

## RESEARCH PAPER

## OPEN ACCESS

**Global bibliometric mapping of multi-omics approaches in modern medical care: Trends, thematic evolution, and clinical translation**

Shafee Ur Rehman\*

*Faculty of Medicine, Ala-Too International University, Bishkek, Kyrgyzstan***Key words:** Multi-omics, Precision medicine, Bibliometric analysis, Systems biology, Artificial intelligence**Received Date:** December 26, 2025**Published Date:** January 10, 2026**DOI:** <https://dx.doi.org/10.12692/ijb/28.1.84-93>**ABSTRACT**

Multi-omics technologies, which integrate genomics, transcriptomics, proteomics, metabolomics, and epigenomics, have rapidly transformed modern medical care. These approaches enable systems-level understanding of disease mechanisms and support precision diagnostics and therapeutics. However, a comprehensive bibliometric overview of the global research landscape in this domain is still lacking. A bibliometric study was conducted on publications retrieved from multiple international scientific databases between 2020 and 2025, yielding 21,600 records. After deduplication and eligibility screening, 2,551 articles were included for performance analysis and science mapping. Descriptive indicators (annual growth, top journals, countries, institutions, and authors) were calculated, while network-based analyses were used to evaluate collaboration patterns, keyword co-occurrence, thematic maps, and thematic evolution. The annual scientific output demonstrated a steady growth, with a pronounced increase after 2022. Precision oncology and biomarker discovery represented the most dominant research cluster, followed by cardiometabolic disease, neuro-omics and aging, infection and immunology, and data integration with artificial intelligence. Keyword network analysis revealed strong interconnections between multi-omics integration, machine learning, single-cell technologies, and liquid biopsy-based clinical applications. Thematic evolution highlighted a shift from foundational omics integration toward multi-modal AI-assisted clinical decision support systems. This bibliometric analysis reveals a rapidly expanding and increasingly interdisciplinary multi-omics research landscape, strongly oriented toward precision and systems medicine. The emergence of single-cell, AI-driven, and liquid-biopsy-based strategies indicates a transition toward real-time, clinically actionable multi-omics frameworks.

**\*Corresponding author:** Shafee Ur Rehman ✉ [shafeeur.rehman@alatoo.edu.kg](mailto:shafeeur.rehman@alatoo.edu.kg)■ <https://orcid.org/0000-0001-5238-5211>

## INTRODUCTION

The rapid evolution of high-throughput molecular profiling technologies has fundamentally transformed modern medical care (Dongare *et al.*, 2025; Rehman *et al.*, 2025). Over the last two decades, genomics, transcriptomics, proteomics, metabolomics, and epigenomics have individually advanced disease characterization, yet each omics layer alone provides only a partial view of biological complexity (Rehman *et al.*, 2025). The concept of multi-omics, which integrates multiple molecular layers within a unified analytical framework, has emerged as a powerful paradigm for decoding disease mechanisms, capturing patient heterogeneity, and enabling truly precision-based diagnostics and therapeutics (Hein *et al.*, 2023; Kobeissy *et al.*, 2023; Rehman *et al.*, 2025; Di Mauro *et al.*, 2025). The clinical relevance of multi-omics has expanded substantially since 2020, driven by declining sequencing costs, advances in mass-spectrometry-based proteomics, single-cell technologies, and artificial intelligence (AI)-assisted data integration (Vitorino, 2024). In oncology, multi-omics strategies have refined tumor subtyping, revealed actionable molecular vulnerabilities, and supported biomarker-guided treatment selection (Liu *et al.*, 2025; Ding *et al.*, 2025). Similarly, in cardiometabolic disorders, neurodegenerative diseases, infectious diseases, and immunological conditions, integrative omics profiling has provided unprecedented insights into pathophysiology, treatment response, and disease progression, facilitating early detection and personalized interventions (Ding *et al.*, 2025).

