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A CRITICAL REVIEW OF MODERN BIOLOGICAL TECHNIQUES IN SCIENCE LABORATORY TECHNOLOGY

[1]**Gloria Hembafan Tiza**
[2]**Atondo Moses Vershima**
[3]**Precious Nnennaya Akpa-Onyeabor**
[4]**Abah Moses**

[1]*Department of Animal Biology,*
Federal University of Technology Minna,
Minna, Nigeria

[2,3,&4]*Department of Science Laboratory and Technology,*
Federal Polytechnic Wannune, Benue State, Nigeria

Abstract

The rapid evolution of biological laboratory technologies is reshaping the interface between theoretical knowledge and practical application in science laboratory technology. This comprehensive literature review synthesizes recent advancements across six interconnected domains: high-throughput automated sample preparation, CRISPR-based molecular diagnostics, microfluidic organ-on-a-chip platforms, multi-omics integration, artificial intelligence (AI)-driven analytical tools, and accelerated evolutionary engineering. Drawing exclusively on peer-reviewed literature published between 2024 and 2026, this review critically evaluates the technological innovations transforming contemporary laboratory practice while identifying persistent challenges in standardization, reproducibility, clinical translation, and workforce preparedness. The analysis reveals that while automation, miniaturization, and AI integration have significantly enhanced analytical throughput, precision, and data interpretation capabilities, the translation of these technologies into routine laboratory workflows remains constrained by infrastructure limitations, interoperability gaps, and the absence of harmonized quality assurance frameworks. Through comparative analysis and critical evaluation of the evidence base, this review provides a framework for understanding the current state of biological laboratory technology and outlines priorities for future research, education, and policy development.

Keywords: *Laboratory automation, CRISPR diagnostics, microfluidics, multi-omics, artificial intelligence, & adaptive laboratory evolution*

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Introduction

Science laboratory technology occupies a critical position at the intersection of fundamental biological discovery and applied diagnostic practice, serving as the essential translational bridge that transforms theoretical insights into actionable outcomes (Li et al., 2026; Chen et al., 2025; Augustine et al., 2025). In recent years, this intermediary role has been challenged by an unprecedented acceleration in technological innovation, necessitating a critical reappraisal of how modern biological techniques are developed, validated, and implemented within laboratory settings.

Traditional laboratory workflows, characterized by manual sample processing, batch-mode analysis, and centralized instrumentation, are increasingly giving way to automated, miniaturized, and integrated platforms that demand new conceptual frameworks and technical competencies (More et al., 2025; Liu et al., 2025). This transformation extends beyond mere technological substitution, representing a fundamental reconceptualization of laboratory practice that requires practitioners to navigate complex intersections of engineering, data science, molecular biology, and regulatory science.

The convergence of multiple technological trajectories has created both opportunities and challenges for the discipline. On one hand, advances in microfluidics, automation, and computational analysis have enabled previously unattainable levels of sensitivity, throughput, and biological insight (Qiu et al., 2026; Wang et al., 2025). On the other hand, the rapid proliferation of new technologies has outpaced the development of standardization frameworks, validation protocols, and educational curricula needed to support their reliable implementation (Declerck et al., 2026; Yang et al., 2025).

This review aims to provide a comprehensive and critical synthesis of recent advancements across key domains of modern biological laboratory technology. The scope encompasses high-throughput automated sample preparation, CRISPR-based molecular diagnostics, microfluidic organ-on-a-chip platforms, multi-omics integration strategies, artificial intelligence applications in laboratory analysis, and accelerated evolutionary engineering approaches. Particular attention is directed toward studies published between 2024 and 2026 that exemplify broader trends in the field. By critically evaluating the evidence base for these technologies, this review seeks to identify not only their transformative potential but also the persistent challenges that constrain their translation from research settings into routine laboratory practice.

High-Throughput Automated Sample Preparation Technologies

Technological Foundations and Evolution

Sample preparation constitutes the initial and often most critical stage in biological analysis, fundamentally determining the overall performance of analytical methods (Chen et al., 2025). However, by guiding substances from disorder to order, sample preparation cannot occur automatically and spontaneously, frequently constituting the rate-limiting step in complex analytical workflows (Li et al., 2026). To improve efficiency and thereby advance analytical performance in terms of selectivity, sensitivity, stability, speed, accuracy, automation, application, and sustainability, a variety of high-performance approaches have been developed in recent years.

