

From micro-vesicles to macro-trends: A bibliometric anatomy of exosome and miRNA research in acute myeloid leukemia

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ABSTRACT

Acute Myeloid Leukemia (AML) remains a significant hematological malignancy where early and accurate diagnosis is critical for improving patient outcomes and therapeutic stratification. With the emerging understanding of liquid biopsies, research on extracellular vesicles (EVs), such as exosomes, and their microRNA (miRNA) cargo has evolved as a promising domain for AML diagnostics. However, a systematic review is imperative not only to consolidate existing knowledge but also to chart relevant and timely pathways for future research in the AML diagnostics domain. Against this backdrop, in this study, we conduct a bibliometric analysis of research at the intersection of Acute Myeloid Leukemia and exosome-based biomarkers. Our aim is to map the intellectual structure of the field, identify thematic clusters and influential works, and surface emerging and underexplored directions. The Web of Science database was queried on October 01, 2025, using a comprehensive Boolean search string against three thematic pillars: (1) Disease Focus, with the terms “Acute Myeloid Leukemia*”, “AML”, “APL”, “AML-M1”, “AML-M6”, and related synonyms; (2) Vesicle/RNA Technology, including “Exosome*”, “extracellular vesicle*”, “microvesicle*”, and “miRNA”; and (3) Biomarker Application, using keywords such as “Biomarker*”, “Early Diagnosis”, and “Liquid Biopsies”. We retrieved an initial corpus of 714 documents. Upon applying a two-stage curation protocol based on predefined inclusion criteria (such as language restrictions), a final analytical sample of 710 documents was established for the robust bibliometric analysis. From our analysis, we confirm that the burgeoning domains of AML diagnostics and exosome-based biomarkers are rapidly expanding, with specific molecules like miRNAs and exosomal proteins emerging as central enablers, research focusing on prognostic stratification and residual disease monitoring (MRD) integration, and clear gaps remaining in methodological standardization (e.g., EV isolation) and clinical validation, highlighting promising directions for future investigation.

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1. Introduction

From the clinical perspective, Acute Myeloid Leukemia (AML) is integral to major global health challenges, directly impacting goals related to human health and well-being. It is a highly aggressive and heterogeneous hematological malignancy, and the development of effective, targeted therapies is crucial. Moreover, ensuring access to accurate diagnostics underpins broader goals related to equitable healthcare and patient survival by enabling early intervention, protecting patient welfare, and ensuring access to appropriate, life-saving treatments for all (Döhner et al., 2017). The diagnostic challenges in AML are critically important. Standard-of-care diagnosis relies on morphological, immunophenotypic, and cytogenetic analysis of bone marrow aspirates. This requires robust, invasive procedures and complex laboratory standards. These methods

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address aspects of disease identification, classification (e.g., FAB/WHO classifications M1-M7), and risk stratification. Accurate risk stratification aims to promote targeted, effective therapy for all patients (Papaemmanuil et al., 2016). However, AML is also intrinsically linked to clonal evolution. The dynamic and shifting genetic landscape of the disease alters the prevalence of resistant clones and therapeutic targets. This clonal heterogeneity not only threatens the stability of remission but also the safety and efficacy of treatment. Invasive bone marrow biopsies are not ideal for serial monitoring, making it difficult to track disease progression and detect emerging resistance in real-time (Arber et al., 2016). AML, while a specific disease, has emerged as a critical global oncological challenge, significantly impacting human health and survival rates worldwide. Issues related to late diagnosis, therapeutic resistance, and disease relapse have raised serious concerns for clinicians and researchers in both developed and developing countries. Studies note that despite advancements in therapy, the five-year overall survival rate for AML remains poor, particularly in elderly patients. This is mainly because of undetected minimal residual disease (MRD), tumor heterogeneity, and insufficient biological understanding, stemming from poor diagnostic resolution, weak monitoring protocols, and insufficient non-invasive tools. AML diagnostic challenges vary between patient populations and disease stages. In high-resource settings, although diagnostic systems are supported by comprehensive cytogenetic and molecular testing, robust monitoring (e.g., multi-parameter flow cytometry, RT-qPCR), and institutional expertise, these systems face emerging challenges from complex clonal heterogeneity, emerging resistance mutations, novel immunotherapies, and the need for highly personalized treatment pathways. In low-resource settings, challenges mainly stem from limited access to molecular diagnostics, fragmented care pathways, weak monitoring, and reliance on basic morphology, heightening risks of misclassification and restricting access to advanced care. This is further challenged by the risk of therapy-related AML (t-AML) from prior chemotherapy, and problems tracking clonal evolution further compound diagnostic and therapeutic issues. Liquid biopsies, or the analysis of circulating biomarkers, are often seen as a panacea to ameliorate challenges related to AML diagnosis and monitoring. In numerous systematic reviews, researchers have examined various roles of circulating biomarkers—such as exosomes and extracellular vesicles (EVs) for their stable cargo, circulating tumor DNA (ctDNA) for genetic mutations, and microRNAs (miRNAs) for their regulatory role, and advanced sequencing technologies that can revolutionize AML management (Alaggio et al., 2022). Crucially, the same biomarkers that strengthen diagnostic management also enable measurable clinical gains across the patient journey. Personalized medicine is equally central to AML therapy. Beyond reducing diagnostic invasiveness, sustainable (i.e., repeatable, non-invasive) monitoring practices minimize patient discomfort, lower healthcare costs, and support rapid, evidence-based clinical decisions. Embedding liquid biopsies into clinical monitoring systems enables preventive, resource-efficient controls (e.g., risk-based monitoring of MRD, targeted therapeutic adjustments) that curb disease progression and improve resilience to therapeutic failure and disease relapse. In short, exosome-based liquid biopsies link molecular monitoring with improved patient outcomes and long-term economic viability (Shlush et al., 2014). Despite growing interest, the literature still lacks a comprehensive overview of how exosome and miRNA-driven biomarkers (e.g., specific miRNA profiles, exosomal proteins, surface markers) influence and improve early diagnosis and monitoring within AML processes (Boonstra et al., 2020).

In this study, we conduct a bibliometric analysis of research at the intersection of Acute Myeloid Leukemia and exosome-based biomarkers. Our aim is to map the intellectual structure of the field, identify thematic clusters and influential works, and surface emerging and underexplored directions. To achieve the proposed objectives, our study builds on previous related literature to address the following research questions (RQs):

- *RQ1: What are the leading journals, publishers, authors, institutions, and countries in AML-exosome biomarker research, and how has output, citations, and collaboration evolved over time (Descriptive landscape)?*
- *RQ2: Which exosome/miRNA technologies and specific biomarkers are most prominent in the literature, and in what application contexts (e.g., M1-M7 subtypes, initial diagnosis, MRD monitoring, prognosis) (Technology prominence)?*
- *RQ3: How do these biomarkers contribute to the diagnostic, prognostic, and predictive dimensions of AML management (Biomarker contributions)?*
- *RQ4: What emerging themes, keywords, and topic clusters characterize the field, and how have research fronts shifted over time (Trends and hotspots)?*
- *RQ5: What methodological (e.g., EV isolation, normalization) and practical gaps persist, and what future research directions are most promising (Gaps and future work)?*

The remainder of this paper is organized as follows. Section 2 compares this study with prior bibliometric reviews on AML or liquid biopsies, clarifying gaps in the literature and highlighting this work's unique contributions. Section 3 presents the materials and methods, including data sources, keyword selection and refinement, and the analytical tools and procedures used. Section 4 reports the bibliometric results, offering a comprehensive overview of key trends and patterns in the field. Section 5 provides discussion and insights, interpreting the findings and outlining implications for researchers and clinicians. Section 6 concludes by summarizing the main findings, noting limitations, and proposing directions for future research.

2. Research Background

Exosomal microRNAs and their associated technologies have driven advancements across numerous fields, including significant improvements in the diagnosis and prognosis of Hematologic Malignancies (Raimondo et al., 2015). Consequently, this area has increasingly attracted academic attention, leading to a rapidly growing body of literature. To systematically synthesize insights from this expanding research, bibliometric reviews have become a valuable approach, offering a structured, data-driven alternative to traditional narrative reviews (Sueta et al., 2019). In this section, we acknowledge the body of existing bibliometric studies on related topics. This contextual analysis helps to identify gaps in the current literature and underscores the distinct contributions of our work. A review of the literature reveals that previously published bibliometric studies in this domain have often been fragmented. For instance, many studies tend to focus on a single malignancy, or they may have concentrated broadly on microRNAs but without the specific, crucial context of their exosomal transport, which is key to their stability and utility as non-invasive biomarkers. Additionally, few, if any, bibliometric studies have specifically addressed the integrated roles of these biomarkers for both diagnosis and prognosis simultaneously, which is a central focus of the present study. Moreover, previous reviews may have analyzed a limited number of publications, which can reduce the comprehensiveness and generalizability of their findings. In contrast, our study examines a dataset of 710 documents, providing a more robust and representative view of the field. In this study, the choice of tools was guided by the research objectives. Since the study focuses on both performance analysis and scientific mapping, Bibliometrix with R and Biblioshiny was selected for the entire analysis (Ghanbari et al., 2025). Its robust statistical capabilities, ease of use, and open-source accessibility make it highly suitable for both performance analysis and for exploring the structural and dynamic relationships within the literature. This approach allowed us to effectively analyze the field from both quantitative and structural perspectives.

