of antibody reproducibility has recently come under intense public scrutiny (Else, 2026). Antibodies are naturally occurring and highly specialized proteins, typically purified from animal serum, that interact with target molecules with exquisite specificity, making them widely used tools in biomedical research. However, they are also among the most variable and least standardized. Their properties are poorly characterized and can vary significantly across applications, suppliers, and labs, making findings difficult to replicate and validate. Community-led efforts have emphasized that rigorous antibody characterization is essential for reproducibility (Ayoubi et al., 2025; Kahn et al., 2024; Rego et al., 2025).

On the contrary, 'open-source antibodies' are produced in the lab, and have fully characterized genetic sequences enabling standardized production, rigorous characterization, and reliable reproduction over time. They directly address long-standing issues of variability and poor documentation that have hindered reliable antibody use in the biosciences. By shifting from traditional lot-dependent, poorly characterized antibodies to sequence-defined, open-source antibodies, the research community gains

access to more stable and reliable tools. This approach supports reproducibility by ensuring that reagents are well-documented, traceable, and accessible for future studies.

Third-party validation of antibodies is essential. Platforms such as YCharOS use consensus methods like knockout-based characterization to verify antibody function. These validation reports help researchers select appropriate antibodies and reduce selective reporting (Ayoubi et al., 2025). Linking antibodies to persistent identifiers such as RRIDs and making validation data publicly available supports discoverability, traceability, and equitable access (Bandrowski et al., 2016; Rego et al., 2025). Therefore, the same general biorepository principles can be usefully applied to this and any other challenging material class.

Limitations and Future Directions for Biorepositories

While biorepositories play a pivotal role in enhancing reproducibility, they continue to face challenges. Not all research materials, like specialized or newly developed materials, are adequately supported, because of the absence of dedicated repositories or standardized deposition practices. This gap can hinder access to and validation of these custom materials.

Sustaining biorepositories also depends on stable funding; many rely on grants, donations, or service fees. Less visible costs, but equally important, are the costs depositing researchers carry in preparing, shipping, and time coordinating with repository staff; these costs rarely appear as explicit line items in grant proposals or data management plans. These unplanned costs become barriers, particularly for under-resourced labs. Biorepository deposition should be treated as a planned, budgeted activity from the outset, not an afterthought. Funders and institutions can act by expecting deposition costs to appear in research budgets, building biorepository deposition timelines into award milestones, and recognizing that material sharing, like data sharing, requires real resources.

The rapid evolution of science means biorepositories must constantly adapt to manage increasingly complex materials, which often require new protocols, expertise, and infrastructure. Disparities in metadata standards, persistent identifiers, and reporting practices across biorepositories complicate discoverability and integration, impeding efforts to track and share materials efficiently.

Finally, cultural and incentive gaps remain persistent barriers. Researchers may not have sufficient motivation, training, or time to deposit their materials with a biological repository or provide sufficient information using standardized practices. As a result, valuable materials remain inaccessible or poorly documented, impeding progress toward more reproducible research.

To address these challenges, several promising strategies are emerging. Expanding biorepository scope to contain underrepresented materials, pursuing hybrid funding models and public–private partnerships, and leveraging technologies such as automation and AI for curation can all bolster long-term stability and efficiency. International collaboration is vital for harmonizing standards, reducing access barriers, and

fostering equitable sharing. Adopting universal metadata standards and persistent identifiers will support seamless integration with publications and improve discoverability.

The challenges described here are not unique to the biosciences. In any experimental field, reproducibility depends on the well-documented characteristics of the physical tools or procedural interventions that shaped the data, such as a bed net in a public health trial, a calibrated chemical reference standard, or a standardized assessment instrument. Fields like the social sciences and materials science already maintain analogous infrastructure for persistent identifiers, provenance, and verification. Biorepositories offer a working model for how that infrastructure can be built and sustained.

How the Research Community Can Support Reproducibility in the Biosciences

Coordinated actions across the research ecosystem are required to support reproducibility in the biosciences.

Researchers should deposit key materials upon acceptance (or even earlier, when possible), cite them using stable identifiers such as biorepository IDs and RRIDs, and independently verify materials for their specific experimental context before drawing and reporting conclusions.

Funders should require material sharing and their documentation, allocate funding for personnel and infrastructure to support deposition and verification, and recognize materials as durable research outputs rather than as expendables.

Publishers and journals should include RRID and identifier fields in submission systems, require deposition of materials in appropriate biorepositories, enforce reporting standards, and collaborate with biorepositories to provide copy-ready citation guidance that makes compliance easy.

Libraries and open infrastructure providers can also support the reliable use of research materials by supporting discovery mechanisms that link publications to deposited materials and sharing guidelines on effective materials reporting with researchers.

Summary

Reproducibility is a cornerstone of scientific progress, ensuring that discoveries can be verified, built upon, and translated into meaningful advancements. In the biosciences, transparent data and code are necessary but not sufficient; reproducibility also requires reliable infrastructure with reliable access to rigorously characterized research materials. Biorepositories play a pivotal role by archiving and safeguarding materials, meticulously curating provenance and metadata, providing visible indicators of material quality, and sustaining durable records that stand the test of time. Working in collaboration, the research community and biorepositories can uphold the integrity of research by supporting research reproducibility, extending published findings to unlock the full potential of scientific research.

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Preview image credited to Matt McKee Photography for Addgene**.** Description: Close-up of a technician's gloved hand as they inspect a barcoded vial that contains bacteria carrying a unique DNA sample called a plasmid, precisely tracked through standardized verification, storage, and distribution workflows at Addgene's laboratory.

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