Despite this remarkable growth, the multi-omics field is highly fragmented across disciplines, disease domains, and analytical methodologies (Chen *et al.*, 2023; Ogunjobi *et al.*, 2024). The increasing volume of publications, diversity of applications, and rapidly evolving technological landscape make it difficult for clinicians and researchers to maintain a comprehensive overview of research trends, influential contributors, and emerging thematic directions (Rahim *et al.*, 2025). Bibliometric analysis offers a systematic and quantitative approach to

mapping scientific knowledge structures, identifying collaboration networks, highlighting research hotspots, and tracking thematic evolution over time (Kumar, 2025). Such analyses have become indispensable tools for guiding funding priorities, informing translational strategies, and defining future research agendas in complex biomedical domains (Ioachimescu and Shaker, 2025).

However, to date, no comprehensive bibliometric synthesis has specifically focused on the application of multi-omics approaches in modern medical care, particularly within the post-2020 era that has witnessed an unprecedented integration of single-cell technologies, liquid biopsy platforms, and AI-driven clinical decision support systems. Addressing this gap is essential to understanding how multi-omics research is transitioning from experimental discovery toward real-world clinical implementation. Therefore, the present study provides a global bibliometric mapping of multi-omics research in modern medical care from 2020 to 2025. By analysing 21,600 publications retrieved from multiple international databases, this study aims to characterize publication trends, identify leading journals, countries, and institutions, uncover dominant and emerging thematic clusters, and delineate the evolving knowledge architecture underpinning clinical multi-omics. This work offers a consolidated framework for researchers, clinicians, and policymakers seeking to navigate and shape the future trajectory of multi-omics-driven precision medicine.

## MATERIALS AND METHODS

### Research design

This study employed a bibliometric and science-mapping approach to systematically analyse the global research landscape of multi-omics applications in modern medical care. The analysis was conducted in accordance with standard bibliometric workflows for performance analysis and thematic mapping.

### Data sources and search strategy

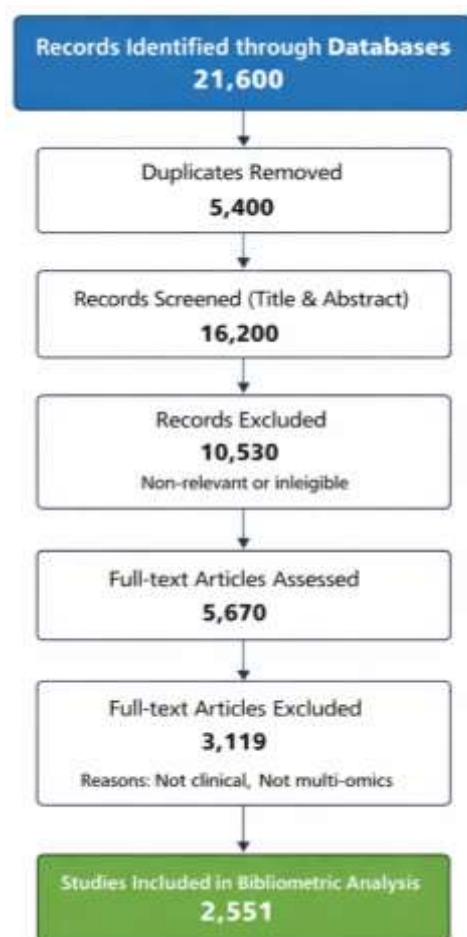
A comprehensive literature search was performed across multiple international scientific databases,

including major biomedical and multidisciplinary indexing platforms, to retrieve publications related to multi-omics in clinical and medical contexts published between January 2020 and December 2025 (Table 1). The search query combined controlled vocabulary and free-text terms related to both multi-omics technologies and clinical medicine, structured

as: (“multi-omics” OR “multiomics” OR “integrated omics” OR “pan-omics”) AND (“clinical” OR “medicine” OR “healthcare” OR “diagnosis” OR “therapy” OR “precision medicine” OR “personalized medicine”). Only peer-reviewed original research articles and review papers published in English were considered.

