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Recent Trends on Multi-omics Studies in Cancer Research: A Bibliometric Study

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***Abstract*—The integration of multi-omics approaches has revolutionized cancer research by providing a comprehensive understanding of cancer pathogenesis beyond single-omics methods. By combining diverse omics data types, multi-omics analyses improve precision in identifying intricate disease-related mechanisms. Despite increasing interest, bibliometric analyses on multi-omics research in oncology remain limited. This study addresses this gap by conducting a bibliometric analysis of multi-omics cancer research trends over the past six years (2019 to February 2025), utilizing data from the Web of Science Core Collection (WoSCC) accessed on 28 February 2025, and analysing it with VOSviewer. The analysis of 3386 publications indexed in WoSCC reveals a significant surge in multi-omics research. China leads with 2055 publications, while the University of Toronto in Canada and the Institut National de la Santé et de la Recherche Médicale (Inserm) in France emerge as major contributors, each accounting for more than 50% of their country's total publications in this domain. Dominant keywords such as multi-omics, prognosis, immunotherapy, machine learning and tumor microenvironment highlight current research priorities. This study provides a comprehensive overview of publication trends, offering valuable insights to guide future research in multi-omics cancer studies. By highlighting major contributors and emerging focal points, this study aspires to foster advancements and inspire future exploration in this pivotal domain.**

***Keywords*—Multi-omics, Bibliometric analysis, VOSviewer, Computational biology**

I. INTRODUCTION

The complexity of biological systems has posed a significant challenge for researchers seeking a holistic understanding of human health. Additionally, the transformation of normal cells into cancerous cells introduces complex behaviors that require study. To comprehend how cancer hallmarks are acquired, it is essential to investigate the underlying mechanisms of cancer cells by employing multiple sources of information. In biological studies, 'omics' or 'omes' refer to comprehensive fields of study related to specific biological molecules within an organism. Examples include genomics, epigenomics, proteomics, metabolomics, and transcriptomics. The distinct characterization of each omics layer provides valuable insights and correlations to diseases. The inception of omics studies can be attributed to the success of the Human Genome Project, which enabled the recognition of disease causes through sequencing and analysing human genomes [1]. With the rapid development of high-throughput technologies, also known as next-generation sequencing, an extensive amount of omics data is being produced at an accelerated volume and in a cost-effective manner. The accumulation of available omics data and clinical information offers significant opportunities for cancer research, including disease subtyping [2-4], biomarker discovery [5, 6], survival analysis [7, 8], subtypes prediction [9, 10], and more.

Previously, single-omics studies analysed disease causality and screening methods to improve patient treatment. Single-omics approaches primarily quantify molecular changes at the tissue level but overlook system-wide interactions across multiple omics layers within the cellular microenvironment, limiting their ability to unravel the complexity of cancer [9]. However, it is now evident that the single-omics approach disregards the molecular interactions across multiple omics layers and fails to unravel the complexity of cancer. As a result, single-omics studies often yield suboptimal prognostic insights due to the exclusion of cross-omics molecular interactions. Therefore, multi-omics analysis provides a more comprehensive

understanding of a given phenotype [11]. Consequently, researchers have made significant efforts to design robust and reliable computational models for improving multi-omics data analysis in clinical settings. For instance, one study prioritized driver genes in colon and rectal cancers by integrating proteomic, genomic and transcriptomic data [12].

According to studies, integrated omics offer the opportunity to understand the flow of information underlying diseases, compared to single-omics analysis [9]. In multi-omics, there is no straightforward one-to-one relationship between the correlation of cancer genotypes and phenotype instead, it involves a complex network of interactions in biological events [13]. Unlike multi-omics analysis, single-omics studies limit the observation of the whole molecular biological interaction in underlying diseases, resulting in unreliable and inaccurate pathogenesis information. The interrelation between omics and conditions in multi-omics provides more insights, such as biological pathways or different processes between the disease and control groups [9, 14]. Consequently, multi-omics has been increasingly applied in cancer research to support treatment decision-making [15]. With its ability to provide a deeper understanding of disease mechanisms and individual variability in treatment response, multi-omics holds great promise for advancing precision medicine and improving patient outcomes.

The utilization of multi-omics analysis has resulted in a significant rise in the number of research publications. Bibliometric analysis is a systematic and comprehensive research approach utilizing quantitative and qualitative methods [16] to evaluate academic publications. This methodology has been widely employed since the late 1800s and early 1900s [17] and has become integral to scholarly research and evaluation. Presently, it is often used to analyse and visualize accumulated scientific knowledge, evaluate the influence of a group of scholars, and extract dominant research topics [18-21]. However, comprehensive bibliometric analyses that capture overarching trends in multi-omics cancer research across various cancer types are scarce. To fill this gap, our study conducts a broad bibliometric analysis over the past six years (2019 to 2025), using the WoSCC database to map publication trends, identify leading contributors, and highlight emerging research themes in multi-omics cancer studies. This work aims to provide researchers with a holistic understanding of the evolving landscape, thereby guiding future investigations and collaborations in this rapidly expanding field. We conducted all searches on the same day (28 February 2025) to prevent bias due to daily updates to the database.