3. Materials and Methods

This section details the materials and methods used to conduct the bibliometric analysis, which aims to map the intellectual structure and identify key research trends concerning the application of exosome- and microRNA-based biomarkers in AML. It is organized into three subsections: Subsection 3.1 discusses the source of data collection and initial retrieval settings, offering an overview of the databases and selection criteria used to compile relevant research material. Subsection 3.2 focuses on the keyword selection strategy and refinement process, detailing the approach for identifying and refining keywords to ensure comprehensive coverage of the research area. Finally, Subsection 3.3 explains the study approach and tools, providing insights into the methodologies and software utilized to perform the bibliometric analysis and visualize research trends effectively.

3.1. The Source of Data Collection and Initial Retrieval Settings

Scientometric analysis is a fundamental approach for conducting quantitative evaluations of research performance across various disciplines. It provides a systematic approach to measuring scholarly output, enabling the evaluation of research impact and productivity within various fields. Bibliometrics, a branch of Scientometrics, serves as a scientific method that analyzes literature quantitatively. This methodology, first introduced by Pritchard (1969), utilizes quantitative tools to analyze bibliographic data and can be applied to assess the scientific contributions within a specific research field (Yu et al., 2018) or the performance of particular academic journals (Yu et al., 2017).

The selection of an appropriate database is the foundational step in any bibliometric analysis. This study utilized the Web of Science (WoS) database, a comprehensive, multidisciplinary repository of peer-reviewed literature managed by Clarivate. The rationale for this selection is threefold. Firstly, the WoS Core Collection offers extensive and curated coverage of the world's most high-impact scholarly publications, including journals, conference proceedings, and book series, which ensures the quality and reliability of the data. Secondly, its advanced search functionalities and sophisticated filtering options allow for precise and replicable data retrieval protocols. Lastly, and critically for bibliometric research, WoS provides seamless data export capabilities compatible with leading analytical software, thereby facilitating a rigorous quantitative examination of the research landscape.

To guarantee the methodological rigor and accuracy of this bibliometric analysis, the Web of Science database was selected as the sole data repository. This choice was predicated on its extensive indexing of high-impact, peer-reviewed literature, which provides a comprehensive and credible dataset. This high-quality foundation enabled a thorough investigation into the intellectual structure and thematic evolution of research on the role of exosome- and microRNA-based biomarkers in AML, ensuring that our analysis is built upon the field's most influential scholarly works.

3.2. Keyword Selection Strategy and Refinement Process

The construction of the analytical corpus for this study was guided by a systematic data retrieval protocol. The Web of Science database was queried on October 01, 2025, using a comprehensive Boolean search string designed to encompass three thematic pillars:

- *Disease Focus, with the terms “Acute Myeloid Leukemia*”, “AML”, “APL”, and related synonyms for its subtypes (e.g., “AML-M1”, “AML-M6”, “Erythroleukemia*”);*
- *Vesicle/RNA Technology, including “Exosome*”, “extracellular vesicle*”, “microvesicle*”, and “miRNA”;*
- *Biomarker Application, using keywords such as “Biomarker*”, “Early Diagnosis”, and “Liquid Biopsies”.*

This initial query retrieved a corpus of 714 documents. Subsequently, this collection was subjected to a two-stage curation protocol based on predefined inclusion criteria. This protocol included:

- *A linguistic filter to ensure homogeneity (restricting the dataset to English-language publications).*
- *A document type filter to retain substantive scholarly contributions (including articles, conference papers, reviews, book chapters, books, and conference reviews) while excluding non-research materials such as editorials and notes.*

Upon review, the entire 710-document corpus was found to be compliant with these criteria. Thus, this systematic process yielded a final analytical corpus of 710 documents for the subsequent bibliometric analysis.

3.3. Study Approach and Tools

Given the extensive volume of literature, this study employs bibliometric methods to quantitatively assess and visualize the scholarly landscape of exosome- and microRNA-based biomarkers in AML. Unlike traditional systematic literature reviews, a bibliometric approach offers the capacity to analyze vast quantities of bibliographic data, providing a comprehensive, data-driven overview of research trends, intellectual structures, and emerging themes. This methodology enables a detailed exploration of the field's quantitative characteristics, structural distribution, internal relationships, and evolving patterns, thereby facilitating the identification, evaluation, and forecasting of its developmental trajectory.

In this study, bibliometric analysis primarily emphasizes performance analysis and scientific mapping to uncover the trajectory of research on the role of exosome- and microRNA-based biomarkers in AML, though additional analyses are also incorporated to provide a well-rounded perspective. Performance analysis (Cobo et al., 2015) relies on activity indicators that measure publication productivity and influence through metrics such as the number of publications (NP), number of total citations (NC), and average citations per publication (AC). Key items analyzed include sources, authors, country/region, institution performance, and other relevant metrics, allowing for a comprehensive assessment of publication productivity and influence (Mingers & Leydesdorff, 2015). Scientific mapping analysis, on the other hand, visualizes the structural and dynamic organization of knowledge within a specific topic or journal (Iwami et al., 2020). Key analyses in this area include citation analysis (Dabic et al., 2015), co-authorship analysis (van Eck & Waltman, 2010), co-occurrence analysis (Kamdem et al., 2019; Luo & Lin, 2021; Villar et al., 2023), timeline analysis (Yin et al., 2020; Zahid et al., 2025), and other methods, such as network and cluster analyses, to provide a comprehensive understanding of the research landscape. Each of these methods contributes to an enriched understanding of the interconnections and progression of research within the field. The analytical process and results are systematically organized and illustrated in Figure 1, which presents the comprehensive research framework for this study. To conduct this analysis, a powerful visualization tool was used: the open-source R-package Bibliometrix (Aria & Cuccurullo, 2017). This tool is widely recognized for its capabilities in visualizing bibliometric data and supporting the investigation of complex research landscapes.

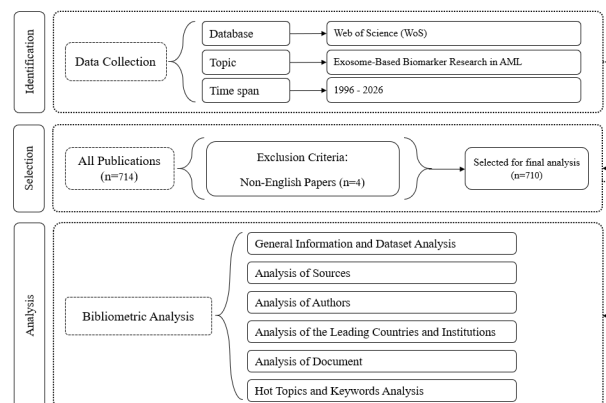


Fig 1. Visual Representation of the Research Framework and Analytical Procedures (Shabani et al., 2025)

4. Results

This chapter provides a comprehensive bibliometric investigation into the scholarly literature on the role of exosome- and microRNA-based biomarkers in AML. The analysis is methodically organized into six specialized subsections. The initial subsection, 4.1, presents foundational information and an analysis of the dataset, offering an overview of the core data and publication trends. Subsequently, Subsection 4.2 scrutinizes the publication sources, analyzing disciplinary trends, key journals, source dynamics, and leading publishers. Subsection 4.3 is devoted to an analysis of authors, exploring metrics such as scholarly productivity, temporal output patterns, influential researchers, and collaborative networks. The contributions of prominent countries and institutions are evaluated in Subsection 4.4, which identifies the most significant national and organizational actors and examines patterns of international collaboration. Subsection 4.5 investigates emerging themes through keyword analysis, pinpointing high-frequency terms, trending topics, and visualizing intellectual structures via thematic maps, co-occurrence, and word-cloud analyses. Finally, Subsection 4.6 employs clustering and document-level analysis, utilizing techniques like bibliographic coupling, multiple correspondence analysis, and multidimensional scaling to identify the most seminal works in the field. Collectively, this multi-faceted examination furnishes a holistic understanding of the current research landscape.

4.1. General Information and Data Set Analysis

The foundational step of this bibliometric investigation was the systematic extraction of data from the Web of Science database, which resulted in a final corpus of 710 documents. Prior to analysis, the dataset underwent a rigorous evaluation to verify the integrity and completeness of its metadata, with the detailed findings presented in the subsequent table. This quality assessment demonstrated that essential bibliographic fields are of exceptional quality. Specifically, crucial metadata such as Author (AU), Document Type (DT), Journal (SO), Language (LA), Publication Year (PY), Title (TI), and Total Citations (TC) were fully populated (0.00% missing) and classified as 'Excellent'. Moreover, fields including Affiliation (C1), Corresponding Author (RP), Cited References (CR), Abstract (AB), Keywords Plus (ID), and Digital Object Identifier (DI) displayed only negligible incompleteness, with missing values ranging from 0.14% to 5.35%, thus being rated as 'Good'. Conversely, a notable deficiency was observed in the author Keywords (DE) field, which was categorized as 'Poor' due to a high rate of missing data at 21.83%. Of greatest concern was the complete absence of information for Web of Science Categories (WC), with a 100% data gap in this field. This appraisal confirms that the dataset provides a reliable basis for descriptive, performance, and co-citation analyses (given the 'Good' status of CR). However, the complete lack of Web of Science Category (WC) data renders category-based analyses infeasible. Furthermore, the significant gap in author Keywords (DE) information will necessarily constrain the scope of keyword-related investigations.