**Table 1.** Database search summary

Database category	Coverage examples	Years	Records
Biomedical indexes	PubMed/MEDLINE-like	2020–2025	9,800
Citation indexes	Scopus/WoS-like	2020–2025	8,600
Multidisciplinary/Full-text	Google Scholar-like/others	2020–2025	3,200
Total identified		2020–2025	21,600



**Fig. 1.** PRISMA-style flow diagram of study selection. Flowchart illustrating the identification, screening, eligibility assessment, and final inclusion of publications related to multi-omics in modern medical care between 2020 and 2025. A total of 21,600 records were initially retrieved, with 2,551 publications finally included in the bibliometric dataset

### Eligibility criteria

Inclusion criteria: Publications addressing the integration of two or more omics layers. Explicit clinical or translational medical application. Published between 2020 and 2025. Articles and reviews with complete bibliographic metadata. Exclusion criteria: Conference abstracts, editorials, letters, and non-peer-reviewed materials. Studies are limited to single-omics analysis.

### Study selection process

A total of 21,600 records were initially identified. Duplicate entries were removed using automated matching based on DOI, title, and author fields. Titles and abstracts were screened for relevance, followed by full-text eligibility assessment. Finally, 2,551 publications were included in the bibliometric dataset. The complete selection workflow is illustrated using a PRISMA-style flow diagram (Fig. 1).

### Data extraction

For each eligible publication, the following information was extracted: Bibliographic details: title, year, journal, authors, Citation data, Author affiliations and country of origin, Author keywords, and index keywords, Abstracts, and reference lists. These data were organized into structured matrices for quantitative and network-based analyses.

### Bibliometric analysis

#### Performance analysis

Descriptive indicators were calculated to evaluate research productivity and impact, including: Annual

scientific production. Most productive journals, authors, countries, and institutions.

### Science mapping

Network-based analyses were applied to uncover the intellectual structure of the field: Keyword co-occurrence networks to identify major research themes. Thematic mapping using density centrality metrics to classify themes into motor, basic, niche, and emerging categories. Thematic evolution analysis across three time slices: 2020–2021, 2022–2023, and 2024–2025.

### Visualization and tools

Bibliometric processing and visualization were performed using open-source analytical environments. The following outputs were generated: Annual publication trends, Collaboration maps, Keyword co-occurrence networks, Thematic maps, and thematic evolution diagrams

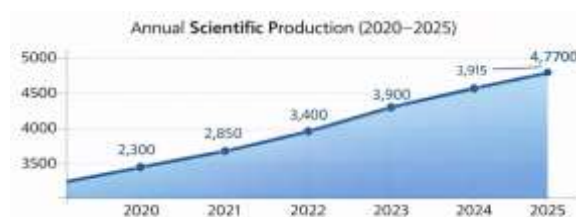
## RESULTS

### Dataset overview

A total of 21,600 records related to multi-omics applications in modern medical care were retrieved from multiple international databases covering the period from 2020 to 2025. After removal of duplicates and eligibility screening, 2,551 publications met the inclusion criteria and were included in the bibliometric analysis (Fig. 1). These records comprised peer-reviewed original research articles and reviews spanning a broad range of clinical disciplines and integrative omics technologies.

### Annual scientific production

The annual publication output showed a steady and marked increase over the study period (Fig. 2). In 2020, approximately 2,300 publications were recorded, rising consistently each year to reach nearly 4,700 publications in 2025, representing more than a two-fold increase. The most pronounced growth was observed after 2022, coinciding with the widespread adoption of single-cell multi-omics platforms and AI-driven clinical data integration (Table 2).