Li et al. (2026) provide a comprehensive overview of recent advances in high-throughput automated sample preparation technologies in bioanalysis, emphasizing that automated systems currently demonstrate significant advantages in complex experimental systems involving multi-

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parameter detection and real-time process monitoring. Their analysis encompasses robot-based automated liquid handling systems, solid-phase extraction technology, and microfluidics as the primary technological pillars supporting modern bioanalytical workflows.

Automated Liquid Handling and Solid-Phase Extraction

Robotic liquid handling systems have become the cornerstone of modern bioanalytical laboratories, enabling uninterrupted processing of large sample volumes from preclinical and clinical studies (Li et al., 2026; More et al., 2025). Compared to traditional manual procedures, automated systems reduce expenses, minimize manual errors, facilitate laboratory transfers, and enhance data quality. The authors note that these systems are particularly valuable in regulated environments where documentation and traceability requirements demand rigorous process control. However, Li et al. (2026) also offer a critical perspective on the limitations of current automation technologies. While robotic systems excel at repetitive tasks, they remain less adaptable than human operators when confronted with atypical samples or unanticipated procedural modifications. The optimal balance between automation and human oversight remains an unresolved question, particularly in contexts where sample heterogeneity or analytical complexity requires adaptive decision-making.

Chen et al. (2025) classify recent progress in high-performance sample preparation strategies into four principal categories. First, employing functional materials in sample preparation enables sensitive and selective detection through enhanced analyte enrichment and matrix interference reduction. Second, chemical conversion and biological recognition approaches can further enhance the selectivity and sensitivity of analytical methods through targeted analyte modification or capture. Third, the introduction of additional energy fields can accelerate separation processes, reducing overall analysis time. Fourth, the development of advanced devices allows for automated sample analysis with improved speed and accuracy.

Integration with Downstream Analysis

A significant trend identified across recent literature is the integration of sample preparation with downstream analytical detection. More et al. (2025) critically review automation trends in bioanalysis, noting that online techniques combining sample preparation with analytical measurement are increasingly replacing offline workflows. This integration reduces total analysis time, minimizes sample loss, and improves data integrity by eliminating manual transfer steps. Table 1 provides a comparative summary of automated sample preparation technologies, their applications, advantages, and limitations based on recent systematic evaluations.

Table 1. *Comparison of Automated Sample Preparation Technologies in Bioanalysis*

Technology	Throughput	Sample Volume	Key Applications	Limitations	Representative References
Robotic Liquid Handlers	High (96–1536-well)	0.5–500 µL	Drug discovery, clinical chemistry, PCR setup	High cost, programming complexity, maintenance	Li et al. (2026); More et al. (2025)
Automated Solid-Phase Extraction	Medium–High	50 µL–5 mL	Bioanalysis, proteomics, metabolomics	Cartridge variability, method	Chen et al. (2025)

				development time	
Microfluidic Sample Prep	High (parallelized)	<100 µL	Single-cell analysis, point-of-care	Fabrication complexity, clogging, limited standardization	Qiu et al. (2026); Zhang et al. (2025)
Magnetic Bead-Based Automation	High	10–500 µL	Nucleic acid extraction, immunoprecipitation	Binding capacity, non-specific adsorption	Augustine et al. (2025)
On-Line SPE-LC/MS	Medium	10–2000 µL	Targeted metabolomics, pharmacokinetics	System complexity, carryover risk	More et al. (2025)

CRISPR-Based Molecular Diagnostics: From Gene Editing to Biosensing

Theoretical Foundations and Technological Evolution

The repurposing of clustered regularly interspaced short palindromic repeats (CRISPR)-associated systems for molecular diagnostics represents one of the most significant paradigm shifts in laboratory technology since the advent of polymerase chain reaction (PCR) (Yang et al., 2025; Augustine et al., 2025). Unlike earlier diagnostic approaches that relied on amplification of target nucleic acids followed by detection, CRISPR-based platforms leverage the programmable specificity of Cas nucleases combined with collateral cleavage activity to achieve sensitivity and specificity that rival, and in some contexts surpass, conventional methods.

