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Research trends and emerging themes in cancer microbiome studies: A bibliometric analysis (2009–2024)

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Abstract

The microbiome has been increasingly recognized as a crucial factor in cancer development and treatment. To guide future research by identifying key trends and thematic directions in cancer microbiome studies, we conducted a bibliometric analysis of 6,454 publications indexed in the Web of Science Core Collection between 2009 and 2024. The United States and China led in publication output and international collaboration. Prominent keywords included "gut microbiome," "colorectal cancer," "immunotherapy," "intratumoral microbiome," and "metabolism." Rapidly emerging research areas encompassed the causal relationship between the microbiome and cancer, the role of microbial metabolites, the impact of dietary interventions on the microbiome, and the interplay between the intratumor microbiome and the tumor microenvironment. Co-citation network analysis revealed widely used analytical tools including QIIME and DADA2 for marker-gene sequencing, LEfSe for identifying taxa with differential abundance, and SIAMCAT for investigating microbiome–host phenotype associations. Research on colorectal and breast cancers dominated the literature, highlighting a relative lack of studies on other malignancies such as brain tumors and sarcomas. These findings offer valuable insights into current research priorities and may guide future cancer microbiome research toward the development of microbiome-based early cancer diagnostics, personalized anticancer therapies, and non-invasive monitoring strategies.

Keywords: Cancer; Microbiome; Bibliometric analysis; Bioinformatics; Biostatistics

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1. Introduction

Cancer, a disease characterized by uncontrolled cell growth and metastatic potential, remains one of the leading causes of mortality worldwide.[1] High-throughput molecular profiling techniques—such as transcriptomics, epigenetics, and proteomics—applied to preclinical models and cancer patients have significantly advanced our understanding of cancer biology and facilitated the identification of biomarkers for prevention, early diagnosis, and treatment. Recent studies have further built on this foundation, providing

deeper insights into environmental contributors and the development of personalized therapeutic strategies.[2,3]

Advancements in microbiome research, fueled by high-throughput next-generation sequencing of marker genes and whole metagenomes, have illuminated the intricate interplay between microbial communities and cancer. Cancer microbiome research focuses on the composition and function of microbial communities associated with cancer development, progression, and treatment outcomes. It encompasses microbial ecosystems residing in the gut, tumor tissues, and biological fluids (e.g., blood or saliva), and examines their roles in tumor initiation, immune modulation, and therapeutic responses. A growing body of evidence suggests that the microbiome can influence the efficacy of immunotherapy, chemotherapy, and radiotherapy, thereby offering promising avenues for microbiome-based diagnostics and interventions.[4-7] Notably, while the intricate relationship between the gut microbiome and colorectal cancer has been extensively studied, other areas such as intratumoral microbiomes and liquid biopsy-based microbiome analyses remain comparatively underexplored.

Microbiome data are inherently heterogeneous, high-dimensional, and often sparse, making analysis and interpretation complex. Reproducibility and standardization remain key concerns, underscoring the need for robust, scalable, and transparent analytical workflows that support multi-omics integration and incorporation of clinical metadata. Unraveling the complex interactions between the microbiome and cancer, therefore, requires sophisticated bioinformatic and biostatistical methodologies capable of integrating vast and diverse data sources.[8,9] Bioinformatics, an interdisciplinary field combining biology, computer science, and information technology, is essential for processing and interpreting high-throughput sequencing data and managing the large datasets generated in microbiome and cancer research. Advanced computational tools and algorithms in bioinformatics enable the identification of microbial signatures linked to cancer,[10,11] provide insights into host microbiome–cancer interactions, and support the development of microbiome-informed therapeutic strategies.[12-14] Biostatistics, which applies statistical techniques to biological research, is equally critical for ensuring data rigor and interpretability in cancer microbiome studies. Through advanced statistical methodologies, biostatistics validates findings, uncovers meaningful associations, and guides the design of robust experimental frameworks. Given the multitude of bioinformatic and statistical methods available for microbiome data analysis, identifying the most influential approaches is essential for accelerating progress in cancer microbiome research.

To effectively guide future investigations and inform research priorities, a comprehensive understanding of emerging trends and thematic developments in the cancer microbiome field is crucial. We therefore conducted a rigorous bibliometric analysis of the scientific literature from the past 15 years. This approach enabled us to (i) track global publication trends, (ii) identify influential studies and analytical tools/methods, (iii) examine temporal keyword patterns and the intellectual structure of the field, and (iv) uncover knowledge gaps and emerging research themes.

By systematically analyzing the scientific literature and associated keywords, our study provides a broad perspective on the development of knowledge in cancer microbiome research, highlighting how this interdisciplinary field has evolved and pinpointing areas for future high-impact efforts.

2. Data and methods

2.1. Data collection

Bibliometric analysis is a quantitative approach for examining academic literature.[15,16] It facilitates understanding of the impact, structure, and trends within a specific field of study. The Web of Science Core Collection (WoSCC) was selected as the sole data source due to its broad coverage of peer-reviewed journals, curated citation information, and consistent metadata. A comprehensive search was conducted within WoSCC to identify pertinent publications. The search query was:

("cancer microbiome"[Abstract] OR "cancer microbiome"[Title] OR "cancer microbiome"[Author Keywords] OR "Article OR Book OR Book Chapter OR Review")

Only publications written in English were included. The dataset covered the period from January 1, 2009, to August 8, 2024. As data for 2024 are partial, year-to-year comparisons should be interpreted with caution. This process yielded 6,454 relevant articles.