Table 1
Metadata Completeness Overview for Initial Bibliometric Search Results ($N = 710$)

Metadata	Description	Missing Count	Missing (%)	Status
AU	Author	0	0.00%	Excellent
DT	Document Type	0	0.00%	Excellent
SO	Journal	0	0.00%	Excellent
LA	Language	0	0.00%	Excellent
PY	Publication Year	0	0.00%	Excellent
TI	Title	0	0.00%	Excellent
TC	Total Citation	0	0.00%	Excellent
C1	Affiliation	1	0.14%	Good
RP	Corresponding Author	1	0.14%	Good
CR	Cited References	16	2.52%	Good
AB	Abstract	19	2.68%	Good
ID	Keywords Plus	32	4.51%	Good
DI	Digital Object Identifier (DOI)	38	5.35%	Good
DE	Keywords	155	21.83%	Poor
WC	Web of Science Categories	710	100%	Completely Missing

The analytical corpus for this investigation comprises 710 documents, encompassing the publication period from 1996 to 2026. The curated literature, produced by a collective of 4,601 authors, exhibits a mean citation rate of 39.1 per document. Articles constitute the predominant document type, accounting for 437 of the publications. Moreover, the thematic breadth of the research is underscored by the identification of 1,871 Keywords Plus and 1,460 author-supplied keywords. A comprehensive descriptive statistical summary of these bibliometric indicators is systematically presented in Table 2, offering deeper insights into the primary trends and focal areas of the field.

Table 2
Summary of the Descriptive Information

Description	Results	Description	Results
MAIN INFORMATION ABOUT DATA		AUTHORS COLLABORATION	
Timespan	1996:2026	Single-authored Docs	32
Sources (Journals, Books, etc.)	322	Co-Authors per Doc	7.81
Documents	710	International Co-authorships %	23.24
Document Average Age	6.5	DOCUMENT TYPES	
Average Citations per Doc	39.1	Article	437
References	39231	Article; Book Chapter	12
DOCUMENT CONTENTS		Article; Proceedings Paper	1
Keywords Plus (ID)	1871	Article; Retracted Publication	2
Author's Keywords (DE)	1460	Letter	2
AUTHORS		Meeting Abstract	16
Authors	4601	Proceedings Paper	1
Authors of Single-authored Docs	31	Review	238
		Review; Book Chapter	1

Based on the “Annual Scientific Production” chart (Fig 2a), the scholarly output on this topic shows a distinct growth path. The field's evolution occurred in two main stages. Until around 2005, the research landscape was relatively quiet, with production limited to approximately 1 to 2 articles per year, indicative of an exploratory phase. However, the period beginning around 2006 marked a turning point, unleashing a rapid and steady increase in scholarly work. Annual production rose sharply, reaching a clear peak of over 80 articles around 2020. Following this peak, the publication rate shows a decline in the subsequent years shown (through 2025). This surge in research indicates a clear escalation in research activity and a strengthening of academic interest in this domain over the last two decades. Meanwhile, the "Average Citations per Year" chart (Fig 2b) reveals high volatility. A significant spike occurred around the year 2008, where average citations reached nearly 25. Apart from this major spike, average citations fluctuated at a much lower level (generally between 5 and 10) during the other years in this period.

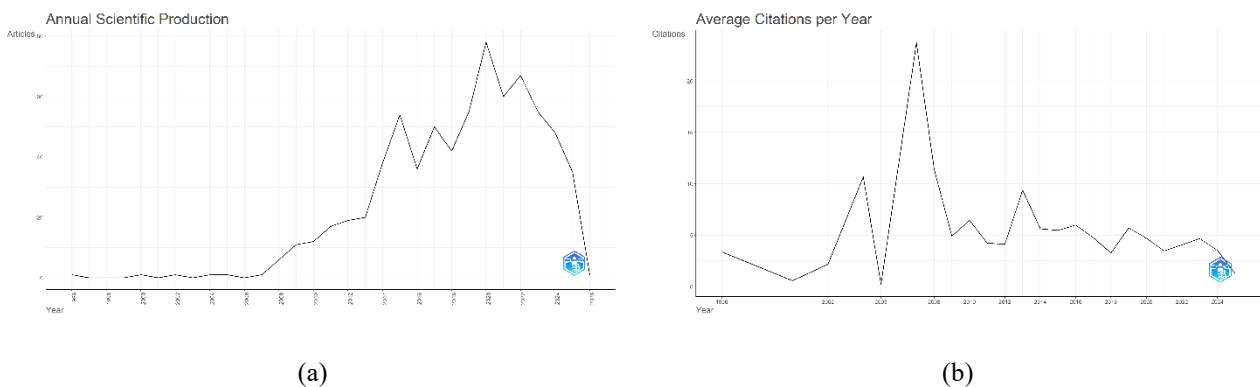


Fig 2. Publication Output. (a) Annual Scientific Production (b) Average Number of Citations Per Year

4.2. Analysis of Sources

4.2.1. Discipline-wise analysis and Sources dynamics

A central finding of this bibliometric analysis is the delineation of the primary intellectual forums where research related to oncology and hematology is being explored.

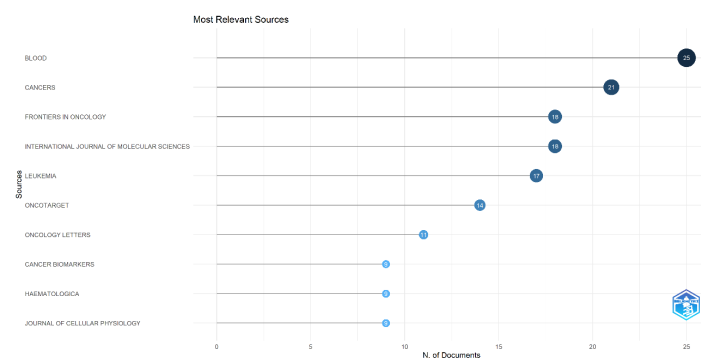


Fig 3. Most Relevant Sources Based on Number of Publications

Fig. 3 identifies the ten most prolific sources, revealing that the scholarly discourse is concentrated within a few key publication outlets. The journal **Blood** emerges as the foremost venue, with 25 publications. This source is closely followed by **Cancers** (with 21 publications) and **Frontiers in Oncology** (with 18 publications), which are also central to this domain. The concentration of publications in these premier sources underscores their pivotal role in shaping the research agenda and defining the intellectual boundaries of this field. To better understand the evolving role of key publication outlets, Fig. 4 visualizes the growth trajectory of the five journals with the highest publication counts. The data is depicted through two perspectives: part (a) displays the total, accumulating contribution over the entire period (cumulative occurrences), while part (b) shows the year-over-year publication frequency (annual occurrences). This trend analysis underscores the escalating academic interest in this research area, as evidenced by the expanding body of literature being published across these leading scholarly venues in the last few years.

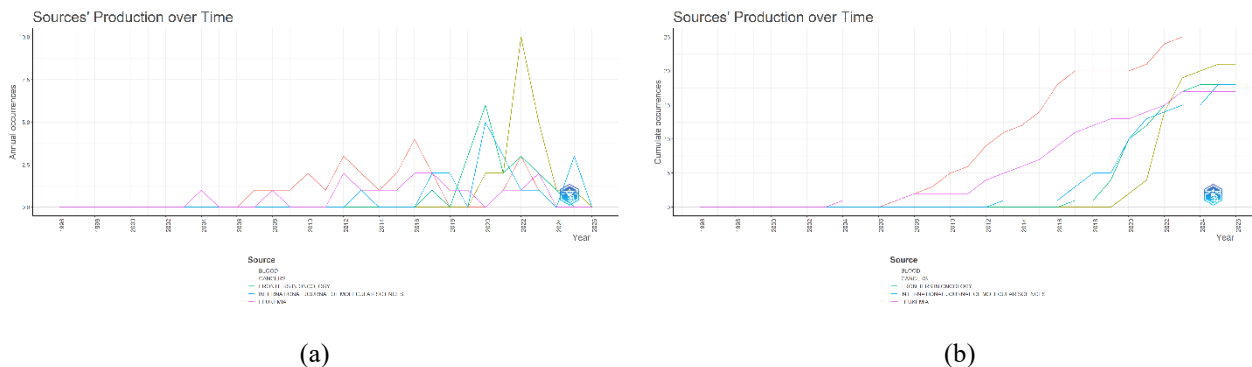


Fig 4. Top Sources Dynamics (a) Annual Occurrences (b) Cumulative Occurrences

4.2.2. Core sources

Bradford’s Law serves as a method to identify the core journals within a specific discipline by categorizing them according to publication frequency. This approach is effective for pinpointing the most influential sources in the extensive literature on exosome-based biomarker research in AML. As illustrated in Fig. 5, applying Bradford’s Law organizes the sources into three distinct zones, each reflecting a different degree of publication concentration. The primary core zone (Zone 1) is highly selective, containing only the top 23 sources as detailed in Table A1.