The theoretical foundation of CRISPR diagnostics rests on the discovery that certain Cas enzymes, particularly Cas12a and Cas13a, exhibit indiscriminate nuclease activity upon target recognition (Pérez Antón et al., 2024). This property enables the coupling of specific nucleic acid detection with signal amplification through cleavage of reporter molecules, achieving attomolar sensitivity without the thermal cycling infrastructure required for PCR.

Recent Advances in Diagnostic Applications

Yang et al. (2025) provide a comprehensive synthesis of CRISPR/Cas-based biosensing platforms in their recent review published in the *Journal of Infection*, highlighting the emergence of these technologies as particularly promising for infectious disease detection. The authors critically evaluate the working principles of various CRISPR systems and their integration with portable point-of-care testing (POCT) platforms, nanomaterials, and novel colorimetric materials. Notably, they emphasize that CRISPR-assisted biosensing offers cost-effectiveness and multiplex detection capabilities that address critical gaps in existing diagnostic infrastructure, particularly in resource-limited settings.

The application of CRISPR diagnostics to drug resistance monitoring represents a particularly significant advancement. Pérez Antón et al. (2024) developed a next-generation diagnostic tool using Specific High-Sensitivity Reporter Enzymatic UnLOCKing (SHERLOCK) technology for surveillance of drug-resistant genotypes in human African trypanosomiasis. Their assay successfully detected the AQP2/3 chimera conferring resistance to pentamidine and melarsoprol in both cultured parasites and field-isolated strains, demonstrating the potential for CRISPR-based platforms to support elimination programmes through enhanced epidemiological surveillance.

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In a complementary approach, Xu et al. (2024) combined CRISPR-Cas9 with nanopore sequencing to develop an amplification-free genomic diagnostic for familial hypercholesterolemia. Their method achieved average coverages of 106× for the LDLR gene and 420× for PCSK9, with continuous reads spanning the entire length of both genes. Critically, the amplification-free approach eliminated PCR-associated artefacts, as demonstrated by the identification of a false-positive 670 base pair deletion in benchmark experiments that was not detected in the CRISPR-nanopore workflow.

Comparative Performance and Critical Evaluation

Table 2 presents a comparative analysis of CRISPR-based diagnostic platforms versus conventional molecular diagnostic methods based on recent performance evaluations.

Table 2. *Comparative Analysis of CRISPR-Based Diagnostic Platforms*

Platform	Cas Enzyme	Sensitivity	Specificity	Key Limitations	References
SHERLOCK (v4)	Cas13a	Attomolar	>99%	RNA stability, target pre-amplification	Pérez Antón et al. (2024); Yang et al. (2025)
DETECTR	Cas12a	Attomolar	>99%	DNA targets only, off-target cleavage	Augustine et al. (2025)
CRISPR-Cas9 Nanopore	Cas9	0.1% allele frequency	99.5%	Complex workflow, specialized equipment	Xu et al. (2024)
HOLMESv2	Cas12b	10 aM	98.5%	Limited commercial availability	Yang et al. (2025)
CRISPR-LAMP	Cas12a + LAMP	10 copies/µL	99%	Requires isothermal amplification	Augustine et al. (2025)

Critical Evaluation and Translational Barriers

Despite these advances, the translation of CRISPR-based diagnostics from research laboratories to routine clinical practice faces substantial barriers. Yang et al. (2025) acknowledge that challenges persist in the integration of CRISPR detection with portable POCT devices, particularly regarding reagent stabilisation, user interface design, and quality control in decentralised settings. Furthermore, the regulatory pathway for CRISPR-based diagnostics remains ill-defined, with uncertainty surrounding whether such platforms should be classified as laboratory-developed tests, in vitro diagnostics, or novel biological products.

A more fundamental limitation concerns the analytical validation of CRISPR-based assays. While sensitivity and specificity are routinely reported under optimised laboratory conditions, performance characteristics in real-world settings with heterogeneous sample matrices and variable operator skill remain inadequately characterised (Pérez Antón et al., 2024). The absence of standardised reference materials and proficiency testing programmes for CRISPR diagnostics impedes meaningful comparison across platforms and laboratories.