All bibliographic data were retrieved exclusively from the WoSCC. While the database is widely used, reliance on a single source may have limited coverage of studies not indexed within it, such as regional or non-English literature. Detailed information, including titles, authors, institutions, countries, publication years, citation counts, journals, H-index values, and keywords, was extracted from WoSCC and exported in BibTex format. The bibliographic data were systematically downloaded and processed utilizing R version 4.4.1.

2.2. Statistical analysis

Bibliometric analyses were conducted using the R package *bibliometrix*,[17,18] which provides a comprehensive array

of tools for citation, co-citation, and network visualization analyses. For the co-citation network analysis, the Walktrap clustering algorithm implemented in the *igraph* package was applied to identify densely connected subnetwork communities within the co-citation network. The default random-walk trap size of 4 was used.[19] For the keyword co-occurrence analysis, multiple correspondence analysis was performed to detect and visualize the underlying structure of keyword relationships using the *mjca* function in the *ca* package. The two most important axes were extracted for visualization, and keywords were graphically represented in this two-dimensional space. Hierarchical clustering with the average linkage method was then used to group keywords into clusters. The optimal number of clusters was determined using silhouette statistics.[20] Thematic labels were manually assigned to each cluster based on dominant keywords identified through word cloud analysis, which was performed using the *wordcloud* package. This approach enhanced interpretability by summarizing the thematic patterns represented within each cluster.

3. Results

3.1. Analysis of scientific publications

Figure 1 illustrates the overall trend in scientific publications on cancer microbiome research. Between 2009 and 2023, a total of 5,604 documents were published. An additional 850 publications from 2024 (as of August 8; not shown in Figure 1) were identified, reflecting ongoing research activity but not a complete calendar year. From 2009 until around 2019, the annual production of articles increased gradually yet consistently. After 2019, the growth rate accelerated sharply, showing an exponential trend likely driven by advances in sequencing technologies, expanded research funding, and growing recognition of the microbiome's role in cancer biology. However, between 2022 and 2023, this growth appeared to moderate, indicating a potential plateau or stabilization in annual publication output.

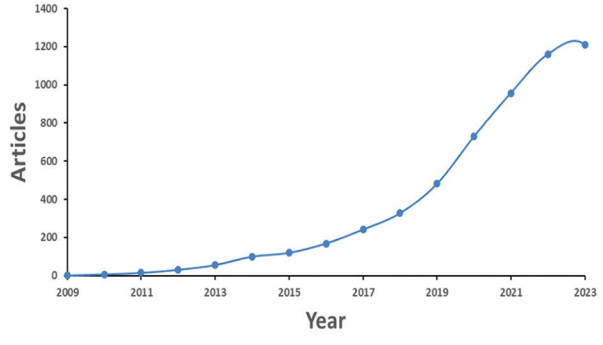


Figure 1. Number of scientific publications on microbiome and cancer (2009–2023) retrieved from the Web of Science Core Collection

3.2. Analysis of countries/regions

The United States led publication output, contributing to 1,917 articles, including both single-country and multi-country collaborations (Figure 2A). The most productive countries following the United States were China (1,485 publications), Italy (264), and India (223). A considerable gap exists between the top two countries and the remainder.

The global collaboration network shown in Figure 2B illustrates international partnerships across continents. The extensive distribution of connections indicates that collaboration in cancer microbiome research is global in scope. The United States and China exhibit the most extensive international collaborations, forming dense intercontinental networks often supported by multi-institutional consortia and large-scale cohort studies. These collaborations emphasize resource sharing and methodological harmonization. European nations such as Germany, the United Kingdom, and Italy, along with East Asian countries, demonstrate moderate participation in these networks. In contrast, regions such as Africa and South America show fewer connections, reflecting lower involvement, potentially due to limited research infrastructure, funding, or access to international partnerships.

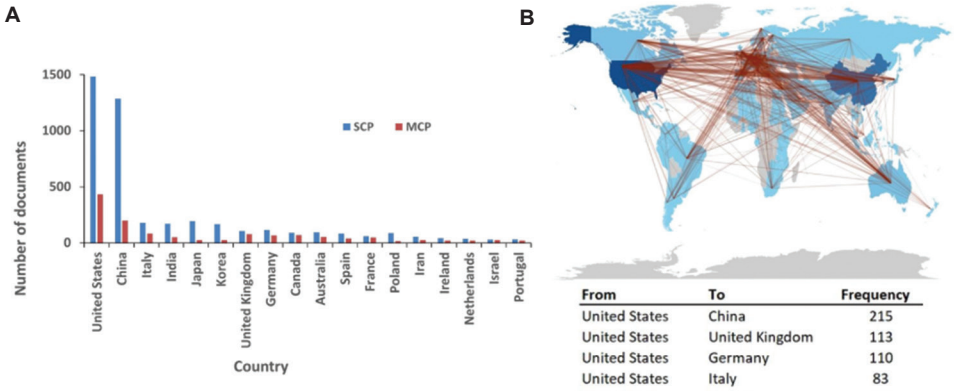
3.3. Contribution of institutions

The University of Texas MD Anderson Cancer Center has been the most productive institution from 2013 to 2024, publishing 582 articles. This output substantially exceeds that of the next four leading institutions: Ohio State University (283), Shanghai Jiaotong University (281), Sun Yat-Sen University (263), and the University of Michigan (260) (Figure 3). These top institutions predominantly focus on high-impact research areas such as immunotherapy, gastrointestinal cancers, and translational microbiome research, as reflected in their publication portfolio.