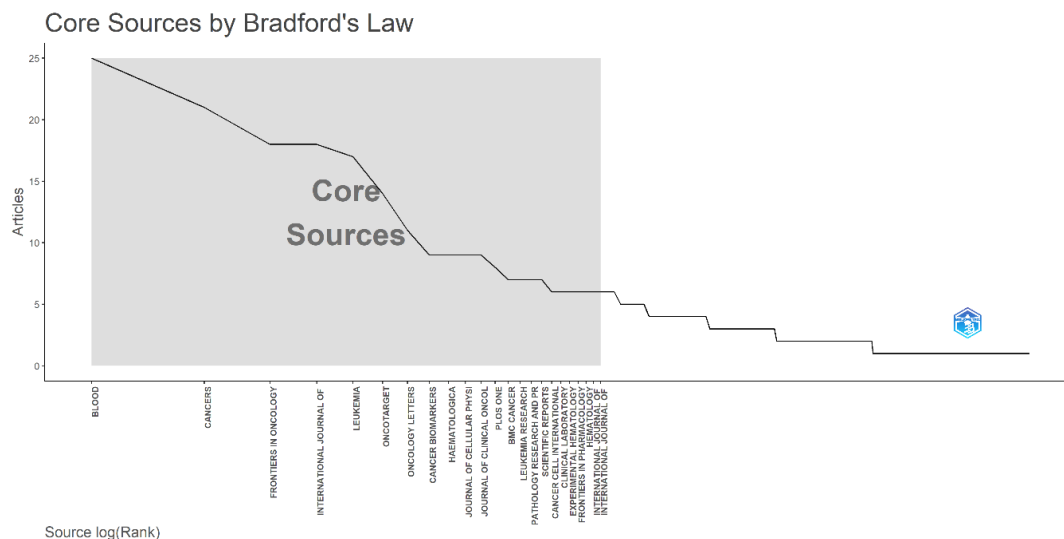


Fig 5. Bradford’s Law (Core Sources)

The nucleus of the research literature, designated as Zone 1 and outlined in Table A1, is composed of the key journals that guide the scholarly conversation in this domain. It is noteworthy that these 23 core sources are responsible for a total of 238 publications (based on the cumulative frequency), establishing them as the primary outlets for research on exosome applications in AML. Their concentration of relevant articles highlights their essential function in advancing the field.

4.2.3. Sources impact

The scholarly influence of various journals on AML and exosome-based biomarker research is detailed in Table 3, which employs three primary bibliometric indicators: the H-index, G-index, and M-index. The table is curated to include the most impactful sources, defined as those with an H-index of at least 8. The H-index provides a composite measure of publication volume and citation impact. For example, “Blood” and “Leukemia” top the list with an H-index of 16, signifying 16 articles with at least 16 citations each. The G-index offers a more nuanced view by emphasizing the most-cited articles in a source's portfolio. Here again, “Blood” is the leader with a G-index of 25. Finally, the M-index normalizes a source's H-index by its publication history timeline, revealing the rate of its impact. The journal “Cancers” stands out with the highest M-index (2.0), reflecting its very strong and immediate influence within the field since its start year of 2020. Overall, this multi-metric analysis effectively highlights the journals that are central to the academic conversation in this domain.

Table 3
Impact Metrics of Key Sources (H-index Threshold: 8)

Source	H index	G index	M index	TC	NP	PY start
Blood	16	25	0.842	2737	25	2007
Leukemia	16	17	0.727	2216	17	2004
Cancers	12	17	2	304	21	2020
International Journal of Molecular Sciences	12	18	0.923	732	18	2013
Oncotarget	12	14	1.091	468	14	2015
Frontiers in Oncology	9	17	1	302	18	2017
Journal of Cellular Physiology	9	9	0.818	375	9	2015
Journal of Clinical Oncology	9	9	0.5	1924	9	2008
Haematologica	8	9	0.333	354	9	2002

4.3. Analysis of Authors

4.3.1. Authors productivity

Lotka's Law is a fundamental bibliometric principle that describes the distribution of scientific productivity. The law posits that the number of authors who produce n publications is inversely proportional to n^2 . Essentially, this means a small cohort of highly prolific authors is responsible for a large portion of the literature, while the vast majority of researchers contribute only one or two papers. The data for exosome-based biomarker research in AML, as depicted in Fig. 6 and Table A2, is consistent with this principle. The findings show a characteristically skewed distribution of author productivity, confirming that a few authors are exceptionally productive in this field.

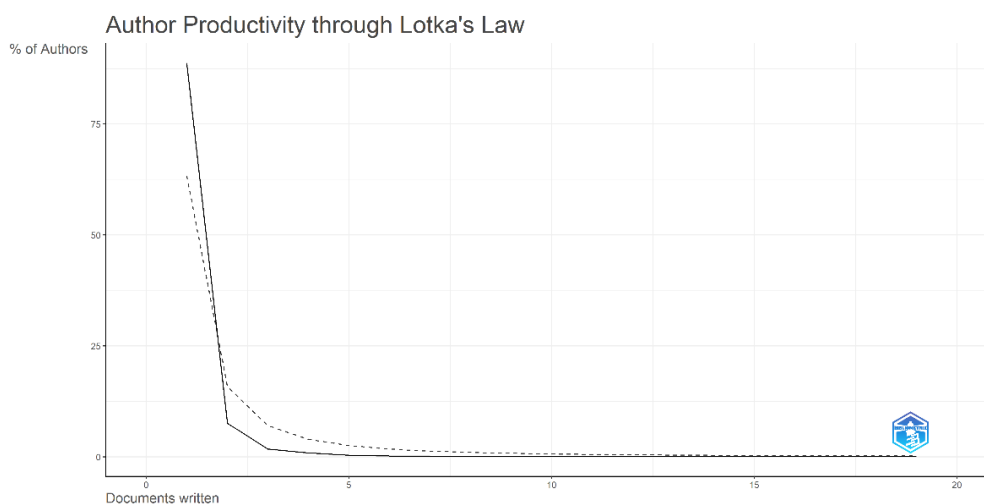


Fig 6. Lotka's Law (The frequency distribution of scientific productivity)

The data presented in Table A2 confirms a highly skewed productivity distribution among the authors in this field. An overwhelming majority of authors, approximately 88.8% (4085 authors), have contributed only a single publication. The proportion of authors decreases sharply with increased output, with 7.5% (347 authors) having written two papers and only 1.8% (81 authors) having written three. This pattern exemplifies a well-known characteristic of academic publishing, where a small cohort of prolific researchers generates a disproportionately large volume of the literature, while most scholars contribute a limited number of works. This phenomenon is a typical feature observed across many scientific disciplines.

4.3.2. Most Relevant Authors and Authors' Impact

This section identifies the leading scholars who have significantly advanced the field of exosome-based biomarker research in AML. The top 10 most prolific authors, ranked by their total number of publications, are presented in Fig. 7. Among the most prominent researchers is **Marcucci Guido**, who has authored 19 publications, demonstrating high productivity in the domain. Other key contributors, **Bloomfield Clara** and **Mrozek Krzysztof**, have published 13 works each (according to the figure), also showing significant contributions to this research area.

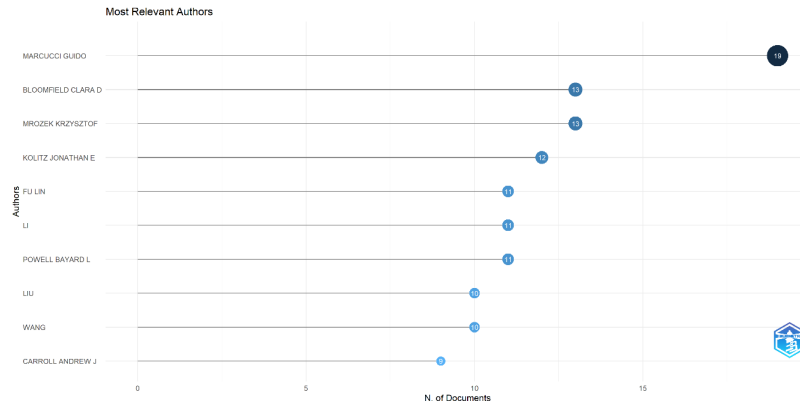


Fig 7. Most relevant authors based on number of publications

Assessing an author's scholarly contribution requires metrics more sophisticated than raw publication counts, especially in highly collaborative research areas. While methods like the fractionalized article count offer a more precise apportionment of credit for multi-authored works, this study employs a more holistic assessment of impact centered on the h-index. This well-established metric integrates both productivity and citation impact, offering a robust view of a researcher's influence.

Table A3 presents a detailed hierarchy of the top 10 most influential researchers, supplementing the h-index with other key indicators to provide a multi-dimensional perspective on their scholarly impact. Based on this analysis, **Marcucci Guido** is identified as the foremost scholar in the field, with an h-index of 18 that underscores his substantial and sustained influence. Following closely are **Bloomfield Clara** and **Mrozek Krzysztof**, with h-indices of 15 respectively, solidifying their positions as leading contributors. The consistent publication records and high citation counts of these researchers confirm their instrumental role in shaping the academic discourse on exosome-based biomarker research in AML.

4.3.3. Authors Productivity Over Time

The publication trajectory of the leading researchers in exosome-based biomarkers in AML is visualized over time in Fig. 8.