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Microfluidic Organ-on-a-Chip and Advanced Cell Culture Platforms

Engineering Principles and Biomimetic Design

Conventional in vitro physiological models, relying on animal studies and two-dimensional cell cultures, are fundamentally limited by interspecies biological discrepancies, ethical constraints, or inadequate replication of human physiology (Qiu et al., 2026). Organ-on-a-chip technology overcomes these challenges through emulating organ-specific microphysiological systems. The transformative power of this innovation lies in multi-channel microfluidic chips that facilitate the formation of three-dimensional cellular organizations and tissue interfaces via integrated porous membranes, micropillar arrays, or perfusable vascular microchannels, simultaneously allowing for precise and dynamic modulation of chemical, biological, and physical factors.

Qiu et al. (2026) systematically examine the development of organ-on-a-chip technology through the lens of multi-channel microfluidics, focusing on four pivotal domains: biomimetic design overview, fabrication methods including soft lithography and three-dimensional printing, applications in pathophysiological investigations and preclinical drug evaluation, and current challenges in structural design, materials, and biological applications.

Vascularized and Multi-Organ Models

The integration of vascular components into organ-on-a-chip platforms represents a significant advancement toward physiological relevance. Poljak et al. (2026) highlight vascularized tumor-on-a-chip models as tools to mimic tumor microenvironment complexity, evaluating engineering advances to bridge translational gaps in screening vascular-targeting and combinatorial cancer therapies. These models enable the study of physical parameters including shear stress, interstitial flow, and permeability, with applications spanning tissue modeling, cancer research, and drug screening.

The lymphatic system, which is integral to fluid balance, immune surveillance, and lipid absorption, has historically been overlooked despite its vital roles. Peng and Lee (2026) review recent advances in lymphatics-on-a-chip microphysiological systems, noting that traditional research modalities have illuminated key molecular and cellular features but fall short in recapitulating human lymphatic function due to limited physiological relevance, throughput, and mechanobiological complexity. Recent microfluidic organ-on-a-chip platforms offer biomimetic platforms that integrate three-dimensional architecture, fluid flow, and biomechanical stimuli alongside human lymphatic endothelial and supporting cells.

Multi-organ chip systems represent the next frontier in physiologically based pharmacokinetic modeling. Sung et al. (2025) demonstrated a four-organ chip integrating liver, kidney, gut, and cardiac tissues for drug toxicity screening, achieving 89% concordance with human clinical outcomes compared to 71% for animal models. However, the authors note that scalability and long-term stability remain significant engineering challenges.

Critical Evaluation of Translation Potential

Table 3 summarizes organ-on-a-chip platforms, their biological applications, and current translational status based on recent systematic reviews.

Table 3. *Organ-on-a-Chip Platforms: Applications and Translational Status*

Platform Type	Cell Sources	Key Applications	Physiological Relevance Features	Current Status	Remaining Challenges	References
Lung-on-a-Chip	Primary human alveolar epithelial, endothelial	Fibrosis modeling, infection, aerosol exposure	Cyclic stretch, air-liquid interface	Preclinical validation	Long-term culture stability	Qiu et al. (2026)
Liver-on-a-Chip	Primary hepatocytes, Kupffer cells, stellate cells	Drug metabolism, hepatotoxicity, NASH modeling	Zonal oxygenation,bile canaliculi	Commercial availability (several platforms)	Limited to short-term studies	Sung et al. (2025)
Kidney-on-a-Chip	Podocytes, proximal tubule epithelial	Nephrotoxicity, glomerular filtration	Flow shear, glomerular barrier	Research use only	Complexity of filtration unit recapitulation	Qiu et al. (2026)
Tumor-on-a-Chip	Patient-derived organoids, immune cells	Drug screening, immunotherapy evaluation, metastasis	Vascularization, hypoxia gradients, stromal integration	Early clinical validation studies	Patient-specific variability, standardization	Poljak et al. (2026)
Heart-on-a-Chip	hiPSC-derived cardiomyocytes	Cardiotoxicity, contractility assessment	Electrical pacing, mechanical load	Research use; regulatory acceptance emerging	Maturation of hiPSC-derived cells	Sung et al. (2025)
Lymphatics-on-a-Chip	Lymphatic endothelial cells, smooth muscle cells	Lymphedema, immune cell trafficking, cancer metastasis	Fluid drainage, junction remodeling, 3D architecture	Proof-of-concept studies	Complex vessel network formation	Peng & Lee (2026)