By examining research trends over these years, this study provides a timely overview of the evolving landscape of multi-omics research in cancer. Understanding these trends can serve as a guide for researchers by highlighting emerging topics, influential contributors and key publication venues. Additionally, this analysis may motivate researchers to explore new directions in multi-omics studies, fostering further advancements in this domain. Our study aims to provide valuable insights through the growth of publications, landmark articles, top keywords, country and institution contributions. This work will serve as a resource for researchers, particularly those new to multi-omics studies, to navigate and expand their understanding of this evolving field.

II. METHODS

A. Data Source and Search Strategy

The paper selection process used in this study is divided into three phases, as illustrated in Fig. 1 and inspired by the approach detailed in [22]. The UTM EZProxy of Universiti Teknologi Malaysia (UTM) Library provides access to WoSCC (https://library.utm.my/). The bibliometric analysis focuses on the publications from WoSCC, which were refined from 2019 to 2025 (February). The *Topic* search field is used in the option of the WoSCC searching tool, which queries on the title, abstract, author keywords and Keywords Plus within a record instead of focusing on specific searches using the Topic search field results in a more efficient search, as it broadens the scope to include all relevant records. The Boolean search string (‘multi-omic’ OR ‘multi-omics’) AND (‘cancer’ OR ‘cancers’) was used. To avoid duplicate records arising from overlap between ‘multi-omic’ and ‘multi-omics’, we applied a NOT operator to exclude redundant articles that appeared in both search terms.

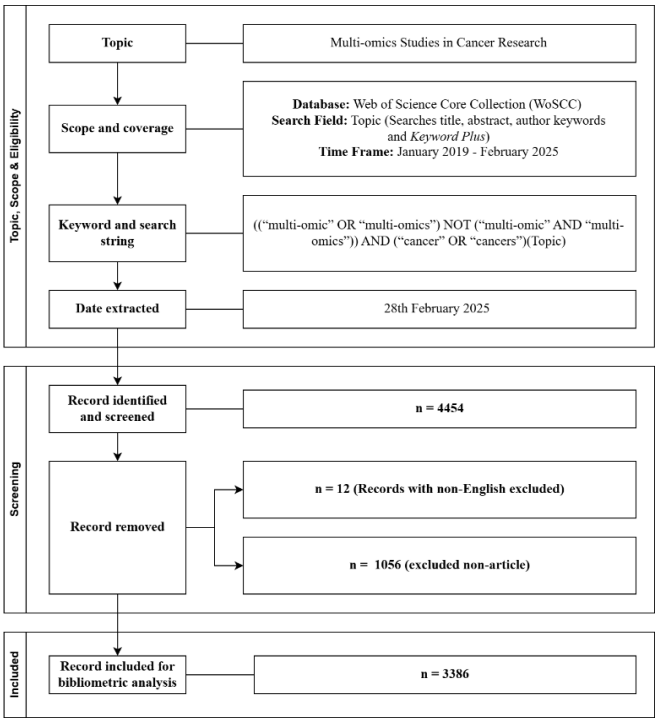

Fig. 1. Flowchart of the three-phase paper selection process for bibliometric analysis of multi-omics cancer research publications from 2019 to February 2025

In this study, we use the keyword search string multi-omic and multi-omics. However, these two keywords have different numbers of articles. Therefore, to eliminate the duplication of articles between these keywords, the NOT operator removes redundant articles that refer to the AND operator. Then, after removing the duplication articles, the search is restricted to cancer OR cancers articles only (using AND operator). We conducted all searches on 28 February 2025 to prevent bias caused by daily updates to the database. The six-year period, including 2025, aims only to observe the current trends of multi-

omics studies. The search focuses on the English language and the document of research articles only. After thoroughly reviewing 4454 records, we excluded 1068 records as they failed to meet the study criteria. Consequently, we have shortlisted 3386 records that satisfy our bibliometric study requirements.

B. Data Analysis

The bibliometric analysis was conducted using VOSviewer. VOSviewer was selected as the primary tool for this bibliometric analysis due to its specialized capabilities in constructing and visualizing bibliometric networks such as co-authorship and keyword co-occurrence maps. It offers an intuitive user interface and efficiently handles large datasets, producing clear, high-quality visualizations that facilitate interpretation of complex relationships in scientific publications. Compared to other tools like CiteSpace, which focuses more on detecting emerging trends and citation bursts, VOSviewer provides a straightforward approach well-suited for mapping collaboration patterns and research themes, aligning closely with the objectives of our study. Additionally, NVivo, while powerful for qualitative data analysis, is less optimized for quantitative bibliometric mapping. Therefore, VOSviewer was deemed the most appropriate tool to comprehensively explore publication trends and collaboration networks in multi-omics cancer research.

We utilized the Analyze Results feature in the Web of Science database to examine and visualize the 3386 shortlisted records. We then exported the selected records in Plain Text File format, including full records based on the topic, scope and eligibility criteria of the study. Due to system limitations, we exported the records in batches of 500 per instance. We performed bibliometric network analysis using VOSviewer, a specialized tool for constructing and visualizing co-authorship and keyword co-occurrence networks. VOSviewer is a specialized tool for generating and visualizing bibliometric maps [23, 24]. The analysis types used in this study are co-authorship and co-occurrence.