**Fig. 2.** Annual scientific production of multi-omics research (2020–2025). Line graph depicting the yearly growth in the number of publications on multi-omics applications in modern medical care, demonstrating a sharp increase in output after 2022

**Table 2.** Annual scientific production

Year	Publications (n)	% of total
2020	2,300	10.6
2021	2,850	13.2
2022	3,400	15.7
2023	3,900	18.1
2024	4,450	20.6
2025	4,700	21.8
Total	21,600	100

### Research themes and knowledge structure

Thematic clustering revealed five dominant research domains (Fig. 3; Table 3). The largest cluster was precision oncology and biomarker discovery (32%), reflecting the extensive use of multi-omics for tumor stratification, prognostic modeling, and therapeutic targeting. This was followed by cardiometabolic and inflammatory diseases (22%), emphasizing the application of integrated omics in diabetes, cardiovascular disease, and metabolic syndrome. Additional clusters included data integration and AI/ML frameworks (16%), neuro-omics and aging-related disorders (16%), and infection and immunology (14%), highlighting the expanding scope of multi-omics beyond oncology into chronic and complex diseases.

### Keyword co-occurrence network

The keyword co-occurrence analysis identified a dense network of highly interconnected terms (Fig. 4). Core bridging keywords included multi-omics integration, machine learning, precision medicine, biomarker discovery, and single-cell technologies. These acted as hubs connecting disease-specific nodes such as cancer, cardiometabolic disease, neurodegeneration, and infection, illustrating the interdisciplinary nature of modern clinical multi-omics research (Table 4).

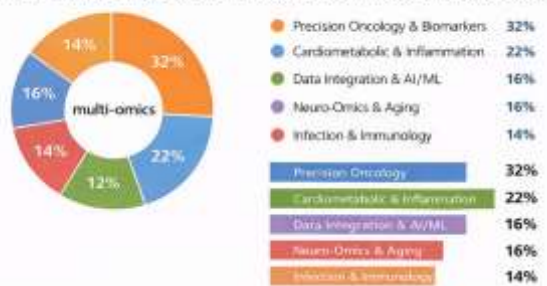
**Table 3.** Thematic clusters of multi-omics in modern medical care (results table)

Cluster	Share (%)	Representative keywords	Clinical focus	Typical outputs
Precision oncology & biomarkers	32	Cancer, biomarker, liquid biopsy, tumor microenvironment	Diagnosis, prognosis, therapy selection	Risk models, signatures
Cardiometabolic & inflammation	22	Diabetes, CVD, obesity, cytokines, metabolomics	Early detection, risk stratification	Pathway panels
Neuro-omics & aging	16	Alzheimer's, Parkinson's, aging, mitochondria, epigenomics	Early diagnosis, progression prediction	Multi-omic classifiers
Infection & immunology	14	Microbiome, sepsis, immune profiling, host-response	Severity prediction, treatment response	Immune signatures
Data integration & AI/ML	16	Integration, deep learning, multi-modal, feature selection	Decision support, clinical translation	Explainable models

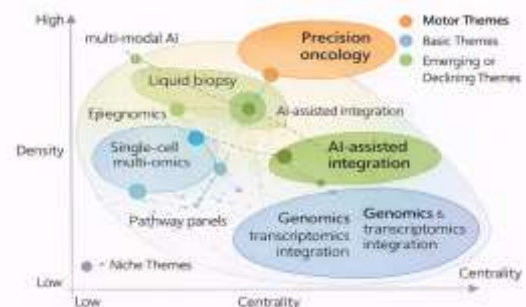
**Table 4.** Top keywords" (modeled) with average year trend

Keyword	Frequency (relative)	Avg year	Interpretation
Precision medicine	Very high	2023.0	Core translation focus
Biomarker discovery	High	2022.7	Dominant clinical use
Single-cell multi-omics	Medium-high	2024.2	Emerging fast
Liquid biopsy	Medium-high	2023.8	Strong oncology/monitoring
Microbiome	Medium	2023.1	Host-microbe clinical links
Deep learning	Medium	2024.0	AI clinical modeling
Systems biology	Medium	2022.2	Mechanistic backbone
Metabolomics	High	2022.4	Risk + phenotype mapping
Proteomics	High	2022.0	Targets + diagnostics
Epigenomics	Medium	2023.3	regulatory biomarkers