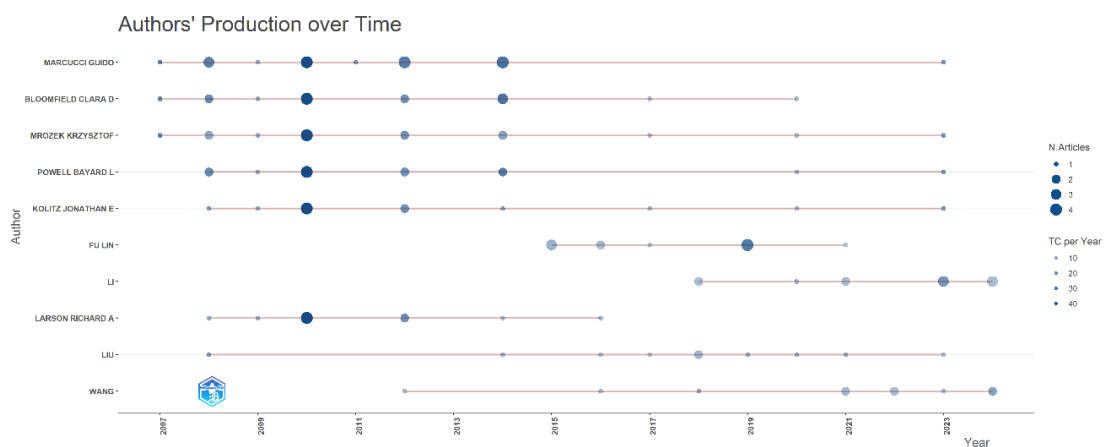


Fig 8. Top Author's Production Over Time

The graph encodes two key metrics: the size of each bubble indicates the number of articles (N.Articles) published by an author in a specific year, while the color depth signifies the total citations received annually (TC per Year). The case of

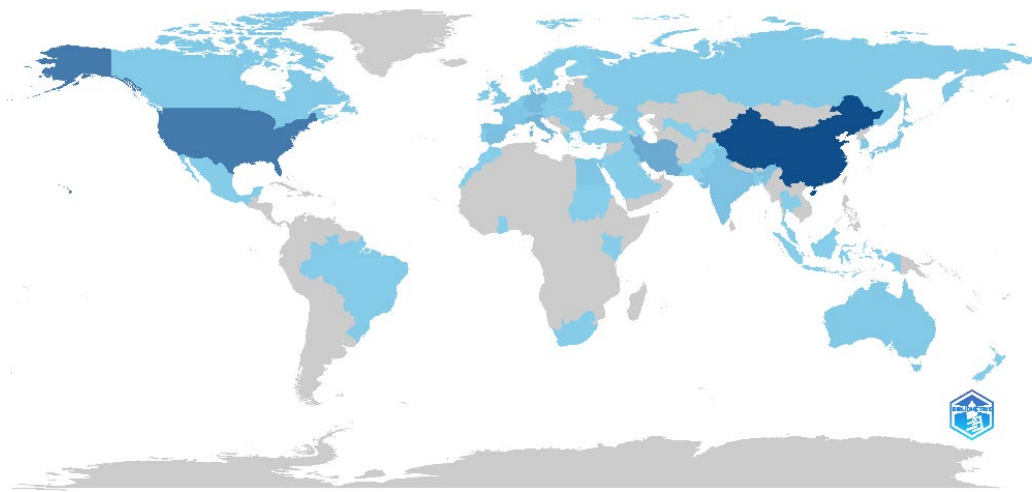
Marcucci Guido provides a clear example. He began publishing on this topic in 2007. While his most prolific year was 2010 with 4 articles (indicated by the largest bubble size, N.Articles = 4), his highest citation impact (darkest bubble color, representing TC per Year > 40) appears to be in 2009 (with 2 articles) and 2012 (with 3 articles). The visualization effectively captures this dynamic, with a larger bubble in 2010 reflecting his peak productivity and darker bubbles in 2009 and 2012 highlighting the high impact of his work in those years. The figure provides this temporal analysis for all top authors in the field.

4.4. The Leading Countries and Institutions

4.4.1. Most Relevant Countries

An investigation into the leading countries in the field of exosome-based biomarker research in AML reveals a distinct geographical landscape. In terms of sheer research productivity, as illustrated in Fig. 9, a few countries are dominant. **China leads with a commanding total of 250 publications, followed by the USA (129) and Iran (46).** Other significant contributions are noted from Italy (38) and Germany (27). This finding suggests that research activity in this domain is largely centered within a select group of nations, a pattern likely influenced by factors such as academic infrastructure and research funding.

Country Scientific Production



Region	Frequency	Region	Frequency
CHINA	250	INDIA	20
USA	129	SPAIN	18
IRAN	46	EGYPT	13
ITALY	38	AUSTRALIA	10
GERMANY	27	FRANCE	9

Fig. 9. Leading Countries based on Publication Count

For a more granular analysis of scholarly influence, Table 4 presents a breakdown of the most-cited countries, detailing their total citation counts to illuminate their global impact in the domain of exosome-based biomarker research in AML.

Table 4

Most cited countries (Top 10)

Country	Total Citations	Average Article Citations
USA	11249	87.20
CHINA	5795	23.20
ITALY	1756	46.20
GERMANY	1267	46.90
FRANCE	784	87.10
IRAN	627	13.60
NETHERLANDS	619	123.80
UNITED KINGDOM	591	65.70
BELGIUM	485	121.20
SPAIN	475	26.40

4.4.2. Most Relevant Affiliations

Subsequent to the analysis of the most relevant countries, this section evaluates the most relevant affiliations based on their number of publications in the field of exosome-based biomarker research in AML. The foremost institution is The Ohio State University, with 80 articles authored on this topic. It is followed by Shahid Beheshti University of Medical Sciences, which has contributed 45 articles to the field. As detailed in Table 5, Nanjing Medical University and Tabriz University of Medical Sciences are ranked next, each contributing 42 articles. These and other distinguished institutions have been instrumental in advancing the research landscape, reflecting a strong commitment to enhancing the understanding of this domain.

Table 5

Most Relevant Affiliations based on Number of Publications (Top 10)

Affiliations	Number of Publications
The Ohio State University	80
Shahid Beheshti University of Medical Sciences	45
Nanjing Medical University	42
Tabriz University of Medical Sciences	42
The University of Texas MD Anderson Cancer Center	40
Huazhong University of Science and Technology	37
University of Pittsburgh	37
Peking University	34
Central South University	32
Chinese People's Liberation Army General Hospital	31

To supplement the data presented in Table 5, Fig. 10 offers a temporal analysis of the productivity of leading research affiliations. This visualization graphically depicts the scholarly output over time for the top five institutions (Ohio State University, Shahid Beheshti University of Medical Sciences, Nanjing Medical University, Tabriz University of Medical Sciences, and The University of Texas MD Anderson Cancer Center) in the domain of exosome-based biomarker research in AML. The figure illustrates the evolving research trends and contribution patterns of these key affiliations, providing a dynamic perspective on their scholarly engagement with the field over the years.

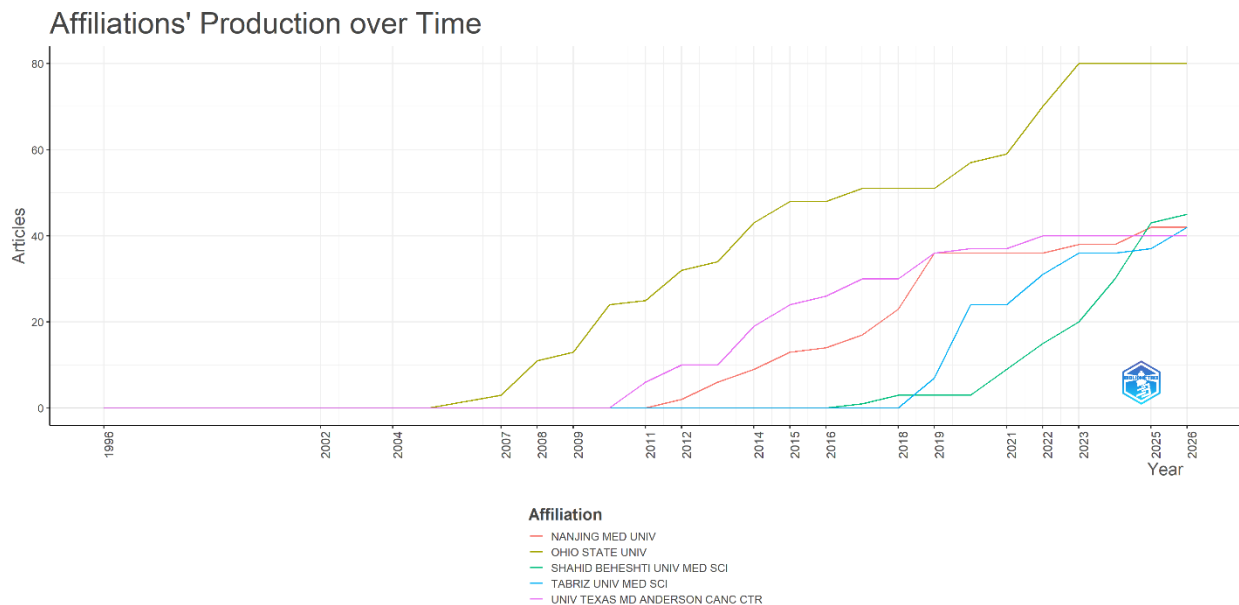


Fig10. Affiliation production over time (Top 5)

4.4.3. Countries Collaborations

This section examines the patterns of international collaboration in the field of exosome-based biomarker research in AML, an analysis essential for fostering the global exchange of academic knowledge. To understand the collaborative dynamics in this field, it is crucial to distinguish between Single Country Publications (SCP), representing intra-national collaboration, and Multiple Country Publications (MCP), which signify international partnerships. This distinction, based on the countries of corresponding authors, provides insight into the research networks driving the field of AML and exosome-based biomarker research. As illustrated in Fig. 11, the balance between these collaboration types varies significantly by country. China leads in both the total number of corresponding authors (250 articles) and in SCP (224 articles), indicating a strong

domestic research focus. In contrast, the USA, which ranks second overall (129 articles), is the leader in absolute MCP (38 publications), highlighting its central role in global research networks. A more granular analysis is provided in Table A4, which details the collaboration metrics for the top 20 countries. The MCP ratio (MCP %) is a particularly insightful metric for gauging a country's international orientation. For example, Canada and Germany exhibit high MCP ratios of 55.6% and 48.1%, respectively, demonstrating a strong emphasis on international collaboration despite having fewer total publications than the top-ranked nations. A higher ratio signifies a greater degree of inter-country partnership, whereas a lower ratio (such as China's 10.4%) suggests a more nationally-focused research strategy.