Multi-Omics Integration and Single-Cell Technologies

The Multi-Omics Paradigm

Multi-omics strategies, integrating genomics, transcriptomics, proteomics, and metabolomics, have revolutionized biomarker discovery and enabled novel applications in personalized oncology (Wang et al., 2025; Chen et al., 2025). Despite rapid technological developments, a comprehensive synthesis addressing integration strategies, analytical workflows, and translational applications has been lacking. Wang et al. (2025) present a comprehensive framework of multi-omics integration, encompassing workflows, analytical techniques, and computational tools for both horizontal and vertical integration strategies, with particular emphasis on machine learning and deep learning approaches for data interpretation. The authors note that landmark projects such as The Cancer Genome Atlas Pan-Cancer Atlas, the Pan-Cancer Analysis of Whole Genomes, MSK-IMPACT, and the Clinical Proteomic Tumor Analysis Consortium have collectively demonstrated the utility of multi-omics in uncovering cancer biology and clinically actionable biomarkers (Wang et al., 2025). These initiatives have established that multi-omics strategies are indispensable for characterizing molecular signatures that drive tumor initiation, progression, and therapeutic resistance.

Single-Cell and Spatial Multi-Omics

Recent technological advances have introduced single-cell multi-omics approaches, including single-cell genomics, transcriptomics, and proteomics, providing unprecedented resolution in characterizing cellular states and activities (Liu et al., 2025; Augustine et al., 2025). Additionally, spatial transcriptomics and spatial proteomics provide spatially resolved molecular data, enhancing understanding of tumor heterogeneity and tumor-immune interactions, which are essential for personalized therapeutic strategies in cancer.

Liu et al. (2025) comprehensively review transformative advances in single-cell omics, emphasizing that foundation models originally developed for natural language processing are now driving transformative approaches to high-dimensional, multimodal single-cell data analysis. Frameworks such as scGPT, pretrained on over 33 million cells, demonstrate exceptional cross-task generalization capabilities, enabling zero-shot cell type annotation and perturbation response prediction. The authors note that scPlantFormer integrates phylogenetic constraints into its attention mechanism, achieving 92% cross-species annotation accuracy in plant systems, while Nicheformer employs graph transformers to model spatial cellular niches across 53 million spatially resolved cells.

Computational Integration and Analytical Workflows

Table 4 presents a comparative overview of multi-omics integration strategies and computational tools based on recent methodological evaluations.

Table 4. *Multi-Omics Integration Strategies and Computational Tools*

Integration Strategy	Analytical Approach	Key Tools/Frameworks	Primary Applications	Limitations	References
Horizontal Integration	Concatenation-based, similarity-based	MOFA, iClusterBayes, DIABLO	Molecular subtyping, biomarker discovery	Assumes matched samples, scalability issues	Wang et al. (2025)
Vertical Integration	Network-based, pathway-based	PARADIGM, OmicsNet, Metacore	Mechanistic interpretation, drug repurposing	Requires prior knowledge, pathway completeness	Wang et al. (2025)
Single-Cell Multi-Omics	Matrix factorization, graph-based	Seurat v5, scVI, totalVI, GLUE	Cell state mapping, regulatory inference	Technical noise, sparsity, batch effects	Liu et al. (2025)
Spatial Multi-Omics	Image alignment, spatial clustering	STUtility, Giotto, SpatialDWLS, Squidpy	Tissue architecture, tumor-immune interactions	Resolution limitations, cost, data complexity	Liu et al. (2025)

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AI Foundation Models	Transformer-based, contrastive learning	scGPT, GeneFormer, scPlantFormer, Niche former	Zero-shot annotation, perturbation prediction	Interpretability, training data biases, generalizability	Liu et al. (2025)

Artificial Intelligence and Machine Learning in Laboratory Technology

AI-Driven Laboratory Automation

The integration of artificial intelligence (AI) and machine learning (ML) into laboratory workflows represents a transformative development in biological laboratory technology. Zhang et al. (2026) review the application of AI in clinical laboratory diagnostics, noting that ML algorithms are increasingly employed for image analysis, result interpretation, quality control, and predictive modeling. In microbiology, deep learning models have demonstrated performance equivalent to expert microbiologists in bacterial colony classification, with sensitivities exceeding 95% for common pathogens (Augustine et al., 2025). Automated microscopy platforms coupled with AI-based image analysis have enabled high-throughput screening of cellular phenotypes. Chen et al. (2025) demonstrated that convolutional neural networks can accurately classify drug-induced cytotoxicity patterns across multiple cell lines, achieving 94% accuracy compared to manual annotation. However, the authors caution that model generalizability across different imaging systems and experimental conditions remains a significant challenge.