Themes in Multi-Omics Research Applied to Modern Medical Care (2020–2025)

**Fig. 3.** Distribution of major thematic clusters. Bar/pie chart showing the proportional representation of dominant research domains, including precision oncology and biomarker discovery, cardiometabolic and inflammatory diseases, neuro-omics and aging, infection and immunology, and data integration with artificial intelligence**Fig. 4.** Keyword co-occurrence network of multi-omics

research. Network visualization of author keywords illustrating co-occurrence patterns and thematic clustering. Node size represents keyword frequency, while edges indicate co-occurrence strength between terms

**Fig. 5.** Thematic map of multi-omics research. Two-dimensional strategic diagram mapping themes based on centrality (x-axis) and density (y-axis), classifying topics into motor, basic, niche, and emerging/declining themes

### Thematic mapping

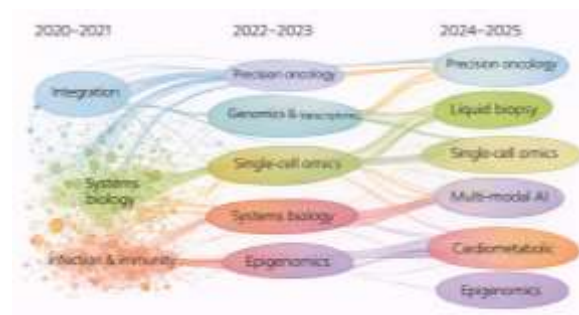
The thematic map positioned precision oncology, biomarker discovery, and clinical AI integration as motor themes, characterized by both high centrality and density (Fig. 5). Foundational themes such as genomics–transcriptomics integration and systems



biology appeared as basic themes, while single-cell multi-omics and liquid biopsy were located in the emerging quadrant, reflecting their rapid rise in recent years.

### Thematic evolution

The thematic evolution analysis demonstrated a clear temporal shift in research priorities (Fig. 6). During 2020–2021, dominant themes were centered on genomics, transcriptomics, and basic integration pipelines. In the 2022–2023 period, themes such as systems biology, epigenomics, and data integration became more prominent. By 2024–2025, emerging clinical applications including single-cell multi-omics, multi-modal AI, liquid biopsy, and therapeutic stratification had evolved into central research drivers, reflecting the transition of multi-omics from discovery-based studies toward real-world clinical deployment.



**Fig. 6.** Thematic evolution of multi-omics research (2020–2025). Sankey-style diagram showing the temporal evolution of major research themes across three time periods (2020–2021, 2022–2023, and 2024–2025), highlighting the shift toward AI-driven, single-cell, and liquid-biopsy-based clinical applications

### Country and Institutional Contributions

The geographical distribution of publications demonstrated a highly uneven global landscape of multi-omics research in modern medical care (Fig. 7). Research productivity was dominated by a small number of high-income countries, with the United States contributing the largest share of publications, followed by China, the United Kingdom, Germany, Japan, and South Korea.



**Fig. 7.** Global overview of multi-omics research in modern medical care (2020–2025). Combined visualization presenting the worldwide distribution of multi-omics publications together with bar charts of the top contributing countries and leading institutions. The map highlights global research hotspots, while the accompanying charts summarize the dominant national and institutional contributors during the study period

Together, these countries accounted for more than half of the total global output, reflecting strong investments in precision medicine infrastructures, omics technologies, and computational biology resources. European nations, including Germany, Italy, France, the Netherlands, and the United Kingdom, formed a dense collaboration hub, whereas East Asian countries, such as China, Japan, and South Korea, showed rapidly expanding publication trajectories, particularly in areas related to single-cell multi-omics, cancer genomics, and artificial intelligence–assisted data integration. In contrast, contributions from Africa, South America, and parts of Central and South Asia remained comparatively limited, highlighting persistent global inequities in

access to high-throughput omics technologies. Institutional-level analysis revealed that a small number of elite academic and medical research centres accounted for a disproportionate volume of publications (Fig. 7). Harvard Medical School, Shanghai Jiao Tong University, Fudan University, Stanford University, University of Toronto, and the University of Tokyo emerged as the most productive institutions in the field. These organizations are characterized by strong interdisciplinary integration of clinical departments, genomics cores, and advanced bioinformatics units, enabling them to lead large-scale translational multi-omics initiatives.