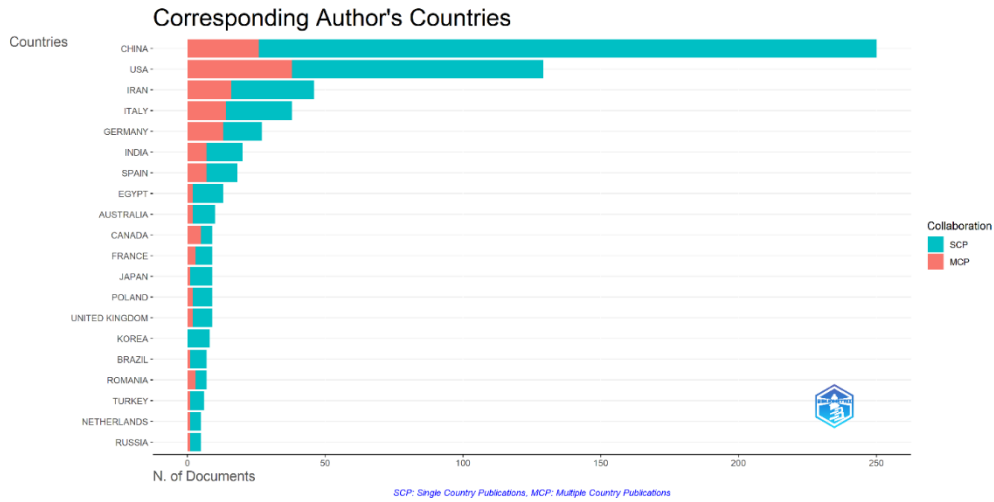


Fig 11. The Visual Representation of the Top Corresponding Authors' Country

4.5. Hot Topics and Keywords Analysis

4.5.1. Most Frequent Words

In this section, we analyze the keywords used in publications from 2000 to 2026. This keyword analysis will help us identify the hot topics within the field. The most frequent author keywords are presented in Fig. 12. The author keyword analysis provides insight into research trends from the perspective of the researchers themselves. In the author keyword analysis (Figure 12), “Acute Myeloid Leukemia” emerges as the most common keyword, with 177 occurrences. This is followed by “prognosis” with 78 occurrences and “microna” with 77 occurrences. This reflects the centrality of the disease itself, along with a strong focus on its clinical outcomes and the emerging molecules under investigation (such as microRNA and biomarkers).

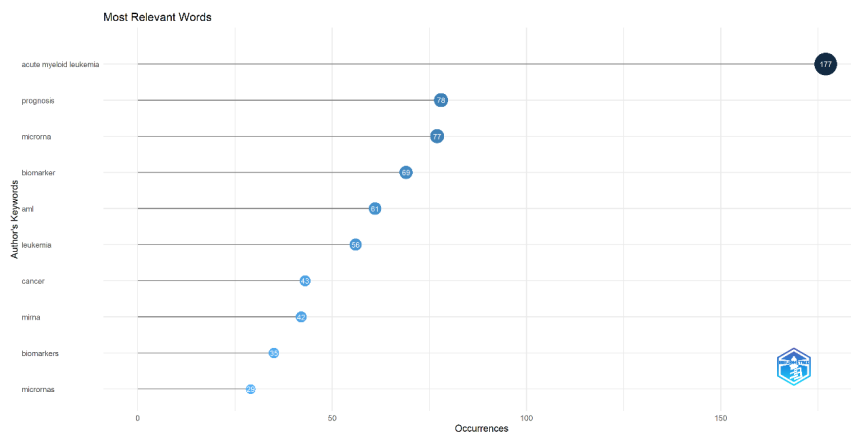


Fig 12. Most Relevant Author Keywords

After conducting the keyword analysis, this section is devoted to further examination of the relationships and patterns in the data. Fig. 13 displays the “Three-Field Plot” analysis, which provides a deeper look at the interactions between authors, disciplinary evolution, and authors' countries. In Fig. 13, the analysis explores the three parameters: Author (AU), Disciplinary Evolution (Author's Keywords - DE), and Author Country (AU_CO). This three-field plot visually represents how authors are connected with their specific keywords and the countries they are associated with. The size of the tiles within the plot indicates the magnitude or significance of the relationships between these parameters. Larger boxes represent stronger connections, meaning that certain authors, keywords, and countries have a more prominent role in shaping the

literature on exosome-based biomarkers in AML. For instance, the strong connection between countries like China, the USA, and Iran and authors (such as Marcucci Guido and Bloomfield Clara D) using keywords like “Acute Myeloid Leukemia”, “Prognosis”, and “Microna” indicates a significant presence in this area of research, as represented by the larger boxes and thicker flow lines.

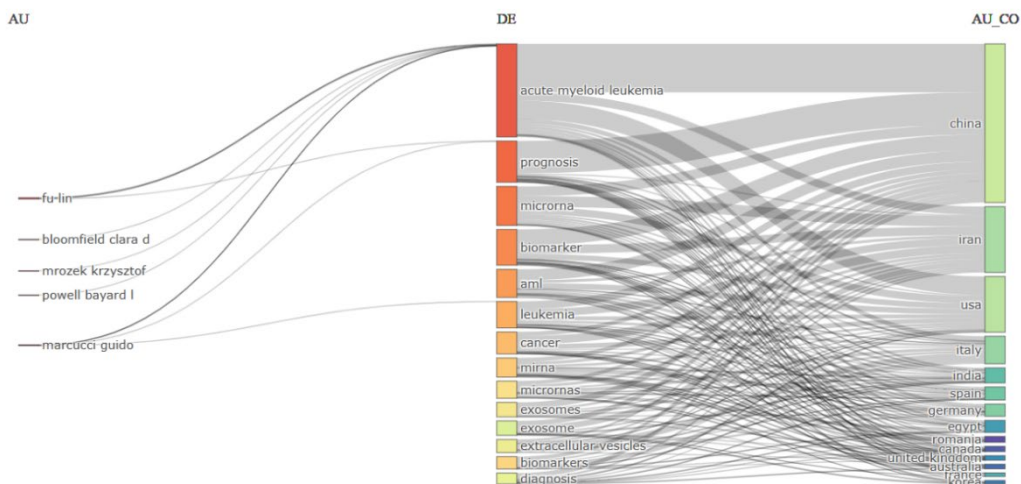


Fig. 13. Three-Field Plot (Author, Disciplinary Evolution (Author’s keywords), and Author Country)

4.5.2. Trend Topics Over Time

A trending topic analysis serves as a valuable mapping tool that aids in illustrating the progression of literature over time. Figure 14 shows the trend topics over time, derived from Author Keywords. This figure represents the frequency of key terms in publications over the years, allowing us to observe how certain topics have gained prominence in the field of exosome-based biomarker research in AML.

As depicted in Fig. 14, core keywords such as “Acute Myeloid-Leukemia”, “Expression”, “Microna”, and “Prognosis” show a significant increase in frequency in recent years (especially around 2019-2020), indicated by the large bubble size (Term frequency). This trend signifies a strong academic focus on understanding the molecular mechanisms and prognostic value in AML. Concurrently, the newer emergence of terms like “exosomes”, “extracellular vesicles”, and “immunotherapy” indicates a shift towards advanced, emerging research fronts within this domain.

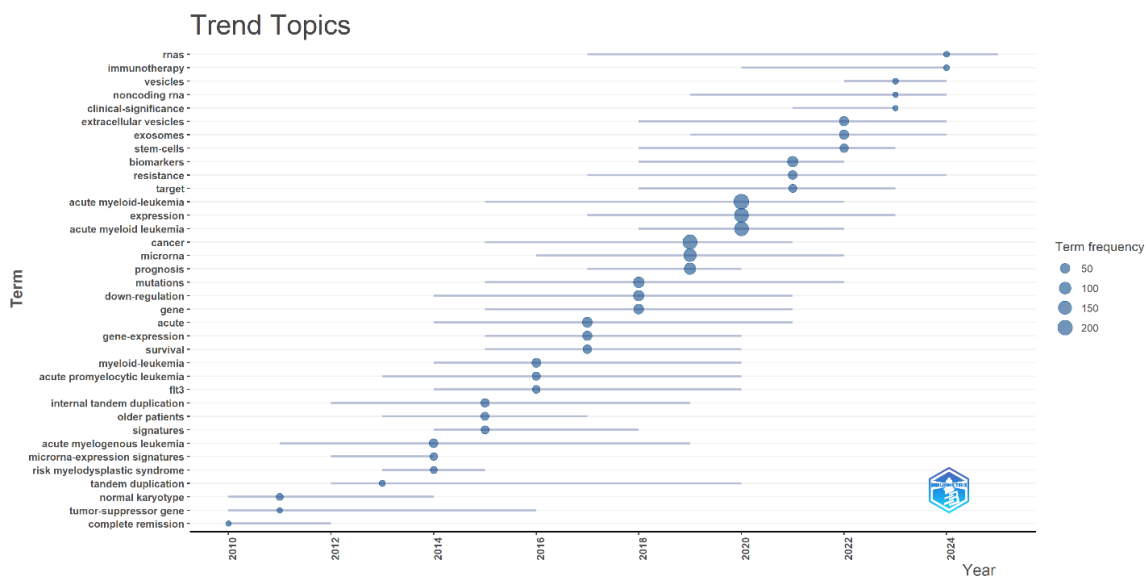


Fig. 14. Trend Topics Over Time Author Keywords

4.5.3. Thematic Map

One of the principal analyses performed in this study involves the development of a thematic map focusing on research in AML and its associated biomarkers. The aim of this analysis is to gain a nuanced understanding of the current landscape and to explore the field's sustainability and future growth potential. By constructing this thematic map, researchers and stakeholders can extract valuable insights into promising research avenues, guiding them toward areas of inquiry that hold potential for further development and innovation. This type of analysis is instrumental in providing strategic knowledge to those invested in advancing the field.