We set a threshold to limit a maximum of 25 authors, organizations, and countries per document. This value was selected based on common bibliometric practices and preliminary data exploration, balancing the inclusion of most multi-authored publications while excluding outlier consortium papers that could disproportionately influence the network structure. This filtering approach helped maintain readability and the interpretability of collaboration and keyword maps.

C. Bibliometric Analysis and Network Visualization

Bibliometric network analyses were conducted using VOSviewer (version 1.6.20) to visualize collaboration patterns and thematic structures within the multi-omics cancer research literature. To ensure clarity and meaningful interpretation of the networks, specific parameter thresholds and settings were applied as follows:

- **Minimum Document and Citation Thresholds:** For country- and institution-level co-authorship networks (Figs. 3 and 4), a minimum threshold of five documents and five citations per entity was set. This filtering excluded sporadic contributors with limited research output or impact, thereby reducing noise and enhancing the robustness of the collaboration maps.
- **Clustering Method:** Node clustering was performed using VOSviewer's built-in modularity-based algorithm, which groups nodes based on the strength of their connections. Nodes within the same cluster represent countries, institutions, or keywords that frequently collaborate or co-occur, with distinct colors assigned to each cluster to highlight closely related groups.
- **Density Visualization Settings:** For keyword co-occurrence analysis (Fig. 5), density visualization was generated using VOSviewer's kernel density estimation with default bandwidth parameters. In these maps, node size corresponds to keyword frequency, while color intensity reflects the local density of keyword co-occurrence, emphasizing dominant research themes.
- **Limits on Contributors per Publication:** To prevent distortion caused by publications with exceptionally large author lists or multiple affiliations (e.g., consortium studies), a maximum limit of 25 authors, organizations, and countries per document was imposed during data processing. This constraint helps maintain the readability and structural balance of the network visualizations by mitigating overrepresentation from a few large collaborations.
- **Keyword Occurrence Thresholds:** For keyword co-occurrence analysis, a minimum occurrence threshold of 10 was applied to filter terms, ensuring only keywords with sufficient frequency were included to generate meaningful networks. This threshold resulted in 506 keywords meeting the criteria for analysis.

These parameter choices were guided by standard bibliometric practice and informed by preliminary data exploration to balance inclusiveness with visualization clarity. The thresholds and settings applied enabled robust, interpretable network maps that accurately reflect collaboration patterns and thematic structures within multi-omics cancer research.

III. RESULTS

A. Quantitative Analysis of Publication Trend

The bibliometric dataset analysed in this study consists of 3386 research articles. Table I provides a summary of the annual publication and citation counts from 2019 to 2025, while Fig. 2 illustrates the annual distribution of publications and citations in multi-omics cancer research from 2019 to early 2025. The bar chart (light purple) represents the number of publications per year, and the line graph (dark blue) represents the corresponding citation counts.

TABLE I. ANNUAL PUBLICATION AND CITATION COUNTS FOR MULTI-OMICS CANCER RESEARCH ARTICLES INDEXED IN THE WEB OF SCIENCE CORE COLLECTION FROM 2019 TO EARLY 2025. THE TABLE PRESENTS RAW COUNTS AND HIGHLIGHTS YEAR-OVER-YEAR PERCENTAGE CHANGES TO ILLUSTRATE GROWTH TRENDS.

Year	Publications	% Change in Publications	Citations	% Change in Citations
2019	155	—	153	—
2020	288	+ 85.2%	1309	+ 756.2%
2021	469	+ 62.8%	4082	+ 211.9%
2022	658	+ 40.3%	7762	+ 90.1%
2023	696	+ 5.8%	11457	+ 47.6%
2024	971	+ 39.5%	16810	+ 46.8%
2025*	152	—	2784	—

Based on Fig. 2, an upward trend in publication volume is evident from 2019 onwards, reaching its peak in 2024. A similar pattern is observed for citations, which also peak in 2024 before declining in early 2025. The lower figures for 2025 are likely due to incomplete data since the counts represent partial-year values up to February, and citations typically accumulate over time. Over the past six years, multi-omics cancer research publications have received an average of 5545.63 citations annually, amounting to a total of 44365 citations.

The annual publication volume from 2019 to 2021 exhibits steady and consistent growth, reflecting intensified research efforts, potentially influenced by the COVID-19 pandemic [25-27]. Factors contributing to this trend include increased funding opportunities in biomedical research and expedited publication processes during this period. This sustained growth underscores the rising importance and urgency attributed to multi-omics cancer research in recent years.