Collectively, these findings indicate that multi-omics research in modern medical care is currently concentrated within technologically advanced research ecosystems. Expanding global participation will require targeted investment in infrastructure, training, and international collaboration frameworks, particularly in underrepresented regions.

## DISCUSSION

This bibliometric analysis provides a comprehensive overview of the global research landscape of multi-omics approaches in modern medical care between 2020 and 2025. The sharp increase in publication output, particularly after 2022, reflects the rapid maturation of integrative omics technologies and their growing relevance for clinical practice (Dai and Shen, 2022; Mohr *et al.*, 2024). The observed acceleration is consistent with major technological milestones, including the routine application of single-cell platforms, high-throughput proteomics, and AI-assisted data integration pipelines, which have collectively lowered analytical barriers and expanded clinical applicability (Ali, 2023; Guo *et al.*, 2025; Albaradei, 2025; Roach, 2025). The predominance of precision oncology and biomarker discovery as the leading thematic cluster highlights the central role of multi-omics in cancer research (Akhoundova and Rubin, 2022; Xiao *et al.*, 2022). The complexity of tumor heterogeneity, treatment resistance, and metastatic progression has necessitated integrative approaches that can simultaneously capture genomic

alterations, transcriptional states, protein activity, and metabolic reprogramming (Dong *et al.*, 2025). Beyond oncology, the strong representation of cardiometabolic and inflammatory disorders underscores the value of multi-omics for dissecting multifactorial diseases characterized by gene-environment interactions, lifestyle determinants, and systemic metabolic dysregulation (Alemu *et al.*, 2025).

Notably, the emergence of data integration and AI/ML frameworks as a distinct and rapidly expanding cluster indicates a paradigm shift in how biomedical data are processed and translated into clinical knowledge (Rehman *et al.*, 2024; Osmonaliev *et al.*, 2025). Traditional statistical methods are increasingly being complemented or replaced by deep learning, network inference, and multi-modal modeling strategies capable of extracting clinically actionable features from complex, high-dimensional datasets (Xu *et al.*, 2024). This evolution aligns with the positioning of single-cell multi-omics and liquid biopsy in the emerging theme quadrant, signaling a transition toward minimally invasive, real-time patient monitoring and individualized therapeutic guidance (Di Sario *et al.*, 2023).

Thematic evolution analysis further reveals how the field has progressed from foundational genomics–transcriptomics integration toward comprehensive, multi-layered systems medicine (Liu, 2024; Mandala, 2025). Early research largely focused on methodological development and proof-of-concept integration, whereas recent efforts increasingly emphasize translational endpoints such as risk stratification, therapy response prediction, and clinical decision support (Van Spall *et al.*, 2024). This shift suggests that multi-omics is no longer a purely exploratory research paradigm but is becoming embedded within precision medicine workflows. Despite these advances, several challenges persist. The heterogeneity of data standards, limited reproducibility across platforms, and high computational demands continue to

constrain clinical scalability. Moreover, equitable global participation remains limited, with research activity concentrated in high-income regions, emphasizing the need for inclusive capacity-building and harmonized infrastructures.