3.4. Analysis of journals

Figure 4 presents a comprehensive overview of the most influential journals in cancer microbiome research. *Cancers* emerged as the leading journal, publishing 259 articles, followed by the *International Journal of Molecular Sciences* (154), *Frontiers in Microbiology* (133), and *Scientific Reports* (130), spanning the period from 1998 to 2023 (Figure 4A).

To further evaluate journal influence, both publication volume and citation impact were analyzed. Among the top-cited journals, *Science*, *Nature*, and *PLOS ONE* ranked highest. Notably, the leading gastroenterology journals *Gut* (impact factor 23) and *Gastroenterology* (impact factor 29.4) ranked fourth and ninth, respectively, highlighting their prominence and sustained interest in gut



From	To	Frequency
United States	China	215
United States	United Kingdom	113
United States	Germany	110
United States	Italy	83
United States	Canada	72
United States	Australia	67
United States	France	65
United States	India	62
United States	Japan	52

Figure 2. Top 18 productive countries based on the corresponding author's affiliations and international collaboration. (A) The number of publications by corresponding author's countries. SCP denotes single-country publications, whereas MCP represents multi-country collaborations. (B) World map of research collaborations, with connecting lines representing international co-authorships. The table below ranks the top 10 countries by frequency of collaborative research.

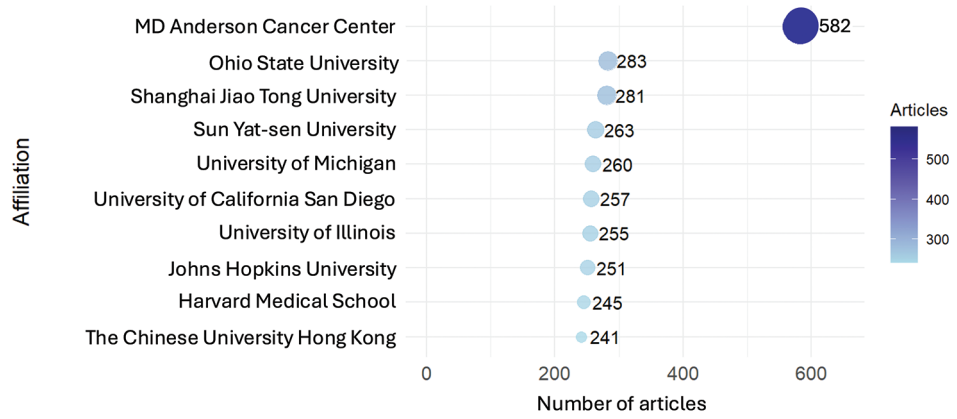


Figure 3. Ten most contributive institutions. Publication volumes of the top 10 institutions in cancer microbiome research.
Note: Dot size and color represent publication volume.

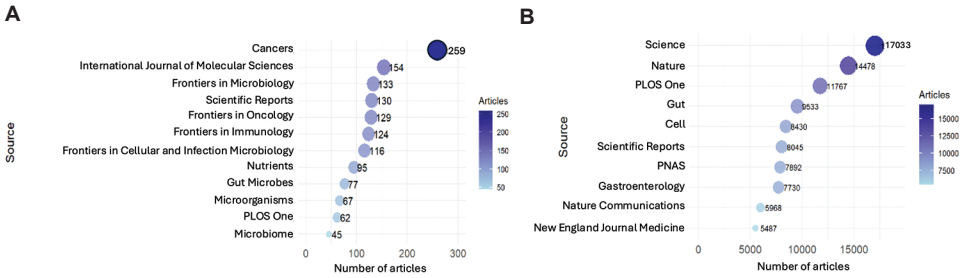


Figure 4. Top relevant journals and highly cited sources (2009–2024). The journals (y-axis) are stratified according to the number of documents (x-axis). (A) Top relevant sources. (B) Most cited sources.
Notes: (A) Dot size and color represent the number of published articles; (B) Dot size and color represent citation count.

microbiome and gastrointestinal cancer research within the scientific community (Figure 4B).

3.5. Highly cited articles

Table 1 lists the 10 most-cited articles in cancer microbiome research. Routy *et al.*,[21] titled "Gut microbiome influences efficacy of programmed cell death protein 1 (PD-1)-based immunotherapy against epithelial tumors," was the most influential study, accumulating 3,394 citations, followed by Gopalakrishnan *et al.*[22] with 2,879 citations and Matson *et al.*[23] with 1,890 citations. These three foundational studies were among the first to demonstrate an association between gut microbial composition and melanoma patients' responses to PD-1-based immunotherapy, establishing a crucial link between the microbiome and immunotherapeutic outcomes. Nejman *et al.*,[24] which investigated tumor-resident microbiota, ranked fourth with 995 citations, while several other high-impact articles focused on the gut microbiome in cancer. Notably, Poore *et al.*[25] analyzed microbiome profiles in blood samples for early cancer diagnosis and have been cited 637 times, underscoring the feasibility of non-invasive liquid biopsy approaches for identifying microbial biomarkers.