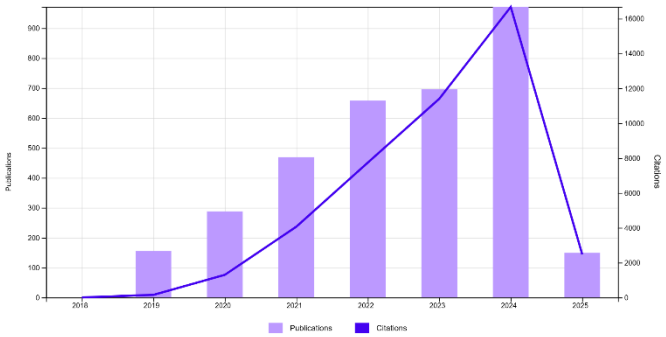

Fig. 2. Annual publication and citation trends in multi-omics cancer research from 2019 through early 2025. Publication and citation counts for 2025 represent partial data collected up to February and should be interpreted with caution

The relatively slower growth observed between 2022 and 2023 may be attributed to several factors. The initial rapid increase in publications during earlier years was likely driven by heightened urgency and increased funding related to the COVID-19 pandemic, which accelerated biomedical research broadly. By 2022, this surge stabilized as research priorities adjusted, and some pandemic-related funding and expedited publication mechanisms normalized. Additionally, the complexity and longer timelines inherent to multi-omics studies may have contributed to a more measured pace of publication growth. Furthermore, global challenges such as supply chain disruptions, workforce shortages, and shifting funding landscapes during the post-pandemic period could have temporarily impacted research productivity. Despite this slower incremental growth, the overall trend remains upward, reflecting sustained interest and investment in multi-omics approaches in cancer research.

From 2023 onwards, the trend of publication rates resumed a steeper increase, possibly driven by advancements in computational methodologies, greater availability of multi-omics datasets, and improved analytical tools facilitating large-scale integrative analyses. Overall, these trends underscore the increasing significance of multi-omics approaches in cancer research and the evolving landscape of scientific contributions in this field.

To further elucidate the publication and citation dynamics over the study period, we calculated the year-over-year percentage changes (Table I). From 2019 to 2020, publications increased sharply by approximately 85.2%, while citations surged by over 750%, reflecting a rapid expansion in multi-omics cancer research interest and impact. Subsequent years showed positive but more moderate growth rates. For example, publication growth slowed to 5.8% between 2022 and 2023, and citations increased by around 47.6% during the same interval. The early 2025 data represent only partial-year counts and thus show lower numbers, which should be interpreted with caution. These trends highlight both an initial surge, likely influenced by factors such as increased funding and expedited publishing during the COVID-19 pandemic, and sustained growth driven by ongoing advancements in multi-omics methodologies and data availability.

B. Collaborative Efforts in the Analysis of Countries and Institutions

Bibliometric data show that 3954 institutions from 86 countries have contributed to multi-omics cancer research. Table II summarizes the top ten countries ranked by publication output, along with their citation counts and leading institutions.

The top three countries, namely China, the United States, and Germany, dominate this research area. China leads with 2055 publications, representing 60.7 percent of the total output, and holds the highest citation count at 21841. The United States follows with 794 publications, accounting for 23.5 percent, and 17793 citations, while Germany ranks third with 187 publications, representing 5.5 percent, and 3766 citations. This concentration reflects significant research capacity and investment in multi-omics cancer studies by these nations.

Leading Chinese institutions include the Chinese Academy of Sciences with 156 publications, Fudan University with 145 publications, Shanghai Jiao Tong University with 142 publications, Sun Yat-Sen University with 141 publications, and the Chinese Academy of Medical Sciences and Peking Union Medical College with 107 publications. These five institutions alone contribute substantially to Chinas dominant position.

In the United States, Harvard University leads with 102 publications, while in Germany the Helmholtz Association contributes 72 publications. These institutions play pivotal roles in driving their countries research outputs. Beyond the top three,

other countries such as the United Kingdom, Canada, Italy, India, South Korea, Australia, and France also contribute notably to multi-omics cancer research. The University of London with 39 publications and the University of Toronto with 57 publications emerge as key institutions in the United Kingdom and Canada respectively. The University of Toronto and Inserm in France, each with 48 publications, account for about half of their countries' total research output, highlighting their importance as national research hubs.

While publication rankings generally align with citation counts, some differences highlight variations in research impact. For example, France, despite fewer publications than Canada, has garnered more citations, suggesting higher average influence or visibility in the field. These findings reveal a research landscape concentrated among a few leading countries and institutions but also underscore opportunities for broader international collaboration.

TABLE II. TOP TEN COUNTRIES RANKED BY PUBLICATION OUTPUT IN MULTI-OMICS CANCER RESEARCH, INCLUDING CORRESPONDING CITATION COUNTS AND THE CONTRIBUTION OF LEADING INSTITUTIONS EXPRESSED AS PERCENTAGES OF THEIR COUNTRY'S TOTAL PUBLICATIONS.

Rank	Country	Count	Citation	Institution	Count
1	China	2055 (60.7%)	21841	Chinese Academy of Sciences	156 (7.6%)
2	United States	794 (23.5%)	17793	Harvard University	102 (12.9%)
3	Germany	187 (5.5%)	3766	Helmholtz Association	72 (38.5%)
4	United Kingdom	146 (4.3%)	3614	University of London	39 (26.7%)
5	Canada	114 (3.4%)	2859	University of Toronto	57 (50.0%)
6	Italy	108 (3.2%)	1873	Consiglio Nazionale delle Ricerche (CNR)	12 (11.1%)
7	India	99 (2.9%)	728	Indian Institute of Technology System	16 (16.2%)
8	South Korea	96 (2.8%)	1099	Seoul National University	39 (40.6%)
9	Australia	92 (2.7%)	2222	University of Queensland	22 (23.9%)
10	France	89 (2.6%)	3089	Institut National De La Sante Et De La Recherche Medicale Inserm	48 (53.9%)

The total link strength metric captures the extent of international collaboration. Fig. 3 highlights this measure for countries and Fig. 4 displays the same for institutions. For Fig. 3, we applied a threshold requiring a minimum of five documents and citations per country. Out of 86 countries, 53 met this threshold, resulting in 53 nodes in Fig. 3, each representing a country. Based on this analysis, United States, China, Germany and United Kingdom exhibit denser and more extensive connections with other nodes on the map, indicating strong international collaboration worldwide.