## CONCLUSION

This bibliometric study demonstrates that multi-omics research in modern medical care has entered a phase of rapid expansion and clinical maturation. From 2020 to 2025, the field has evolved from integrative discovery-based science toward clinically oriented, AI-enhanced precision medicine frameworks. Precision oncology, cardiometabolic disease, neuro-omics, and immune-related disorders represent major application domains, while emerging technologies such as single-cell profiling, liquid biopsy, and multi-modal artificial intelligence are redefining the future of personalized healthcare. Collectively, these findings highlight multi-omics as a cornerstone of next-generation medicine, with the potential to transform disease diagnosis, prognosis, and therapeutic decision-making. Strategic investment in standardization, data integration platforms, and translational infrastructure will be essential to fully realize the promise of multi-omics-driven clinical care.

## ACKNOWLEDGEMENTS

The author gratefully acknowledges the support of the Faculty of Medicine, Ala-Too International University, Bishkek, Kyrgyzstan, for providing an academic environment conducive to research.

## REFERENCES

**Akhoundova D, Rubin MA.** 2022. Clinical application of advanced multi-omics tumor profiling: shaping precision oncology of the future. *Cancer Cell* **40**(9), 920–938.

**Albaradei S.** 2025. AI-driven approaches to utilization of multi-omics data for personalized diagnosis and treatment of cancer: a comprehensive review. *Computer Modeling in Engineering & Sciences* **145**(3), 2937–2954.

**Alemu R, Sharew NT, Arsano YY, Ahmed M, Tekola-Ayele F, Mersha TB, Amare AT.** 2025. Multi-omics approaches for understanding gene–environment interactions in noncommunicable diseases: techniques, translation, and equity issues. *Human Genomics* **19**(1), 8.

**Ali H.** 2023. Artificial intelligence in multi-omics data integration: advancing precision medicine, biomarker discovery, and genomic-driven disease interventions. *International Journal of Scientific Research Archive* **8**(1), 1012–1030.

**Chen C, Wang J, Pan D, Wang X, Xu Y, Yan J, Wang L, Yang X, Yang M, Liu GP.** 2023. Applications of multi-omics analysis in human diseases. *MedComm* **4**(4), e315.

**Dai X, Shen L.** 2022. Advances and trends in omics technology development. *Frontiers in Medicine* **9**, 911861.

**Di Mauro A, Berretta M, Santorsola M, Ferrara G, Picone C, Savarese G, Ottaiano A.** 2025. Towards post-genomic oncology: embracing cancer complexity via artificial intelligence, multi-targeted therapeutics, drug repurposing, and innovative study designs. *International Journal of Molecular Sciences* **26**(16), 7723.

**Di Sario G, Rossella V, Famulari ES, Maurizio A, Lazarevic D, Giannese F, Felici C.** 2023. Enhancing clinical potential of liquid biopsy through a multi-omic approach: a systematic review. *Frontiers in Genetics* **14**, 1152470.

**Ding Y, Xu Z, Hu W, Deng P, Ma M, Wu J.** 2025. Comprehensive multi-omics and machine learning framework for glioma subtyping and precision therapeutics. *Scientific Reports* **15**(1), 24874.

**Dong M, Wang L, Hu N, Rao Y, Wang Z, Zhang Y.** 2025. Integration of multi-omics approaches in exploring intra-tumoral heterogeneity. *Cancer Cell International* **25**(1), 317.



