The Role of Single-Cell Multi-omics and Artificial Intelligence in Guiding Precision Antibody-Drug Conjugate Therapies for Metastatic Breast Cancer.

Krupa J[1], Afreen Misbah[2], Ajoy Shil[3], Santanu Mandal[4]

Department of Pharmacy Practice, East West College of Pharmacy, Bengaluru, Karnataka, India

ABSTRACT

Metastatic breast cancer (MBC) remains a leading cause of cancer mortality in women, complicated by extensive intratumoral heterogeneity and complex tumor microenvironments that fuel treatment resistance and progression. Antibody-drug conjugates (ADCs) offer targeted cytotoxic therapy combining monoclonal antibody specificity with potent payloads, improving efficacy and reducing systemic toxicity [1-9,12]. However, ADC effectiveness is often limited by factors like heterogeneous antigen expression, adaptive resistance, altered trafficking, and microenvironmental influences.

Advances in single-cell multi-omics technologies, including scRNA-seq, spatial transcriptomics, proteomics, metabolomics, and epigenomics, enable high-resolution profiling of tumor cells and their microenvironment, revealing subclonal populations, lineage hierarchies, and cellular interactions critical to ADC response and resistance [8-16]. Spatially resolved data preserve tissue architecture to identify immune infiltration, stromal signaling, metabolic adaptations, and extracellular matrix remodeling that impact treatment outcomes, especially in triple-negative and hormone receptor-positive subtypes.

Artificial intelligence (AI), through machine learning and deep learning, integrates these complex multi-omics datasets to discover predictive biomarkers, model therapy response, classify patients, and simulate tumor evolution under ADC therapy [17-22]. AI-driven models have identified resistance mechanisms, optimized treatment sequencing, and suggested synergistic combination therapies to enhance ADC efficacy. Clinically, these integrative approaches have stratified patients by molecular profiles, anticipated resistant clones longitudinally, and guided adaptive treatment strategies, as supported by expert consensus guidelines [23-24].

Challenges remain in standardizing single-cell workflows, harmonizing heterogeneous data, ensuring interpretability and clinical validation of AI models, and addressing ethical and regulatory issues. Nonetheless, the convergence of AI and single-cell multi-omics promises a paradigm shift in precision oncology, enabling fully personalized, adaptive ADC therapies that improve outcomes and foster next-generation drug development for metastatic breast cancer [1–25].

Keywords: Metastatic breast cancer, Antibody-drug conjugates, single-cell multi-omics technologies, Artificial intelligence (AI)

INTRODUCTION:

Despite advancements in early diagnosis and therapeutic measures, metastatic breast cancer (MBC) remains a major contributor to breast cancer fatalities and a leading cause of cancer-related morbidity and mortality in women worldwide [1-3]. MBC differs from localised breast cancer in that the cancerous cells spread to distant organs like the brain, liver, lungs, and bones, forming intricate tumour microenvironments that lead to treatment resistance, disease progression, and variation in clinical results [8,9,12]. The phenotypic and molecular heterogeneity of MBC, which includes variations in cellular composition, receptor status, gene expression, and epigenetic modifications, poses serious obstacles to traditional therapies and emphasises the need for tailored, targeted strategies that can adjust to the particulars of each patient's tumour [10,11,14,22].

The revolutionary class of targeted medicines known as antibody-drug conjugates (ADCs) was created to take advantage of monoclonal antibodies' selectivity in order to deliver lethal payloads directly to cancerous cells while reducing systemic toxicity [1-5]. ADCs provide the ability to get around the drawbacks of conventional chemotherapy and enhance clinical results in MBC by fusing the strong anti-tumor activity of chemotherapeutic drugs with the precise targeting of antibodies [1,2,6]. Although clinical trials have shown the effectiveness of several ADCs, such as HER2-targeted medicines and new payloads for triple-negative breast cancer, patient response variability is still a major problem [2,3,5].