Fig. 3 illustrates six clusters of countries based on total link strength in co-authorship networks. Nodes represent individual countries, while edges denote collaborative publication relationships. For instance, if researchers from two countries have co-authored a publication, a link is created between those two countries. The size of each node corresponds to the number of publications, with China having the largest node due to its highest publication count, followed by the United States, Germany and United Kingdom. Consequently, the China node is the most prominent in the map, as the node weight in this analysis is based on the number of publications.

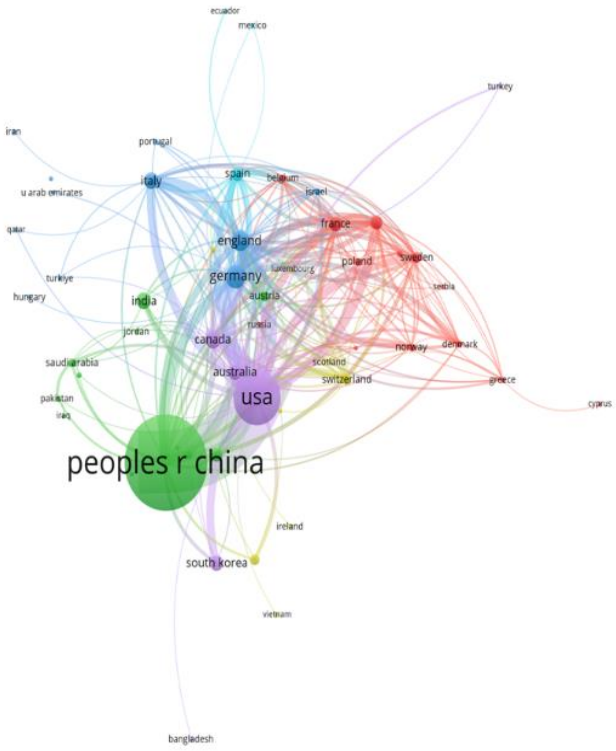

Fig. 3. Co-authorship network map of countries involved in multi-omics cancer research based on a minimum of five documents and citations. The size of each node represents the number of publications, the thickness of connections indicates collaboration strength, and different colors represent clusters of frequently collaborating countries

For Fig. 4, institutions were required to have at least five documents and citations to be included on the map. Out of 3954 institutions, 434 met this threshold. Fig. 4 displays nine clusters of institutions with the strongest co-authorship links. The nodes on the map represent institutions and the links represent co-authorship relationships. A link is created when researchers from two institutions have co-authored a publication. Among the clusters, Cluster 1 (indicated by red nodes), Cluster 2 (represented by green nodes), and Cluster 3 (highlighted by blue nodes) are the most prominent on the map. The size of the nodes

in Fig. 4 corresponds to the total link strength of the institutions. As a result, institutions with higher total link strength have more prominent node labels. Notable examples include Shanghai Jiao Tong University, Chinese Academy of Sciences, Fudan University, Harvard Medical School and Sun Yat-Sen University, which are among the most significant nodes on the map.

C. Landmark Articles

Out of 3386 articles, we retrieved ten highly cited papers from WoSCC, as presented in Table III. The most cited paper, with 819 citations, was authored by Yachida *et al*. and focused on 'Metagenomic and metabolomic analyses reveal distinct stage-specific phenotypes of the gut microbiota in colorectal cancer' [28]. Based on publications from 2019 to 2025, the top ten landmark articles in multi-omics studies have addressed various types of cancer, including colorectal, breast, hepatocellular carcinoma, ovarian, lung adenocarcinoma, renal cancer and endometrial carcinoma.

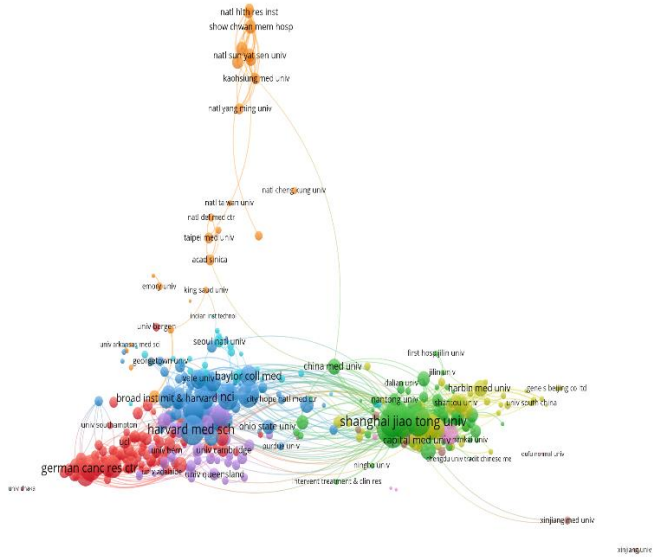

Fig. 4. Network map showing institutional co-authorship in multi-omics cancer research with a threshold of at least five documents and citations. Node sizes correspond to collaborative activity levels, links indicate co-authorship relationships, and colors denote clusters of closely collaborating institutions.