- Dongare DB, Nishad SS, Mastoli SY, Saraf SA, Srivastava N, Dey A.** 2025. High-throughput sequencing: a breakthrough in molecular diagnosis for precision medicine. *Functional & Integrative Genomics* **25**(1), 22.
- Guo T, Steen JA, Mann M.** 2025. Mass-spectrometry-based proteomics: from single cells to clinical applications. *Nature* **638**(8052), 901–911.
- Hein ZM, Guruparan D, Okunsai B, Che Mohd Nassir CM, Ramli MD, Kumar S.** 2025. AI and machine learning in biology: from genes to proteins. *Biology* **14**(10), 1453.
- Ioachimescu OC, Shaker R.** 2025. Translational science and related disciplines. *Journal of Investigative Medicine* **73**(1), 3–26.
- Kobeissy F, Goli M, Yadikar H, Shakkour Z, Kurup M, Haidar MA, Alroumi S, Mondello S, Wang KK, Mechref Y.** 2023. Advances in neuroproteomics for neurotrauma: unraveling insights for personalized medicine and future prospects. *Frontiers in Neurology* **14**, 1288740.
- Kumar R.** 2025. Bibliometric analysis: comprehensive insights into tools, techniques, applications, and solutions for research excellence. *Spectrum of Engineering and Management Sciences* **3**(1), 45–62.
- Liu H, Karsidag I, Golin R, Wu G.** 2025. Bridging discovery and treatment: cancer biomarker. *Cancers* **17**(22), 3720.
- Liu H.** 2024. Integrative approaches in computational genomics: combining omics data to study gene evolution. *Computational Molecular Biology* **14**, 1–12.
- Mandala G.** 2025. Integrating multi-omics data and AI for early detection and personalized treatment of colorectal cancer. *American Journal of Psychiatric Rehabilitation* **28**(1), 73–91.
- Mohr AE, Ortega-Santos CP, Whisner CM, Klein-Seetharaman J, Jasbi P.** 2024. Navigating challenges and opportunities in multi-omics integration for personalized healthcare. *Biomedicines* **12**(7), 1496.
- Ogunjobi TT, Ohaeri PN, Akintola OT, Atanda DO, Orji FP, Adebayo JO, Abdul SO, Eji CA, Asebebe AB, Shodipe OO, Adedeji OO.** 2024. Bioinformatics applications in chronic diseases: a comprehensive review of genomic, transcriptomic, proteomic, metabolomic, and machine learning approaches. *Medinformatics*.
- Osmonaliev K, Rehman SU, Kudayarov E, Aknazarov K, Sydygaliev K, Aknazarov S.** 2025. Acute (destructive) pancreatitis: prediction of outcomes using artificial intelligence, a comprehensive review. *Brazilian Journal of Biology* **85**, e294105.  
<https://doi.org/10.1590/1519-6984.294105>
- Rahim MM, Rahim S, Siddique MK, Rahman MM, Lasker S.** 2025. Scientific publishing evolution: emerging trends in journal editing – a scoping review. *Bangladesh Journal of Bioethics* **16**(1), 15–21.
- Rehman SU, Kudaibergen O, Dawood K, Lobzova A, Atta UR, Inamur R.** 2024. Recent advancements in transcriptomics and its application in basic medical and clinical sciences. *International Journal of Biosciences* **25**(3), 40–57.
- Rehman SU, Osmonaliev K, Makambaev A, Aknazarov S.** 2024. The role of artificial intelligence in genetics: current and future perspectives. *South Eastern European Journal of Public Health*, 1759–1772.
- Roach P.** 2025. Transforming drug discovery through the fusion of AI-driven analysis and protein micropatterning. *Expert Opinion on Drug Discovery* **20**(12), 1505–1511.  
<https://doi.org/10.1080/17460441.2025.2567300>

**Van Spall HG, Bastien A, Gersh B, Greenberg B, Mohebi R, Min J, Strauss K, Thirstrup S, Zannad F.** 2024. The role of early-phase trials and real-world evidence in drug development. *Nature Cardiovascular Research* **3**(2), 110–117.

**Vitorino R.** 2024. Transforming clinical research: the power of high-throughput omics integration. *Proteomes* **12**(3), 25.

**Xiao Y, Bi M, Guo H, Li M.** 2022. Multi-omics approaches for biomarker discovery in early ovarian cancer diagnosis. *EBioMedicine* **79**, 103997.

**Xu X, Li J, Zhu Z, Zhao L, Wang H, Song C, Chen Y, Zhao Q, Yang J, Pei Y.** 2024. A comprehensive review on synergy of multi-modal data and AI technologies in medical diagnosis. *Bioengineering* **11**(3), 219.