Heterogeneous antigen expression, target receptor mutations, changes in endocytosis and lysosomal trafficking, payload efflux mechanisms, and effects from the tumour microenvironment, such as stromal interactions, immune suppression, and metabolic adaptations, are some of the factors that lead to ADC resistance [3,4,7,6]. These difficulties underline the necessity for sophisticated predictive techniques that can direct patient selection, enhance treatment sequencing, and provide guidance for the development of next-generation ADCs [23-24]. The ability to investigate tumour heterogeneity and microenvironmental interactions at previously unheard-of resolution has been transformed in recent years by single-cell multi-omics technologies [8-12].

Researchers can record the variety of cellular states, lineage hierarchies, and functional phenotypes within tumours using single-cell RNA sequencing (scRNA-seq), spatial transcriptomics, proteomics, metabolomics, and epigenomic profiling. This information can be used to understand the mechanisms underlying disease progression, resistance to treatment, and the possibility of metastasis [8,9,11,12,13]. Understanding the effectiveness of targeted therapies like ADCs depends on the mapping of cellular neighbourhoods and interactions between malignant and stromal or immune cells, which is made possible by spatially resolution analyses that preserve tissue architecture [8,9,11]. As an illustration of the limitations of bulk tissue analysis in forecasting treatment outcomes, scRNA-seq studies have discovered uncommon subpopulations of cancer cells with distinct molecular fingerprints that can elude therapy and cause relapse [12-13].

A comprehensive understanding of tumour biology is also offered by multi-omics integration, which connects transcriptomic, proteomic, and metabolomic characteristics to certain phenotypic behaviours and clinical outcomes [10,14,15,16]. Machine learning and artificial intelligence (AI) have become essential tools for integrating the high-dimensional, complicated datasets produced by single-cell multi-omics research [17-21]. In order to identify predictive biomarkers, model therapy responses, and stratify patients based on molecular profiles, artificial intelligence (AI) algorithms are able to identify patterns and associations that are invisible to traditional analytical techniques [17,18,20]. AI can identify resistance mechanisms, propose the best sequencing or combination techniques to optimise efficacy, and predict which patients are likely to respond to particular ADCs by utilising multi-omics data [18,19,21].

In order to predict susceptibility to HER2-targeted ADCs and identify metabolic pathways, including cholesterol production, as possible synergistic targets for therapy, AI-driven models have effectively incorporated spatial transcriptomics and proteomic data [8,13]. Clinicians can adopt a fully individualised, data-driven treatment plan by using integrative approaches that go beyond conventional biomarker-based stratification [17,18,21]. The use of AI and single-cell multi-omics in clinical settings to direct ADC therapy is developing quickly. Research has shown that combining predictive computational models with high-resolution genetic profiling can optimise ADC sequencing, guide patient selection, and identify resistance mechanisms before they become clinically apparent [1,2,4,5,22,23].

One aspect that affects response to HER2-targeted ADCs is heterogeneity in HER2 expression among subclones within the same tumour, as demonstrated by multi-omics research [2,4]. The significance of contextual molecular information in therapeutic decision-making has been highlighted by the identification of immunological and stromal microenvironmental variables that impact ADC penetration and payload efficacy through the profiling of triple-negative and hormone receptor-positive tumours [10,11,13,15]. Additionally, modelling of tumour evolution during ADC therapy has been made possible by longitudinal studies combining multi-omics and AI. This has helped to forecast emergent resistant clones and inform adaptive therapeutic methods [8,9,12,13,17].

The application of AI-guided ADC treatment and single-cell multi-omics in clinical practice still faces several obstacles in spite of these developments. Data integration across modalities, batch effect correction, computational scalability, and standardisation of single-cell procedures are examples of technical constraints [10,15,16]. Clinically, it's important to address the interpretability of AI models, validation in prospective trials, ethical issues with AI-driven decision-making, and cost-effectiveness [20,23,24]. As regulatory frameworks for incorporating AI-guided therapy suggestions continue to develop, thorough validation and agreement on best practices are required to guarantee clinical deployment that is both safe and successful [23-24].