The study of gut microbiome has become increasingly popular in recent times and this is proven by the two articles related to the gut microbiome garnered the highest citations. It has been researched on a range of health conditions, including obesity, diabetes, liver diseases, cancer and neurodegenerative disorders. This indicates that gut microbiome study extends beyond cardiovascular disease [29]. According to Li *et al*. [30], much scientific research has been dedicated to the gut microbiome in the past two decades. There are over 50000 research articles on this topic in the WoSCC alone, with a consistent increase in publications over time. Thus, the gut microbiome is a subject of great interest in scientific research. The scientific community is highly interested in the microbiome and it has also captured the attention of the public and businesses, which is evident from its press coverage [31]. Support from governments and international organizations, particularly in financial aid, has been instrumental in the growth of this research field. For example, the United States National Institutes of Health (NIH) invested $216 million in the Human Microbiome Project in 2016 [30].

Two of the most highly cited landmark articles in our dataset focus on the gut microbiome, underscoring its emerging significance within multi-omics cancer research. The gut microbiome represents a complex and dynamic ecosystem that influences cancer pathogenesis, treatment response, and patient outcomes through intricate molecular interactions. Multi-omics approaches enable comprehensive characterization of microbial communities alongside host genomics, transcriptomics, metabolomics, and proteomics, providing deeper insights into these interactions.

The prominence of gut microbiome studies highlights how integrative multi-omics analyses are advancing our understanding of cancer biology beyond traditional single-omics methods. This integrative perspective facilitates identification of novel biomarkers and therapeutic targets, particularly in cancers such as colorectal carcinoma, where microbial dysbiosis plays a critical role. The high citation impact of these studies reflects growing research interest and the translational potential of microbiome-focused multi-omics investigations in oncology.

D. Keywords

To analyse keywords in bibliometric data, co-occurrence analysis was applied to all keyword units. A total of 9751 keywords were identified, out of which only 506 keywords met the minimum threshold of having at least 10 occurrences. Fig. 5 displays the density visualization of the keyword analysis, where eight clusters were identified. The most significant node in the map represents the keyword with the highest occurrence. Nodes in the map represent total link strength, and their size corresponds to the frequency of keyword usage. From Fig. 5, keywords such as *expression*, *cancer*, *multi-omics* and *prognosis* appear in a larger font size compared to other keywords, indicating that they are the most frequently used terms in the research articles. The keyword *expression* is part of Cluster 1 (represented by green nodes), while *immunotherapy* and *prognosis* belong to Cluster 2 (represented by red nodes).

A total of 5853 author keywords were identified, of which 169 keywords met the minimum threshold of at least 10 occurrences each. Fig. 6 presents the overlay visualization of the co-occurrence analysis for author keyword units, revealing seven distinct clusters. The most prominent node in the map represents keywords with the highest occurrence across all records, including *multi-omics* (533 occurrences), *prognosis* (300 occurrences), *immunotherapy* (277 occurrences), *machine learning* (166 occurrences) and *tumor microenvironment* (146 occurrences). The node colors correspond to the average citation values, with Cluster 1 (indicated by yellow nodes) receiving the highest citations. This cluster highlights the application of computational methods and interdisciplinary approaches in multi-omics research, encompassing keywords such as artificial intelligence, machine learning, deep learning, feature selection, autoencoders, cancer subtype classification, survival analysis, and others.

In addition, a total of 4731 KeyWords Plus were identified, of which 330 keywords met the minimum threshold of at least 10 occurrences each. The top five KeyWords Plus, based on their frequency, include *expression* (828 occurrences), *cancer* (741 occurrences), *cells* (322 occurrences), *survival* (241 occurrences), and *identification* (228 occurrences). These high-frequency keywords reflect the dominant themes and focus areas within the dataset, particularly in fields such as oncology, molecular biology and biomedical research.

TABLE III. THE TEN MOST HIGHLY CITED LANDMARK ARTICLES IN MULTI-OMICS CANCER RESEARCH PUBLISHED BETWEEN 2019 AND EARLY 2025, LISTING FIRST AUTHOR, YEAR, JOURNAL, AND CITATION COUNT