3.6. Co-citation network of cancer microbiome literature

To identify influential studies and elucidate the structural framework of knowledge dissemination in cancer microbiome research, we constructed a co-citation network of the top 50 cited references and calculated their betweenness and closeness centrality scores using CoCitNet analysis (Figure 5; Table S1).

Betweenness centrality quantifies how often a node (i.e., a cited reference) acts as a bridge along the shortest paths between other nodes, thereby influencing the flow of information, resources, or interactions within the co-citation network. Nodes with higher betweenness centrality scores serve as key intellectual bridges that connect distinct thematic areas and facilitate information exchange across otherwise separate research domains. In the analyzed co-citation network, Yu *et al.*,[26] which examined the link between *Fusobacterium nucleatum* and colorectal cancer chemoresistance, exhibited the highest betweenness score (38.61), followed by Bullman *et al.*[27] and Routy *et al.*[21]

Closeness centrality represents a node's proximity to all other nodes in a network and measures how efficiently a node can reach all other nodes in the network. Higher closeness scores indicate greater accessibility and faster information dissemination across the citation space. Based on closeness centrality, CoCitNet analysis identified three distinct thematic clusters among the top 50 references in cancer microbiome research:

- Cluster 1 (green nodes; closeness = 0.01429): 21 articles focus primarily on bioinformatic and

Table 1. Top 10 most-cited cancer microbiome studies

Document	Journal	Title	Publication year	Citation	Normalized citation
Routy *et al.*[21]	*Science*	Gut microbiome influences efficacy of PD-1–based immunotherapy against epithelial tumors	2018	3,394	29.5
Gopalakrishnan *et al.*[22]	*Science*	Gut microbiome modulates response to anti–PD-1 immunotherapy in melanoma patients	2018	2,879	25.0
Matson *et al.*[23]	*Science*	The commensal microbiome is associated with anti-PD-1 efficacy in metastatic melanoma patients	2018	1,890	16.4
Nejman *et al.*[24]	*Science*	The human tumor microbiome is composed of tumor type–specific intracellular bacteria	2020	995	21.8
Pushalkar *et al.*[63]	*Cancer Discovery*	The pancreatic cancer microbiome promotes oncogenesis by induction of innate and adaptive immune suppression	2018	796	6.9
Bullman *et al.*[27]	*Science*	Analysis of *Fusobacterium* persistence and antibiotic response in colorectal cancer	2017	897	10.0
Baruch *et al.*[64]	*Science*	Fecal microbiota transplant promotes response in immunotherapy-refractory melanoma patients	2021	801	28.1
Feng *et al.*[65]	*Nature Communications*	Gut microbiome development along the colorectal adenoma–carcinoma sequence	2015	871	8.1
Poore *et al.*[25]	*Science*	Microbiome analyses of blood and tissues suggest cancer diagnostic approach	2020	637	14.0
Zeller *et al.*[66]	*Molecular Systems Biology*	Potential of fecal microbiota for early-stage detection of colorectal cancer	2014	762	6.2

Abbreviation: PD-1: Programmed cell death protein 1.

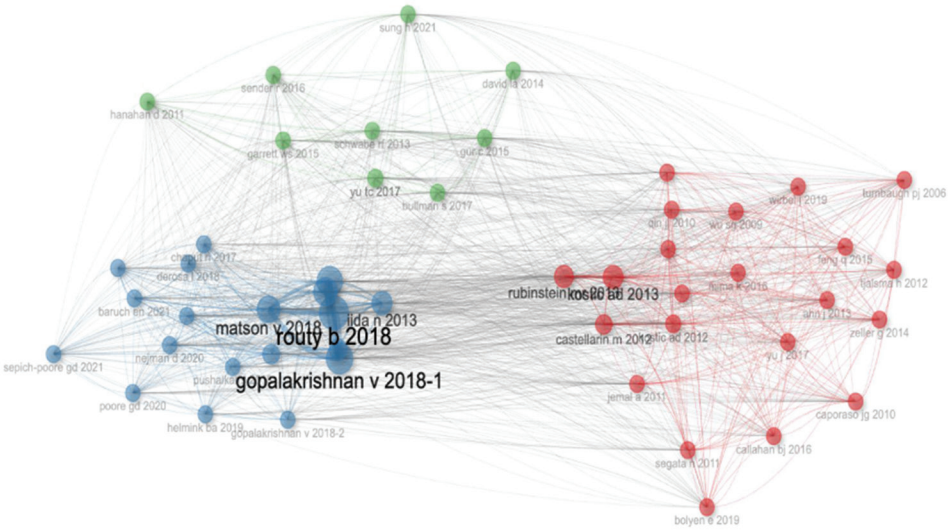


Figure 5. Article co-citation network. Co-citation network of the 50 most cited references in cancer microbiome research. Node colors represent thematic clusters based on closeness centrality: Green (bioinformatic/statistical tools), blue (gut microbiome and immunotherapy), and red (*Fusobacterium*-related and foundational works).
Note: Node size indicates citation count, and edge thickness denotes co-citation frequency, with thicker lines representing stronger connections.

statistical analysis methods, including QIIME (Bolyen *et al.*;[28] Caporaso *et al.*[29]), DADA2 (Callahan *et al.*[30]), LEfSe (Segata *et al.*[31]), and SIAMCAT (Wirbel *et al.*[32]).