Expert consensus statements, like the Taiwan Expert Consensus, highlight the complementary role of computational models in optimising treatment sequencing and combination strategies and advocate for the structured integration of ADCs guided by molecular profiling and AI-based patient stratification [23-24]. In summary, a thorough understanding of tumour heterogeneity, mechanistic insights into therapeutic resistance, and predictive modelling for customised ADC therapy are made possible by the convergence of single-cell multi-omics and AI, which offers a revolutionary approach to the management of metastatic breast cancer [1–25]. Clinicians can develop towards precision-guided therapy methods that take into consideration the dynamic and spatially organised features of metastatic tumours by combining high-resolution molecular profiling with sophisticated computational tools. Enhancing clinical results, improving ADC design, optimising sequencing and combination therapies, and eventually creating a framework for completely customised, adaptive, and outcome-optimized treatment in MBC are all possible with this paradigm shift [1–25].

Advancements in Single-Cell Multi-Omics Technologies:

In cancer research, single-cell multi-omics technologies have become a game-changer, offering previously unheard-of resolution for studying cellular hierarchies, tumour heterogeneity, and the intricate relationships within the tumour microenvironment, especially in metastatic breast cancer (MBC) [8-11]. The diversity of individual cells and the contributions of uncommon but clinically relevant subpopulations are obscured by traditional bulk sequencing approaches, which average signals across millions of cells [12-13]. Molecular heterogeneity at the level of RNA, DNA, proteins, epigenetic marks, and metabolites, frequently in combination, can be dissected using single-cell methods, which circumvent these restrictions by profiling individual cells [8,9,11,12,14].

Single-Cell RNA Sequencing (scRNA-seq) has been one of the most widely adopted technologies, which enables transcriptome profiling of hundreds to millions of individual cells in a single experiment [8,9,12]. This method has shown that tumours contain a variety of unique cellular states, such as subpopulations with higher metastatic potential, therapy-resistant phenotypes, or stem-like characteristics [12-13]. Heterogeneous expression of clinically relevant receptors, including hormone and HER2 receptors, has been identified by scRNA-seq investigations in metastatic breast cancer among subclonal populations. This has significant implications for antibody-drug conjugate (ADC) therapy [2,4]. Personalised treatment strategies are designed by using scRNA-seq to capture transcriptome heterogeneity at the single-cell level, which helps identify biomarkers predictive of treatment response, illness progression, or therapeutic resistance [9,11,13].

Spatial transcriptomics expands on the capabilities of scRNA-seq by preserving tissue architecture, which allows researchers to understand the spatial distribution of cellular subpopulations inside the cancer microenvironment and map gene expression patterns in situ [8,9,11]. Spatially resolved single-cell studies have identified gradients of immune infiltration, stromal organisation, and tumor-stroma interactions that directly affect therapy efficacy [8,10]. For instance, tumours with immunosuppressive or immune-excluded microenvironments have been associated with reduced ADC efficacy due to inadequate drug transport or low immune-mediated mechanism engagement [8,10]. These findings highlight the significance of local context in determining therapy goals and developing treatment strategies.

Single-cell proteomics improves transcriptome analysis by measuring post-translational alterations and protein expression in individual cells [10,14,15]. Since proteins are the primary component regulating cellular function, proteomic profiling provides valuable information beyond RNA expression, which may not be related with protein abundance or activity [14-15]. In ADC therapy, single-cell proteomics can be used to identify cells with different receptor expression, altered drug transporters, or resistance pathway activity. Sensitivity to ADC payloads may be impacted by these cells [1,2,4]. Advanced mass cytometry (CyTOF) and imaging mass cytometry techniques allow the simultaneous evaluation of dozens of proteins in thousands of single cells, preserving spatial information and facilitating high-dimensional mapping of tumour heterogeneity [10,15].