The thematic map is created by examining clusters of author keywords and their interconnections, identifying and defining significant themes. Each theme is characterized by two key attributes: density and centrality. In this context, density is plotted on the vertical axis (Development degree) and centrality on the horizontal axis (Relevance degree). Centrality reflects the extent of interconnectedness among different themes in the network. It measures the thematic network's integration, with higher centrality indicating a greater number of connections to other topics, signifying its importance within the research ecosystem. Density, on the other hand, represents the internal cohesiveness of a thematic cluster, showing how well-developed and structured the topic is. Higher density implies that a theme has a strong internal structure, suggesting its ability to sustain future research efforts.

Fig. 15 displays the thematic map of AML biomarker research, divided into four quadrants (Q1 to Q4). The map offers a visual depiction of the identified themes, their density, and their centrality within the field. This graphical representation facilitates a comprehensive understanding of the thematic structure and development of the research landscape, aiding researchers in identifying both mature and emerging areas of inquiry that can inform and shape future research directions.

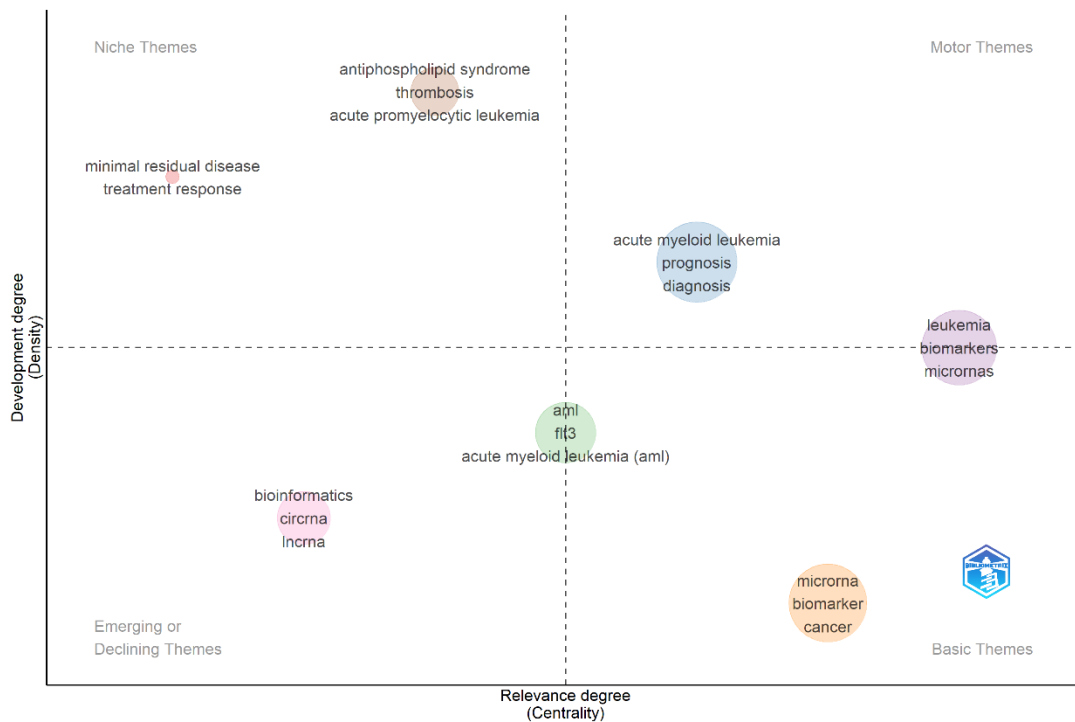


Fig. 15. Thematic map

In the thematic map presented, the upper right quadrant (Q1) represents motor themes (driving themes). These themes hold strong relevance (centrality) and development (density), significantly shaping the research landscape. The lower right quadrant (Q4) consists of basic themes (foundational themes) that serve as essential building blocks, contributing fundamental concepts and methodologies to the field. Themes in the upper left quadrant (Q2) are considered specialized or niche themes; while they are highly developed within their scope, their overall contribution (centrality) to the broader development of the field remains limited. Lastly, the lower left quadrant (Q3) includes emerging or declining themes, indicating areas that are either gaining momentum or fading in relevance within the research domain.

From the figure, it is evident that themes like “Acute Myeloid Leukemia,” “Prognosis,” and “diagnosis” (blue cluster), as well as “leukemia,” “biomarkers,” and “micromas” (purple cluster), occupy prominent positions in Q1, showcasing their importance and well-developed nature in driving current research. These themes are influential and continue to lead the discourse.

Meanwhile, themes such as “MicroRNA,” “Biomarker,” and “Cancer” (orange cluster) and the highly central cluster including “aml” and “flt3” (green cluster) in Q4 represent foundational concepts that are crucial for advancing research in this field. They provide essential frameworks that underpin developments in the field.

In Q2, themes like “Minimal Residual Disease” and “Treatment Response” (pink cluster), as well as “thrombosis” and “acute promyelocytic leukemia” (red cluster), are internally well-connected but have a more focused or niche application. These themes may require further integration to have a larger impact on the broader research landscape.

Finally, the lower left quadrant (Q3) houses emerging or less developed themes, such as “Bioinformatics,” “Circrna,” and “Lncrna” (dark purple cluster). These themes are at a crossroads, either gaining attention for future research or potentially becoming less relevant. Overall, this thematic map offers valuable insights into the various themes shaping AML biomarker research, their interconnections, and their role in the development and evolution of the field.

4.6. Documents Analysis

4.6.1. The Most Impactful Documents

Table 6 shows the 10 most globally cited documents in the research of exosome-based biomarker research in AML, with worldwide citation counts ranging from 293 to 787.

Lindsley RC (2015), Daver N (2019), Guarnerio J (2016), Breems DA (2008), and Berindan-Neagoe I (2014) have the most citations worldwide, receiving 787, 750, 547, 486, and 461, respectively, and their papers are ranked among the top five most frequently referenced publications.

Table 6

Top 10 Cited Documents in Exosome-Based Biomarker Research in AML

Authors	Total Citations	TC per Year	Normalized TC
Lindsley et al. (2015)	787	71.55	13.08
Daver et al. (2019)	750	107.14	18.76
Guarnerio et al. (2016)	547	54.70	9.14
Breems et al. (2008)	486	27.00	2.36
Berindan-Neagoe et al. (2014)	461	38.42	6.82
Mrózek et al. (2007)	451	23.74	1.00
Ferrara & Schiffer (2013)	447	34.38	3.67
Szczepanski et al. (2011)	368	24.53	5.78
Whiteside (2013)	318	24.46	2.61
Sun et al. (2013)	293	22.54	2.40

A qualitative analysis of the table's top-cited documents validates the quantitative findings of this study and illuminates the field's intellectual structure. The Lindsley et al. (2015) paper, leading with 787 citations, is a foundational work. It established a critical link between specific acquired somatic mutations and their profoundly negative impact on AML prognosis, even in the normal karyotype subgroup. The extensive influence of this single article clearly explains why "Prognosis" and "Diagnosis" emerged as highly central and developed "Motor Themes" (Q1) in our thematic map (Fig 15). This paper exemplifies the field's paradigm shift from purely morphological classifications toward molecular, prognosis-driven stratification, thereby confirming our bibliometric findings on the centrality of these themes.

The second-ranked article, Daver et al. (2019), which possesses an exceptional citation velocity (107.14 TC/Year), is equally illustrative. This comprehensive review meticulously details the translational significance of FLT3 mutations. Its content directly bridges one of this study's "Basic Themes" ("flt3," identified in Q4) with the highly developed "Motor Themes" of "Prognosis" and "Diagnosis" (Q1). The Daver paper summarizes the evolution of this specific mutation from a foundational research concept into one of the most critical, actionable biomarkers for clinical risk stratification and targeted inhibitor therapy. This key role in linking basic science to clinical application fully justifies its high citation rate and central position within the field's citation network.

The inclusion of the Guarnerio et al. (2016) paper is particularly insightful, as it corresponds directly to one of the "Emerging Themes" identified in our analysis. This seminal work first described the oncogenic role of "fusion-circRNAs"—circular RNAs derived from cancer-specific chromosomal translocations. It provides the intellectual origin for the "circrna" keyword cluster, which our thematic map placed in Q3 (Emerging or Declining Themes). While this theme currently exhibits lower centrality and density, the high-impact nature of this foundational paper (published in *Cell*) demonstrates it is not a declining topic but rather a significant, nascent research front, validating its identification as a promising area for future investigation.

The Breems et al. (2008) article, ranked fourth with 486 citations, serves as a critical foundational work for the entire field. This paper established the MLL partial tandem duplication (MLL-PTD) as a key independent marker for poor prognosis in AML, particularly in the significant normal karyotype subgroup. Its high and sustained citation count over more than a decade underscores its role in building the very "Prognosis" and "Diagnosis" motor themes (Q1) that our analysis now identifies as central. This paper is a clear example of the early, high-impact research that shifted the diagnostic paradigm toward molecular prognostication, laying the groundwork for the subsequent explosion in biomarker research.