Predictive Modeling and Laboratory Information Systems

ML models are increasingly being integrated into laboratory information management systems (LIMS) for predictive quality control and workflow optimization. More et al. (2025) note that AI algorithms can predict instrument maintenance requirements, optimize sample batching, and flag anomalous results that warrant repeat analysis. In clinical chemistry, random forest models have been shown to reduce repeat testing rates by 23% through improved delta check algorithms (Zhang et al., 2026). However, critical concerns regarding algorithmic transparency, validation requirements, and regulatory oversight remain unresolved. The "black box" nature of many deep learning models presents particular challenges for clinical laboratory adoption, where interpretability is essential for diagnostic decision-making (Zhang et al., 2026; Liu et al., 2025).

Accelerated Evolutionary Engineering

Principles and Acceleration Strategies

Adaptive laboratory evolution is a powerful strategy for enhancing microbial traits by harnessing the principles of natural selection in controlled environments (Declerck et al., 2026). It has enabled significant advances in microbial growth, stress tolerance, and product yield across a variety of organisms, while also providing insight into evolutionary mechanisms. Unlike rational engineering approaches that require comprehensive knowledge of host metabolic pathways, evolutionary engineering circumvents these limitations by generating a wide diversity of phenotypes followed by selection for improved traits. However, Declerck et al. (2026) note that the traditional adaptive laboratory evolution workflow is time- and resource-intensive, relying on prolonged cultivation to allow beneficial mutations to emerge and be maintained in the population. Depending on the experimental setup and desired outcome, selection time can range from 25 days to 8 months, and exceptionally up to 15 years as demonstrated in the famous Lenski long-term evolution experiment.

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To address these temporal constraints, a range of evolutionary engineering tools have been developed to accelerate adaptive laboratory evolution by increasing mutation rates and genetic diversity in evolving strains (Declerck et al., 2026). These acceleration methods are categorized based on portability (applicability across different microorganisms), genomic targetability (specificity of mutagenesis), and reliability (minimal off-target mutations and mutational reproducibility).

Integration with Automation and High-Throughput Screening

The combination of accelerated evolution with high-throughput screening platforms and automated sample preparation systems offers particular promise for rapidly generating and characterizing microbial strains with industrially relevant phenotypes. Declerck et al. (2026) outline future directions for accelerated adaptive laboratory evolution, including the integration of genome-wide and targeted mutagenesis, computational modeling, laboratory automation, and broader application beyond model organisms. By applying defined selective pressures, automated evolution platforms can achieve targeted strain improvement with minimal human intervention.

Table 5 summarizes accelerated evolution strategies, their mechanisms, and applications based on recent reviews.

Table 5. *Accelerated Adaptive Laboratory Evolution Strategies*

Strategy	Mechanism	Mutation Rate Increase	Targetability	Applicable Organisms	Key Limitations	References
Chemical Mutagenesis (EMS, MNNG)	DNA alkylation, base mispairing	10–100×	Non-targeted	Broad	Random mutations, potential toxicity	Declerck et al. (2026)
UV Mutagenesis	Thymine dimer formation	10–50×	Non-targeted	Broad	DNA repair variation, low specificity	Declerck et al.(2026)
OrthoRep (Error-Prone Polymerase)	Mutagenic plasmid replication	10^5–10^6×	Targeted to plasmid	Yeast, limited bacteria	Plasmid stability, organism restriction	Declerck et al. (2026)
CRISPR-Cas9 Mutagenesis	Targeted double-strand breaks, error-prone repair	Variable (targeted)	High	Broad	Off-target effects, delivery efficiency	Augustine et al. (2025)
Automated Evolution Platforms (e.g., eVOLVER)	Continuous culture with adaptive control	N/A (selection-based)	N/A	Microbial	Equipment cost, complexity	Declerck et al. (2026)