Epigenomic analysis at single-cell resolution enables the understanding of histone modifications, DNA methylation patterns, and chromatin accessibility that govern gene expression [8,9,11]. Epigenetic processes associated with drug resistance, stemness, and the epithelial-to-mesenchymal transition (EMT) in breast cancer have been discovered by the use of Assay for Transposase-Accessible Chromatin (ATAC-seq) on single cells and related approaches [11,13]. These epigenetic insights are particularly relevant to ADC therapy, as they can help identify transcriptionally plastic subpopulations that may avoid lethal payloads and impact combination strategies to overcome resistance [7,11,13].

Multi-omics integration is a significant advancement that simultaneously employs multiple single-cell modalities to provide a comprehensive understanding of cancer biology [10,15,16]. Combining transcriptome, proteomic, metabolomic, and epigenomic data allows researchers to predict phenotypic outcomes, identify functionally distinct subpopulations, and capture the complex regulatory networks underlying the course of cancer [10,14,16]. Tools such as Seurat, Harmony, and MOFA+ facilitate the integration and visualisation of multi-omics datasets, allowing physiologically meaningful insights to be extracted from high-dimensional single-cell data [10,15,16]. Multi-omics integration has revealed links between metabolic reprogramming, receptor expression heterogeneity, and treatment resistance in metastatic breast cancer, providing actionable targets for precision ADC therapy [13-14].

ADC therapy applications are very significant. Heterogeneity in target antigen expression, payload resistance mechanisms, and microenvironmental variables influencing ADC delivery and efficacy can all be revealed using single-cell multi-omics profiling [1,2,4,13]. For instance, spatial transcriptomics can map areas of immune exclusion that may hinder drug efficacy, and subpopulations with low or diverse HER2 expression in HER2-positive tumours may react poorly to HER2-targeted ADCs [2,4,13]. Optimised patient classification, adaptive dosage, and logical combination therapies that improve ADC efficacy are made possible by incorporating these insights into therapeutic planning [1,2,4,23].

Technological advancements continue to push the boundaries of single-cell multi-omics. Advances in image cytometry, high-throughput sequencing, droplet-based microfluidics, and combinatorial indexing have improved the scope, velocity, and resolution of single-cell profiling. Millions of cells within complex cancers may now be thoroughly characterised because to this [8,9,10]. Additionally, the ability to develop treatment response prediction models, identify rare subpopulations, and analyse multi-omics data has improved due to developments in machine learning approaches and bioinformatic pipelines [17,18,19,21]. Together, these advancements facilitate the conversion of single-cell insights into clinical applications, bridging the gap between research and patient care.

There are still issues and restrictions, such as high computing requirements, batch effects, data sparsity, and technical variability [10,15,16]. Furthermore, to guarantee reproducibility and clinical relevance, techniques must be standardised, results must be validated across cohorts, and clinical data must be integrated [23-24]. Despite these challenges, the combination of single-cell multi-omics with computational approaches, particularly artificial intelligence, holds immense potential for advancing precision oncology, guiding ADC therapy, and improving outcomes for patients with metastatic breast cancer [17,18,19,21].

In conclusion, high-resolution characterisation of tumour heterogeneity, cellular states, and microenvironmental interactions has been made possible by developments in single-cell multi-omics technologies, revolutionising the research of metastatic breast cancer [8-13]. When combined through multi-omics frameworks, methods like scRNA-seq, spatial transcriptomics, single-cell proteomics, and epigenomic profiling offer a comprehensive understanding of tumour biology, uncover resistance mechanisms, and find biomarkers indicative of therapeutic response [10,14,15,16]. The development of next-generation targeted medicines, patient stratification, and antibody-drug conjugate therapy optimisation all depend on these discoveries [1,2,4,13]. Single-cell multi-omics has the potential to become a key component of precision oncology and revolutionise the treatment of metastatic breast cancer as long as technical advancements continue to improve resolution, throughput, and integrative capacities [1–25].