Rank	Title	First author	Year	Journal	Citation	Ref.
1	Metagenomic and metabolomic analyses reveal distinct stage-specific phenotypes of the gut microbiota in colorectal cancer	Yachida, S	2019	Nature Medicine	819	[28]
2	A single-cell and spatially resolved atlas of human breast cancers	Wu, SZ	2021	Nature Genetics	663	[32]
3	IOBR: Multi-Omics Immuno-Oncology Biological Research to Decode Tumor Microenvironment and Signatures	Zeng, DQ	2021	Frontiers in Immunology	596	[33]
4	Integrated Proteogenomic Characterization of HBV-Related Hepatocellular Carcinoma	Gao, Q	2019	Cell	589	[34]
5	Interaction between drugs and the gut microbiome	Weersma, RK	2020	Gut	506	[35]
6	The m^{6}A reader YTHDF1 promotes ovarian cancer progression via augmenting EIF3C translation	Liu, T	2020	Nucleic Acids Research	485	[36]
7	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma	Gillette, MA	2020	Cell	438	[37]
8	High-Spatial-Resolution Multi-Omics Sequencing via Deterministic Barcoding in Tissue	Liu, Y	2020	Cell	436	[38]
9	Molecular Subsets in Renal Cancer Determine Outcome to Checkpoint and Angiogenesis Blockade	Motzer, RJ	2020	Cancer Cell	317	[39]
10	Proteogenomic Characterization of Endometrial Carcinoma	Dou, YC	2020	Cell	283	[40]

Fig. 7 presents the network visualization of the co-occurrence analysis for all KeyWords Plus units, revealing seven distinct clusters within the map. Each cluster represents a group of closely related keywords, indicating thematic subdomains or research trends. For instance, Cluster 1 emphasizes molecular and cellular mechanisms, featuring keywords such as *antibody*, *B-cell* and *pathogenesis*, while Cluster 2 focuses on molecular biology, including terms like *glycolysis*, *hypoxia* and *degradation*. The visualization highlights not only the frequency of keyword co-occurrence but also the interconnectedness of research topics, providing insights into the structure and evolution of the field.

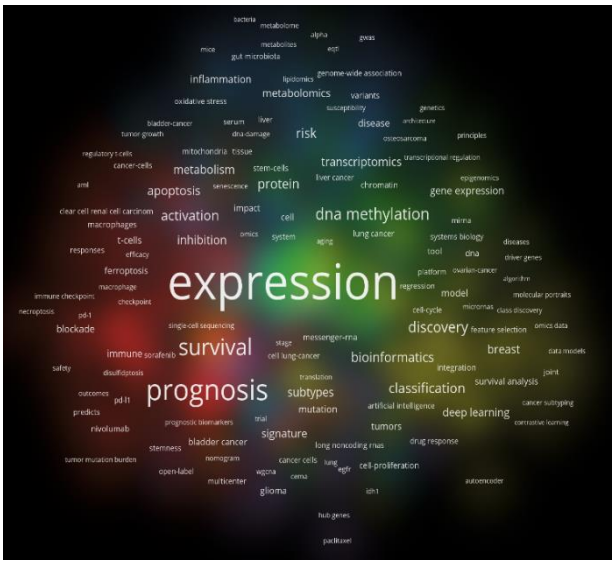

Fig. 5. Density visualization of keyword co-occurrence in multi-omics cancer research publications. Node size reflects keyword frequency, and warmer colors indicate areas with higher densities of co-occurring keywords, highlighting dominant research themes.

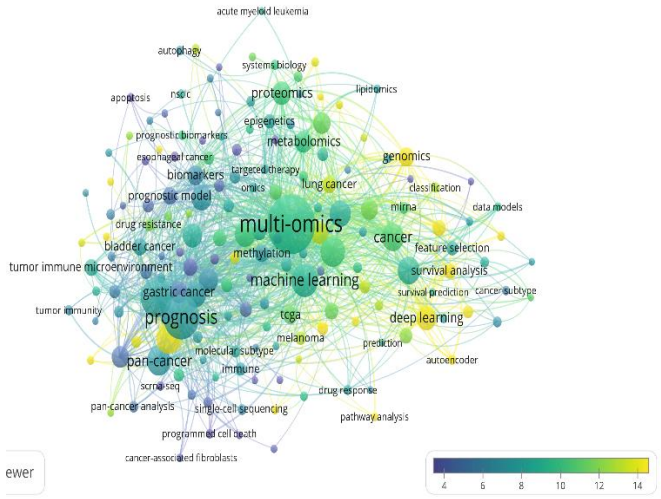

Fig. 6. Overlay visualization of author keyword co-occurrence in multi-omics cancer research. Node size indicates frequency of keyword usage, while node color represents average citation impact, thereby identifying influential research topics.

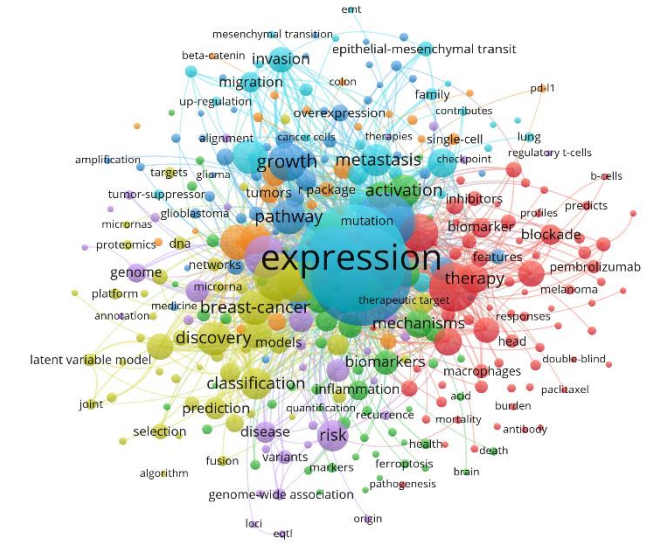

Fig. 7 Network visualization of KeyWords Plus co-occurrence analysis depicting thematic clusters within multi-omics cancer research. Nodes are sized by keyword frequency, edges represent co-occurrence links, and colors distinguish thematic groups.