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Cross-Cutting Challenges and Future Directions

Standardization and Quality Assurance

The absence of harmonized protocols, reference materials, and validation frameworks persists as a fundamental barrier across all technology domains reviewed. For organ-on-a-chip platforms, Qiu et al. (2026) emphasize the need for standardized fabrication methods and performance metrics. For CRISPR diagnostics, Yang et al. (2025) call for the development of reference standards and proficiency testing programs. For multi-omics integration, Liu et al. (2025) identify inconsistent evaluation metrics and unreproducible pre-training protocols as major impediments to cross-study comparison.

Interoperability and Data Integration

The integration of advanced technologies with existing laboratory infrastructure poses significant practical challenges. Qiu et al. (2026) note that while organ-on-a-chip platforms offer physiological relevance, their adoption in conventional laboratory settings requires substantial modifications to workflows, equipment, and personnel training. Similarly, the implementation of automated sample preparation systems demands reconsideration of laboratory layout, quality management systems, and standard operating procedures. The computational and data management requirements of modern biological techniques are increasingly beyond the capacity of traditional laboratory information management systems. Liu et al. (2025) emphasize that the volume and complexity of single-cell multi-omics data necessitate sophisticated computational infrastructure and specialized bioinformatics expertise that may not be readily available in many laboratory settings.

Workforce Development and Education

The successful translation of advanced biological techniques into routine laboratory practice depends critically on the development of a workforce equipped with necessary interdisciplinary skills. Traditional training in biological laboratory technology must expand to encompass engineering principles, data science, and automation technologies. This educational transformation requires not only curriculum revision but also the development of new pedagogical approaches that integrate theoretical understanding with hands-on experience in advanced laboratory technologies. Table 6 outlines priority areas for future research, standardization, and workforce development based on the synthesis of literature.

Table 6. *Priority Areas for Advancing Biological Laboratory Technology*

Domain	Stakeholders	Timeline	Key References
Standardization	Professional societies, regulatory agencies, industry	2–5 years	Yang et al. (2025); Liu et al. (2025)
Validation	Academic medical centers, IVD manufacturers, FDA	3–7 years	Pérez Antón et al. (2024); Qiu et al. (2026)
Interoperability	Vendors, informatics consortia	3–5 years	More et al. (2025); Zhang et al. (2026)
Workforce Training	Educational institutions, accreditation bodies	2–5 years	Liu et al. (2025); Declerck et al. (2026)
Regulatory Frameworks	FDA, EMA, regulatory harmonization bodies	Ongoing	Yang et al. (2025); Sung et al. (2025)
Sustainability	Laboratory managers, manufacturers, researchers	1–5 years	Li et al. (2026); Chen et al. (2025)

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Conclusion

The paper examined recent advances in automated sample preparation, CRISPR-based diagnostics, microfluidic organ-on-a-chip platforms, multi-omics integration, artificial intelligence applications, and accelerated evolutionary engineering within the context of modern biological laboratory technology. The analysis reveals that while these technologies offer transformative potential for enhancing analytical performance, physiological relevance, and experimental efficiency, their translation into routine laboratory practice is constrained by persistent challenges in standardization, integration, interoperability, and workforce development. The convergence of automation, miniaturization, AI, and computational analysis represents a paradigm shift in biological laboratory practice, requiring practitioners to navigate increasingly complex technological landscapes. Bridging the gap between theoretical innovation and practical implementation demands not only continued technological development but also coordinated efforts in standardization, validation, and education. As laboratory technologies continue to evolve at an accelerating pace, the discipline of science laboratory technology must adapt to embrace interdisciplinary approaches that integrate engineering principles, data science capabilities, and biological expertise.

The evidence synthesized in this review indicates that the future of biological laboratory practice lies not in the isolated adoption of individual technologies but in their thoughtful integration into comprehensive laboratory workflows that prioritize reliability, reproducibility, and translational relevance. Achieving this vision will require sustained collaboration among researchers, educators, industry partners, and regulatory bodies to establish the frameworks, standards, and training programs necessary to realize the full potential of modern biological techniques in science laboratory technology.

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