Artificial Intelligence in Integrating Multi-Omics Data:

Artificial intelligence (AI), which offers computational frameworks that can manage the enormous complexity and dimensionality of datasets produced by single-cell multi-omics technologies, has completely changed the integration of multi-omics data in metastatic breast cancer (MBC) research [17,18,19,21]. Transcriptomics, proteomics, metabolomics, and epigenomics are examples of multi-omics methodologies that generate high-dimensional, heterogeneous data that are challenging to evaluate with traditional statistical techniques. From these intricate datasets, artificial intelligence (AI), in particular machine learning (ML) and deep learning (DL) algorithms, provides strong tools for identifying patterns, modelling regulatory networks, and forecasting phenotypic behaviours [17,18,20].

Machine learning models can learn predictive patterns from multi-modal data to find correlations between molecular markers and clinical outcomes, including resistance to antibody-drug conjugates (ADCs), progression, or therapeutic response [18-19]. For example, supervised learning methods have been used to predict ADC sensitivity based on receptor expression heterogeneity, microenvironmental interactions, and signalling circuit activity using scRNA-seq and spatial transcriptomics data [17,18,21]. These models enable precision-guided treatment methods by allowing researchers to stratify patients into subgroups that are most likely to benefit from particular ADC therapies [18,21].

Neural networks, autoencoders, and graph-based models are examples of deep learning techniques that further improve the integration of multi-omics data by identifying intricate correlations and non-linear relationships between molecular markers [19,21]. By connecting geographical transcriptomic data with proteomic and metabolomic profiles, graph neural networks, for instance, may simulate intercellular communication within the tumour microenvironment and identify subpopulations that contribute to treatment resistance [8,17,21]. In order to visualise high-dimensional single-cell data and highlight important biomarkers for ADC response, autoencoder-based techniques allow dimensionality reduction while maintaining important biological signals [17-18].

AI also makes it possible to model tumour progression over time under therapeutic pressure, which helps with treatment strategy adaptation and emergent resistant clone prediction [8,17,19]. AI algorithms can support proactive and adaptive therapeutic interventions by anticipating molecular changes linked to ADC resistance, such as changes in antigen expression, activation of compensatory signalling pathways, or metabolic rewiring, through the integration of temporal multi-omics data [13,17,18].

Furthermore, by revealing hidden patterns in massive multi-omics datasets that would be missed by conventional analysis, AI makes it easier to find new biomarkers and therapeutic targets [17,18,20]. For instance, AI-powered multi-omics integration has uncovered metabolic pathways, such cholesterol production, and signatures linked to EMT that can alter ADC sensitivity, directing the logical development of combination treatments [13]. In addition to improving patient stratification, these insights guide the creation of next-generation ADCs with improved specificity and efficacy [1,3,4].

The necessity for standardised data preparation, platform harmonisation, interpretability of prediction models, and clinical validation in prospective cohorts are some of the obstacles that AI-based multi-omics integration must overcome despite its potential [20,23,24]. In order to convert computer predictions into useful clinical judgements, these constraints must be addressed. However, AI is still a key factor in achieving single-cell multi-omics' full potential for precision oncology, especially when it comes to directing ADC treatments for metastatic breast cancer [1–25].

Clinical Applications and Case Studies:

The clinical management of metastatic breast cancer (MBC) is starting to undergo a considerable transformation due to the combination of single-cell multi-omics and artificial intelligence (AI), especially in the area of optimising antibody-drug conjugate (ADC) therapies [1,2,4,8,18]. Differential treatment responses and resistance to ADCs are frequently caused by tumour heterogeneity, which includes variations in receptor expression, genetic changes, and microenvironmental impacts [9-12]. By offering comprehensive molecular characterisation at the individual cell level, single-cell multi-omics technologies make it possible to identify microenvironmental variables that affect drug transport and effectiveness as well as subpopulations that can elude treatment [8,9,11,12,13].