- Cluster 2 (blue nodes; closeness = 0.01493): 19 articles centered on the relationship between the gut microbiome and immunotherapy in melanoma, including Routy *et al.*,[21] Matson *et al.*,[23] and Gopalakrishnan *et al.*,[22] all showing relatively high betweenness values.
- Cluster 3 (red nodes; closeness = 0.01754): 9 articles addressing the link between *Fusobacterium* and colorectal cancer (Yu *et al.*;[26] Bullman *et al.*;[27] Gur *et al.*[33]) and including comprehensive review articles (Schwabe and Jobin;[34] Garrett[35]) as well as foundational works on the hallmarks of cancer (Hanahan and Weinberg[36] and global cancer statistics Sung *et al.*)[37]

3.7. Keywords and co-occurrence network

To identify key research terms used in cancer microbiome studies, we analyzed 9,538 Keywords Plus (KWP), which appeared 50,267 times in total (Table S2). KWP terms from the WoSCC represent words and phrases that frequently occur in the titles of references cited by microbiome and oncology articles but are not present in the titles of the articles themselves.[37]

A word cloud analysis revealed that the most common keyword was "gut microbiome" (831 occurrences), followed by "colorectal cancer" (593) and "inflammation" (565) (Figure 6A). A keyword co-occurrence network analysis identified two major subnetworks: one consisting of "gut microbiota," "inflammation," and "cancer risk," and another centered around "colorectal cancer" and "*Fusobacterium nucleatum*" (Figure 6B and C).

To elucidate the conceptual structure of cancer microbiome research, the co-occurrence patterns of keywords were further analyzed using multiple correspondence analysis—a dimensionality reduction method that facilitates visualization of relationships among categorical variables such as keywords.

A subsequent hierarchical cluster analysis of keywords revealed four major conceptual clusters, which were manually annotated based on dominant keywords as follows (Figure 6D):

(i) Cluster 1: Diet and inflammation/metabolism
(ii) Cluster 2: Intratumor microbiome and immunity
(iii) Cluster 3: Immunotherapy
(iv) Cluster 4: Gastrointestinal cancer and gut microbiome.

The "Gastrointestinal cancer and gut microbiome" cluster encompassed gastrointestinal diseases such as ulcerative colitis and colorectal cancer, along with bacteria causally linked to these conditions, such as *Helicobacter pylori* and *F. nucleatum*. The "Diet and inflammation/metabolism" cluster covered a broader range of interconnected themes: diet, obesity, metabolism, inflammation, and infection. This relationship aligns with established knowledge that an unhealthy diet promotes inflammation and metabolic dysregulation.[38] Interestingly, the "Immunotherapy" cluster was positioned in close proximity to the "Intratumor microbiome and immunity"