The size and color of nodes in the network correspond to the frequency and impact of the keywords, respectively, allowing for a clear interpretation of their significance. Keywords with larger nodes indicate higher occurrences, while smaller nodes represent less prominent terms. This layered representation enables the identification of both established and emerging research areas, offering valuable guidance for future studies and interdisciplinary collaborations.

IV. DISCUSSION

This bibliometric study, utilizing VOSviewer, analysed 3386 publications retrieved from the WoSCC to explore current trends in multi-omics cancer research over the past five years. The annual publication and citation output from January 2019 to February 2025 demonstrates a consistent growth pattern, indicating sustained growth and demand in this field. The increasing trends in both publications and citations suggest that multi-omics studies in cancer research are experiencing a period of rapid expansion.

The study involved contributions from 86 countries and 3954 institutions, highlighting the global engagement in this domain. China emerged as the leading contributor, with 2055 publications accounting for over 50% of the total publications worldwide. Other prominent countries, including the United States, Germany, and the United Kingdom, also demonstrated strong international collaborations. Among institutions, the Chinese Academy of Sciences, Fudan University, Shanghai Jiao Tong University, Sun Yat-Sen University, and the Chinese Academy of Medical Sciences & Peking Union Medical College were the most active in producing publications related to multi-omics cancer research globally.

Notably, the University of Toronto in Canada and the Institut National de la Santé et de la Recherche Médicale (Inserm) in France were the most active institutions in their respective countries, contributing significantly to the publication output. While China leads in the total number of publications and citations, its average citation rate is lower compared to countries like France, indicating differences in research impact and influence.

The most highly cited article in the dataset is “Metagenomic and metabolomic analyses reveal distinct stage-specific phenotypes of the gut microbiota in colorectal cancer” by Yachida *et al*., which received 819 citations. This landmark article, along with others, highlights the involvement of various cancer types such as colorectal, breast, hepatocellular carcinoma, ovarian, lung adenocarcinoma, renal cancer and endometrial carcinoma in multi-omics research. The gut microbiome, a subject of significant scientific interest, is prominently featured, with two articles related to this topic receiving the highest citations.

In total, 9751 keywords were identified, including 5042 author keywords and 4731 KeyWords Plus. These keywords can be categorized into several thematic groups, such as types of omics data, approaches to multi-omics studies, biological and molecular mechanisms and specific cancer types, reflecting the diverse and interdisciplinary nature of this research field.

A. Limitations

It is important to acknowledge certain limitations in this bibliometric study. First, the study focused exclusively on the WoSCC database, which may have excluded relevant studies from other databases, potentially introducing bias. Second, the analysis was restricted to English-language publications, meaning that non-English studies were not included. This exclusion may have led to the omission of valuable research that could have influenced the findings.

In this study, the search strategy focused on the keywords ‘multi-omic’ OR ‘multi-omics’ combined with ‘cancer’ OR ‘cancers’ to ensure retrieval of publications directly related to multi-omics cancer research. Related synonyms such as ‘tumor,’ ‘tumour,’ and ‘neoplasm’ were not included in the search terms to maintain specificity and manage the scope of the dataset. We

recognize that excluding these synonyms may have omitted some relevant articles. Thus, future bibliometric analyses could expand keyword inclusion to capture a broader range of relevant literature. Despite these limitations, the retrieved bibliometric data provides valuable insights and offers researchers objective information on recent trends in multi-omics studies in cancer research.

V. CONCLUSIONS

In this bibliometric study, VOSviewer was employed to analyse publications related to multi-omics studies in cancer research. The findings reveal a significant and exponential increase in the number of publications and citations in this field over the past five years, a trend that is expected to continue. The peak in publication output during 2020 and 2021 can likely be attributed to the COVID-19 pandemic, which provided researchers with additional time and resources, thereby boosting productivity. The study analysed 3386 articles from 86 countries, 3954 institutions, 9751 keywords, 5042 author keywords, and 4731 KeyWords Plus. China and the United States emerged as the top-ranking countries in terms of contributions. Among institutions, the University of Toronto in Canada and the Institut National de la Santé et de la Recherche Médicale (Inserm) in France stood out, each contributing more than 50% of the total citations within their respective countries. Author keyword analysis identified *multi-omics, prognosis, immunotherapy, machine learning* and *tumor microenvironment* as the most frequently occurring keywords, highlighting the dominant themes and emerging trends in multi-omics cancer research. The bibliometric findings offer a structured overview of research trajectories, facilitating strategic directions for future computational and multi-omics investigations.

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CONFLICTS OF INTEREST

The authors declare that there is no conflict of interest regarding the publication of this paper.

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