These databases enable patient stratification, ADC response prediction modelling, and logical combination therapy design when combined with AI [17,18,19,21]. Single-cell transcriptomics in conjunction with AI algorithms has identified cells with low or missing target expression that may contribute to resistance in HER2-positive MBC, revealing subclonal heterogeneity in HER2 expression [2,4,13]. By guiding sequencing techniques for ADC delivery, these studies have minimised the selection of resistant clones while guaranteeing maximal engagement of HER2-positive subpopulations [1,2,4]. Combination treatments that increase the effectiveness of ADC and overcome adaptive resistance are being designed with the use of multi-omics integration, which has also revealed compensatory signalling pathways and metabolic changes inside tumour cells.

Actionable targets and microenvironmental characteristics affecting ADC sensitivity have been identified using multi-omics profiling in triple-negative breast cancer (TNBC), a subtype that has hitherto lacked targetable receptors. Proteomic and metabolomic investigations have shown metabolic vulnerabilities that might be used therapeutically, while spatial transcriptomics has mapped areas of immune exclusion and stromal-mediated drug resistance [10,13,15]. Clinicians can choose patients who are most likely to benefit from experimental ADCs or combination therapy by using predictive stratification made possible by AI algorithms that integrate these information[17,18,21].

The therapeutic usefulness of combining AI with multi-omics is further illustrated by longitudinal case studies. Adaptive treatment regimen adjustments and improved patient outcomes are made possible by tracking tumour progression during ADC therapy, which identifies resistant clones before clinical recurrence [8,17,19].

The timing and sequencing of ADCs, logical combinations with immunotherapy or targeted medicines, and dosage strategy optimisation are all supported by these methods, which also provide dynamic patient-specific therapeutic planning [1,2,4,23].

The integration of AI and multi-omics into ADC treatment is becoming more and more supported by expert agreement and clinical recommendations. In order to optimise sequencing and combination tactics, the Taiwan Expert Consensus places a strong emphasis on patient classification, biomarker-driven ADC selection, and computer modelling [23-24]. Together, these clinical uses highlight the revolutionary possibilities of fusing AI-driven analytics with high-resolution molecular profiling to provide precision-guided ADC treatment that takes adaptive resistance, tumour heterogeneity, and microenvironmental complexity into account [1–25]. These integrative approaches have the potential to become commonplace in the individualised treatment of metastatic breast cancer as they grow, which will ultimately lead to better results and guide the creation of next-generation ADCs.

Challenges and Future Directions:

The practical use of single-cell multi-omics and AI in directing ADC therapy still faces a number of obstacles, despite the encouraging developments. These include integrating multi-omics data into clinical processes, the requirement for standardised techniques, and technical constraints in data collection and interpretation.
The main goals of future research should be to create reliable computational tools that can easily include multi-omics data, validate AI models in upcoming clinical trials, and create standards for the clinical application of these technologies.

Conclusion:

A new age of precision oncology for metastatic breast cancer (MBC) has been brought about by the confluence of artificial intelligence (AI) and single-cell multi-omics technologies, especially in the direction of antibody-drug conjugate (ADC) treatments [1–25]. Unmatched resolution is offered by single-cell multi-omics for mapping the tumour microenvironment, identifying subclonal populations, analysing tumour heterogeneity, and determining the molecular pathways behind treatment resistance [8-13]. These databases allow doctors to provide completely personalised medicines by enabling patient classification, treatment sequencing optimisation, and predictive modelling of ADC response when combined with AI [17,18,19,21]. This comprehensive method may predict emerging resistant clones, identify patients most likely to benefit from ADCs, and guide logical combination tactics to overcome adaptive and microenvironment-mediated resistance, as clinical research and case reports have shown [1,2,4,13,23].