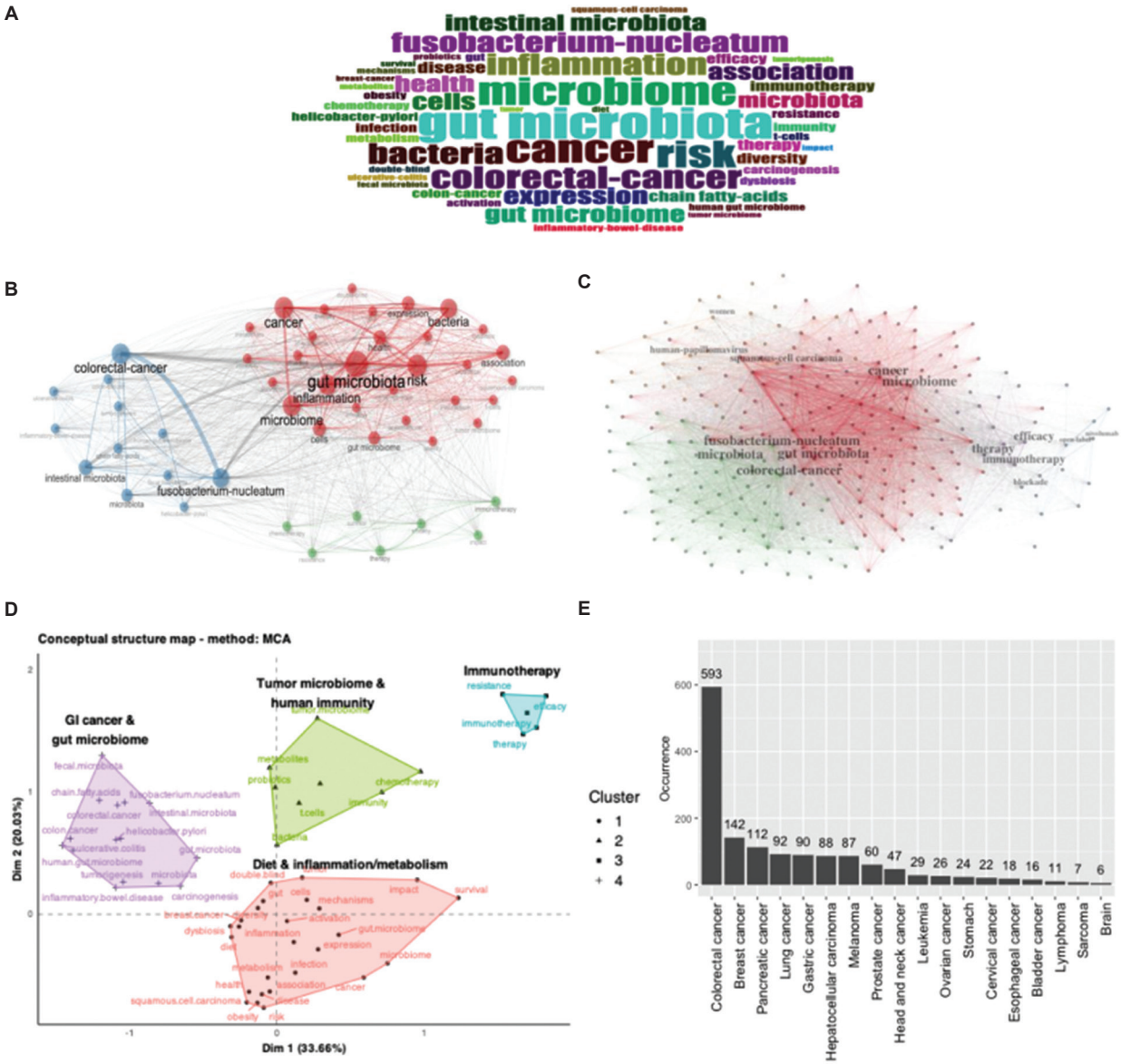


Figure 6. Keywords and co-occurrence network/map. (A) Word cloud analysis of microbiome and cancer publications (2009–2024); frequently occurring and high-impact keywords are shown in larger, bolder fonts. (B) Keyword co-occurrence network, where each keyword is represented as a node. Lines indicate co-occurrence, with thicker lines denoting higher co-occurrence frequency. (C) Co-word networks connecting keywords that appear together within the same publication. (D) Multiple correspondence analysis of the keyword co-occurrence map. (E) Frequency distribution of cancer-type-related keywords.
Abbreviation: GI: Gastrointestinal.

cluster on the conceptual structure map, more so than to the "Gastrointestinal cancer and gut microbiome" cluster. This spatial relationship suggests an emerging research focus on leveraging insights into the intratumor microbiome to develop more effective immunotherapy strategies.

To further delve into cancer-specific keywords, we isolated terms related to individual cancer types (Figure 6E). "Colorectal cancer," "breast cancer," and "pancreatic cancer" were the most frequently referenced, whereas "lymphoma," "sarcoma," and "brain cancer" appeared least often, indicating disparities in research focus across cancer types.

3.8. Research hotspots and frontiers

To provide an overview of the evolving landscape and trends in cancer microbiome research, Figure 7 presents the temporal distribution (1st quartile, median, and

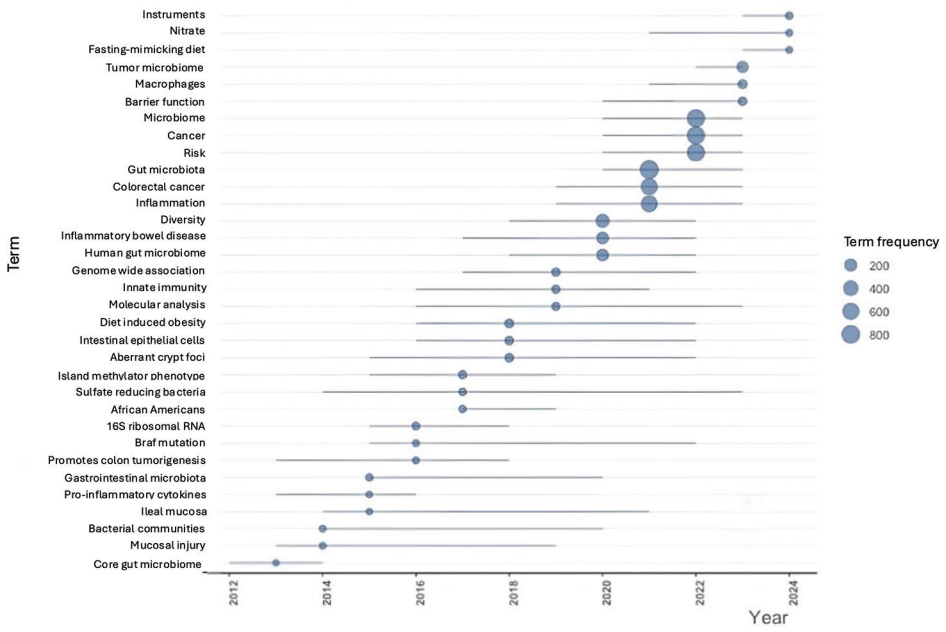


Figure 7. Temporal trends in keyword frequency. Temporal distribution of keyword prevalence in cancer microbiome research.
Notes: Lines indicate the interquartile range of publication years for individual keywords; dots mark the median of publication years, with dot size corresponding to keyword frequency.

3rd quartile) of KWP. In addition, the most cited articles associated with these terms are summarized in Table S3.

Emerging research areas, reflected by KWP terms such as "instruments" (2023–2024), "nitrate" (2021–2024), and "fasting-mimicking diet" (2023–2024), indicate a recent shift toward investigating the causal relationships between the microbiome and cancer, the roles of microbial small molecules and metabolites, and the impact of dietary interventions on the microbiome–cancer axis. Furthermore, KWP terms such as "tumor microbiome" (2022–2023), "macrophages" (2021–2023), and "barrier function" (2020–2023) highlight the growing interest in the intratumoral microbiome, the tumor microenvironment, and microbial metabolic pathways.

High-frequency KWP terms, including "gut microbiota" (831 mentions), "microbiome" (734), "colorectal cancer" (593), "inflammation" (565), and "risk" (538), represent core concepts within the field. These recurring terms highlight the sustained relevance of gut microbiome research and its connections to gastrointestinal cancers, immune regulation, and cancer risk, suggesting that this area remains a major focus for further investigation. However, it is important to note that while frequency indicates recurring attention, it does not necessarily reflect topic popularity or scientific impact.

Certain KWP terms, such as "island methylator phenotype" (24 mentions), "diet-induced obesity,"[37] and "sulfate-reducing bacteria,"[14] continue to receive consistent yet niche attention within specific research areas. In contrast, several terms that once held greater prominence have fluctuated in usage over time. For instance, "core gut microbiome" peaked between 2012 and 2014, while "proinflammatory cytokines" were most prominent between 2013 and 2016.

4. Discussion

To elucidate the latest research trends and identify potential research gaps in cancer microbiome studies, we conducted a comprehensive bibliometric analysis of global research output using appropriate keywords. While prior bibliometric studies have addressed microbiome research in specific cancers or regions, none, to our knowledge, have systematically analyzed cancer microbiome research across all cancer types.[39,40] By encompassing diverse cancer types and integrating both topical and methodological trends, our study provides a comprehensive overview that distinguishes it from earlier, more narrowly focused analyses.

Our findings revealed that most cancer microbiome research was conducted independently or collaboratively in the United States and China, with a substantial gap between these two countries and others. This disparity underscores a major concern in the field, as limited research activity in less developed regions hinders a more comprehensive

understanding of global microbial diversity and its impact on human health. To address this disparity, future efforts should prioritize international collaboration and capacity building, particularly in underrepresented regions such as parts of Africa and South America. Establishing global research partnerships can foster knowledge exchange, co-authorship, and resource sharing, while training programs and technical support can strengthen local expertise in microbiome sampling, sequencing, and analysis. In parallel, expanding access to open-source bioinformatics tools and public data repositories would empower researchers in low-resource settings to engage in microbiome research without requiring substantial infrastructure investment.

While most cancer microbiome studies have traditionally focused on the gut microbiome,[6,41-43] recent research by Dohlman *et al.*[44] and Hurst *et al.*[45] has highlighted the growing interest and importance of microbiomes residing within tumor tissues and liquid-biopsy samples. These studies emphasize the potential of non-invasive sample sources, such as liquid biopsies, for broader applications in early cancer detection and disease monitoring.

Over the past 15 years, bioinformatic and statistical analyses have become central to cancer microbiome research.[46-48] Accordingly, one of the main objectives of this study was to investigate recent trends in the use of bioinformatic tools and statistical analysis methods. Through co-citation network analysis of key reference articles, we identified four key bioinformatic and statistical tools and methods—QIIME, DADA2, LEfSe, and SIAMCAT—that are widely used in cancer microbiome research. In brief, QIIME is a comprehensive software suite for microbial community analysis, broadly used to analyze microbial marker gene sequencing data.[12,49] DADA2 is a powerful bioinformatics tool for amplicon sequence variant (ASV) analysis, offering functionality for sequencing error correction, ASV inference, and taxonomic classification.[50] LEfSe is designed to identify biomarkers with differential abundance between biological groups.[51] It employs statistical tests such as the Kruskal–Wallis test, calculates linear discriminant analysis effect sizes, and generates cladograms to visualize taxonomic hierarchies. SIAMCAT provides a versatile pipeline for statistical inference of associations between microbial communities and host phenotypes, incorporating modules for microbiome data preprocessing, statistical modeling, biomarker extraction, and model evaluation and interpretation. It is important to note that QIIME and DADA2 were developed primarily for marker gene sequencing (e.g., 16S ribosomal RNA) rather than whole metagenome sequencing. Our co-citation analysis did not identify any tools specifically tailored for preprocessing whole metagenome sequencing data. This indicates that a significant portion of cancer microbiome research still relies on marker gene sequencing, likely due to its lower cost and reduced computational requirements compared to whole-genome sequencing (WGS).[52]

However, WGS offers several advantages, including comprehensive taxonomic and functional profiling, the ability to discover novel microorganisms, and reduced analytical bias.[49] As sequencing costs continue to decline, WGS is expected to be increasingly adopted in cancer microbiome research. Bioinformaticians working in this field will need to become proficient in analytical methods specifically designed for analyzing raw WGS data. Beyond its higher cost, a main barrier to the widespread adoption of WGS is the lack of standardized bioinformatics pipelines for raw sequencing data preprocessing. Therefore, the development of standardized and computationally efficient bioinformatics pipelines spanning from quality control of raw sequencing data to taxonomy/function annotation will encourage greater utilization of the more informative WGS data, thereby improving the accuracy and reproducibility of cancer microbiome data analysis.