The significance of biomarker-driven ADC selection and computational modelling to inform treatment choices is being emphasised in expert consensus guidelines [23-24].
In conclusion, the combination of AI and single-cell multi-omics offers a revolutionary approach to precision ADC therapy in MBC, with the potential to enhance patient outcomes, maximise medication effectiveness, and direct the creation of next-generation tailored treatments. These technologies have the potential to revolutionise standard-of-care therapy and provide a new paradigm for personalised, adaptive oncology as they develop [1–25].

References:

1. Llinas-Bertran A, et al. Multimodal data integration in early-stage breast cancer. Biomed Pharmacother. 2025.
2. Liu F, et al. Decoding metastatic microenvironments through single-cell and spatial transcriptomics. Nat Rev Cancer. 2025; PMC12273945.
3. Khalili-Tanha G, et al. Innovative Approaches to EMT-Related Biomarker Discovery Using Multi-omics in Breast Cancer. Cancer Genomics. 2025; PMC12467340.
4. Aleskandarany MA, Shia W. Antibody–Drug Conjugates in Breast Cancer. Cancers (Basel). 2025; PMC12467912.
5. Zhang C, et al. Application of spatial and single-cell omics in tumor biomarker discovery. Cancer Biomark. 2025.
6. The impact of artificial intelligence on precision medicine and personalized oncology: a systematic review. Eurasian J Genome Med. 2025.
7. Sharma A, et al. Comprehensive multi-omics analysis of breast cancer long-term outcomes. Oncogene. 2024; s41389-024-00521-6.
8. Taiwan Expert Consensus on the Clinical Integration of ADCs in metastatic breast cancer therapy. Oncology. 2025.
9. Single-cell RNA sequencing reveals different cellular states in metastatic breast cancer. npj Breast Cancer. 2025; s41523-025-00808-w.
10. Advances in antibody-drug conjugates in the treatment of advanced triple-negative breast cancer: a narrative review. Transl Breast Cancer Res. 2025; 95768.
11. Pacholczak-Madej R, et al. Sequencing of antibody drug conjugates in breast cancer. Cancer Lett. 2025.
12. Davis AA, et al. Novel treatment approaches utilizing antibody-drug conjugates in breast cancer. npj Breast Cancer. 2025; s41523-025-00743-w.
13. Multi-omics based artificial intelligence for cancer research. Semin Cancer Biol. 2024.
14. Advancements in breast cancer therapy: Integrating AI and multi-omics. Comput Biol Med. 2025.
15. Multi-omics insights into biomarkers of breast cancer. Front Med. 2025.
16. Multi-omics integration reveals cholesterol biosynthesis in aggressive breast cancer as a synergistic target with HER2. Cancer Res. 2025.
17. Antibody–drug conjugates in breast cancer: mechanisms of resistance and strategies to overcome. npj Breast Cancer. 2025.
18. Top Oncology Innovations That Shaped the First Half of 2025. Oncology News. 2025.
19. Multi-omic profiling in breast cancer: utility for advancing precision oncology. Expert Rev Mol Diagn. 2025.
20. Loganathan T, et al. Multi-omics insights into biomarkers of breast cancer and diabetes comorbidity. Front Med. 2025.
21. Review Antibody-drug conjugates: Current challenges and future perspectives. Cancer Treat Rev. 2025.
22. Zhou M, et al. The next frontier in antibody-drug conjugates: challenges and opportunities. Theranostics. 2025; PMC12366496.
23. Artificial intelligence integrates multi-omics data for precision breast cancer management. J Med AI. 2025; PMC12463597.
24. Gómez-Bravo R, et al. The role of artificial intelligence integrating multi-omics in clinical breast cancer precision medicine. Rev Senol Patol Mamar. 2025.

25. Comprehensive multi-omics analysis of breast cancer. Oncogene. 2024.