Our analysis of keyword temporal trends offers valuable insights into the main research topics and evolving patterns within the field. Early cancer microbiome studies, primarily relying on 16S ribosomal RNA gene sequencing, focused on analyzing the composition and differential abundance of gut microbes across various health conditions. Since 2017, the field has expanded to include microbiome-wide association studies (MWAS), investigating links between the microbiome and conditions such as obesity and inflammatory bowel disease, both of which are strongly linked to human immunity and cancer. These MWAS have also started integrating multi-omics data, such as epigenetics and gene expression, to provide a more comprehensive view. However, much of this research is still limited to correlation analysis. Since 2023, there has been a growing interest in causal analysis in microbiome research. We also anticipate increased attention to prospective intervention studies, particularly those examining how dietary changes can reshape the human microbiome to improve cancer prevention and therapeutic outcomes.

Through keyword co-occurrence pattern analysis, we identified seven major keyword clusters related to immune response, immunotherapy response, and survival prediction. While immunotherapy has revolutionized cancer treatment, its efficacy remains limited.[50-52] Radiotherapy and chemotherapy continue to serve as fundamental therapeutic modalities.[53,54] Investigating the potential of the microbiome as a predictor of response to

radiation and chemotherapy represents a valuable research direction to enhance cancer treatment outcomes.[55-57]

In addition, as expected, the microbiome has been most extensively studied in gastrointestinal cancer, including colorectal,[41,53] pancreatic,[54,55] gastric[56,57] cancer, and hepatocellular carcinoma,[58,59] due to the direct connection between the gut microbiome and the gastrointestinal tract, which facilitates both sampling and mechanistic investigation, making it a prime area for microbiome-related studies. In contrast, brain tumors have been among the least studied cancer types. The blood–brain barrier tightly regulates the passage of substances, including bacteria and their metabolites, into the cerebral environment, thereby limiting the feasibility of brain-resident microbiome investigations. Consequently, recent studies on brain cancer have shifted toward exploring the brain–gut axis.[60,61] For instance, several studies have unveiled significant differences in gut microbiota composition among glioma patients and reported that alterations in gut bacterial metabolites are associated with glioma progression.[62] In addition, sarcomas represent another underexplored group in microbiome research. Their underrepresentation may stem from multiple factors, including their relative rarity, limited availability of high-quality tissue or biopsy samples, and the challenges of modeling microbiome interactions in specialized environments such as the central nervous system. In addition, the absence of well-established mechanistic pathways linking microbiota to these cancer types may have impeded research progress. Future studies could explore whether research output aligns with disease prevalence by comparing publication volume with cancer incidence data across cancer types.

Furthermore, our analysis of the latest trends and emerging topics in cancer microbiome research reveals a paradigm shift from merely identifying core microbiomes and characterizing compositional profiles to a deeper understanding of their functional mechanisms. This growing focus involves investigating the microbiome–metabolite linkage, the interplay between the intratumoral microbiome and the tumor microenvironment, and their collective influence on host immune responses. In addition, there is a growing interest in leveraging microbiome signatures as biomarkers for personalized medicine, facilitating early cancer diagnosis, predicting response to immunotherapy, and enhancing therapeutic efficacy. Notably, strategies such as dietary modulation to reprogram the gut microbiome toward a more beneficial composition are gaining traction as complementary approaches to improve cancer treatment outcomes.

While the current bibliometric analysis provides valuable insights into global research trends in cancer microbiome studies, it is crucial to acknowledge the inherent biases and methodological limitations that may influence the findings. One major limitation of this study is the overrepresentation of English-language articles. Because the analysis relies on the WoSCC database, which predominantly indexes journals published in English, research articles written in other languages are inherently underrepresented. This linguistic bias may result in an underestimation of contributions from non-English-speaking countries, particularly those with emerging research communities. Consequently, the global research landscape depicted in this analysis may not fully capture the diversity of perspectives and advancements in cancer microbiome research. Furthermore, the reliance on a single database such as WoSCC introduces selection bias, as it does not encompass all relevant journals, including regional or emerging titles. While WoSCC is recognized for its comprehensive coverage of high-impact publications, studies published in less prominent journals or indexed in other databases such as Scopus or PubMed may be underrepresented, potentially distorting perceived research trends. These limitations underscore the need for greater inclusivity and methodological rigor in future bibliometric investigations. Expanding analyses to include multiple databases and non-English literature would yield a more comprehensive and representative overview of global research activity.

It is also important to recognize that citation-based metrics assume all citations reflect positive scholarly impact, which is not always the case. Articles may be cited in critical or controversial contexts, rather than as indicators of scientific consensus or influence. Therefore, citation frequency should be interpreted with caution and ideally complemented by qualitative assessments or sentiment analyses in future research. Future bibliometric studies could also explore alternative indicators of topic popularity by incorporating citation dynamics, thematic evolution over time, and network centrality measures, thereby providing a more nuanced understanding of research impact.

5. Conclusion

Through a comprehensive bibliometric analysis of research publications and keywords, the present study provides valuable insights into current research priorities and emerging trends within the field of cancer microbiome research. These insights can inform future research directions and support evidence-based decision-making in this rapidly evolving research field.

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Conflict of interest

The authors declare that they have no competing interests.

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Availability of data

Raw data will be made available on request to the corresponding author.

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