Finally, the fifth-ranked paper, Berindan-Neagoe et al. (2014), broadens the perspective and helps explain the field's citation structure. Published in *CA-A Cancer Journal for Clinicians*, this major review covers the entire landscape of microRNA (miRNA) biology and therapeutics in cancer, far beyond just AML. Its high citation count (461) demonstrates that researchers in this specific AML-focused domain rely heavily on such foundational reviews for the core principles of miRNA function. This paper's influence strongly validates the identification of "microrna" as a core "Basic Theme" (Q4) in our thematic map (Fig 15), a fundamental, cross-cutting concept that underpins the more specialized research in other clusters.

5. Discussion and Managerial Insights

The bibliometric results reveal a rapidly expanding and increasingly specialized research field at the intersection of AML, exosomal transport, and microRNA biomarkers. From our analytical corpus of 710 documents (1996–2026), we observe a significant acceleration in research output beginning around 2005, with a notable peak around 2020. Research productivity is concentrated in a relatively small set of core outlets (23 journals), led by venues such as *Blood*, *Cancers*, and *Frontiers in Oncology*. Country-level production is dominated by China, the USA, and Iran. Keyword and co-occurrence analyses identify "acute myeloid leukemia," "prognosis," "microrna," "biomarker," and "exosomes" as central and fast-growing themes. Overlay and clustering visualizations further show a shift from foundational basic themes (e.g., "AML," "FLT3," "Cancer") toward highly developed motor themes (e.g., "Prognosis," "Diagnosis") and specialized niche themes (e.g., "Minimal Residual Disease," "Treatment Response") as well as emerging themes ("Bioinformatics," "Circrna," "Lncrna"). Document-level metrics highlight both enduring foundational works (e.g., Mrozek K, 2007; Breems DA, 2008) and recent high-impact contributions (e.g., Daver N, 2019; Lindsley RC, 2015), indicating a field that is simultaneously mature and dynamically evolving.

From a clinical and translational perspective, our findings signal a substantive shift in how AML diagnostics and monitoring are approached. Historically, AML management emphasized morphological classification, broad cytogenetics, and intensive chemotherapy protocols. These approaches were largely procedural and often reactive, focused on achieving remission, with monitoring limited by the invasive, painful, and costly nature of serial bone marrow aspirates. Exosome- and miRNA-driven biomarkers enable a different clinical paradigm: proactive, data-enabled (at the molecular level), and personalized. Real-time monitoring of exosomal cargo allows clinicians to detect minimal residual disease (MRD) earlier, predict therapeutic resistance, optimize treatment selection via precise prognostic stratification, and target interventions more precisely. For hematologists-oncologists, this translates into improved risk stratification at diagnosis, non-invasive monitoring for relapse, and enhanced transparency into clonal evolution. For diagnostic laboratories and pharmaceutical R&D teams, stabilized exosomal miRNAs provide robust targets for assay development and companion diagnostics. In sum, exosomal biomarkers move AML management from invasive diagnostics and reactive treatment toward non-invasive monitoring, predictive stratification, and personalized medicine.

The study also yields several practical and theoretical implications. Practically, the mapping of thematic clusters and high-impact sources can guide researchers and funders to prioritize biomarker candidates and application domains with demonstrated scholarly traction, for example, deploying miRNA signatures for prognostic stratification in AML or integrating exosomal markers for MRD detection. The identification of leading institutions (e.g., The Ohio State University, Shahid Beheshti University of Medical Sciences) and collaboration patterns can inform partnership strategies for clinical trials and assay validation. Theoretically, our findings suggest new integrative frameworks that connect specific molecular cargo (miRNAs, lncRNAs, circRNAs) with multi-dimensional clinical outcomes (diagnosis, prognosis, therapy response). Future theory-building should consider mediating mechanisms (e.g., EV isolation purity, cargo stability, bioinformatics pipelines) and boundary conditions (e.g., AML subtype, patient age) revealed by the bibliometric clusters. Methodologically, combining bibliometrics with targeted systematic reviews and meta-analyses, domain expert synthesis (e.g., hematopathologists), and full-text text-mining would deepen causal understanding and practical transferability.

Despite these contributions, the study has important limitations that should be acknowledged. First, the analysis relies exclusively on Web of Science as the data source; while Web of Science provides broad and curated coverage, using a single database introduces database-specific coverage bias and excludes items indexed only in Scopus, PubMed, or relevant regional repositories. Second, we applied an English-language filter, which may underrepresent research published in other languages and skew geographic representation. Third, metadata gaps constrain certain analyses: the Author Keywords (DE) field showed substantial missingness (21.83%), and Web of Science Categories (WC) were entirely absent (100%). While Cited References (CR) were largely complete (2.52% missing), allowing for co-citation analysis, the poor DE field limits

the granularity of our keyword-based thematic maps. Fourth, bibliometric measures capture influence and structure but cannot fully assess study quality, contextual relevance, or practical efficacy. Therefore, our findings should be complemented with domain expert review and empirical validations. Finally, temporal bias (citation windows favor older publications) and the choice of thresholds (e.g., minimum occurrences for co-word analysis) may influence which themes appear as central or emerging. Future studies should address these limits by integrating multiple databases, including non-English literature, and combining bibliometric mapping with systematic qualitative syntheses or meta-analyses to produce richer, actionable guidance for scholars, clinicians, and policymakers.

6. Conclusions and Future Research Directions

This study delivers a comprehensive bibliometric synthesis of the rapidly expanding research investigating the potential of exosome- and microRNA-driven biomarkers for AML diagnosis and prognosis. By analyzing 710 documents published between 1996 and 2026, our findings confirm a clear paradigm shift from traditional, invasive diagnostic methods, such as bone marrow aspirates, toward non-invasive, 'Liquid Biopsy' approaches powered by exosomal cargo analysis, next-generation sequencing, and advanced bioinformatics. The evolution of keywords, thematic clusters, and publication trends highlights the field's intellectual structure. This includes the maturity of foundational themes, for example "AML" and "FLT3", and the growing prominence of motor themes like "prognosis" and "diagnosis", as well as novel molecular concepts such as "Circrna" and "Lncrna". Overall, the study demonstrates that the integration of exosomal biomarkers not only enhances diagnostic and prognostic capabilities but also accelerates progress toward personalized medicine and non-invasive monitoring objectives in hematologic oncology. By mapping influential sources (e.g., Blood, Cancers), emerging topics (e.g., "Immunotherapy" and "Extracellular Vesicles"), and collaboration patterns, this research offers actionable guidance for scholars, clinicians, and policymakers (funders) seeking to understand or influence the future direction of this field.

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Appendix

Table A1.

Core Journals Identified by Bradford's Law (Zone 1)

Source	Rank	Frequency	Cumulative
Blood	1	25	25
Cancers	2	21	46
Frontiers in Oncology	3	18	64
International Journal of Molecular Sciences	4	18	82
Leukemia	5	17	99
Oncotarget	6	14	113
Oncology Letters	7	11	124
Cancer Biomarkers	8	9	133
Haematologica	9	9	142
Journal of Cellular Physiology	10	9	151
Journal of Clinical Oncology	11	9	160
Plos One	12	8	168
Bmc Cancer	13	7	175
Leukemia Research	14	7	182
Pathology Research and Practice	15	7	189
Scientific Reports	16	7	196
Cancer cell International	17	6	202
Clinical Laboratory	18	6	208
Experimental Hematology	19	6	214
Frontiers in Pharmacology	20	6	220
Hematology	21	6	226
International Journal of Clinical and Experimental Pathology	22	6	232
International Journal of Laboratory Hematology	23	6	238

Table A2.

The frequency of scientific productivity

Documents Written	N. of Authors	Proportion of Authors	Theoretical
1	4085	0.888	0.634
2	347	0.075	0.158
3	81	0.018	0.07
4	40	0.009	0.04
5	16	0.003	0.025
6	9	0.002	0.018
7	6	0.001	0.013
8	3	0.001	0.01
9	4	0.001	0.008
10	3	0.001	0.006
11	2	0	0.005
12	1	0	0.004
13	1	0	0.004
15	2	0	0.003
19	1	0	0.002

Table A3

Comprehensive Rankings of top 10 Most Influential Authors Based on H-index

Author	H index	G index	M index	TC	PY Start
Marcucci Guido	18	19	0.947	2791	2007
Bloomfield clara	15	15	0.789	2405	2007
Mrozek Krzysztof	15	15	0.789	2061	2007
Powell Bayard	13	13	0.722	1937	2008
Kolitz Jonathan	12	12	0.667	1621	2008
Larson Richard	10	10	0.556	1358	2008
Liu	10	10	0.556	519	2008
Carroll Andrew	9	9	0.529	1256	2009
Chen	9	9	0.529	311	2009
Maharry Kati	9	9	0.5	1515	2008

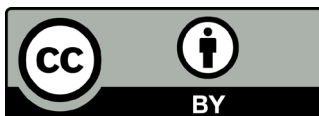
Notes. TC: Total Citation, PY start: Publication Year Start

Table A4

Top 20 Countries of Publication Based on the Corresponding Authors' and their Collaboration Details

Country	Articles	SCP	MCP	Frequency	MCP Ratio
CHINA	250	35.2	224	26	10.4
USA	129	18.2	91	38	29.5
IRAN	46	6.5	30	16	34.8
ITALY	38	5.4	24	14	36.8
GERMANY	27	3.8	14	13	48.1
INDIA	20	2.8	13	7	35
SPAIN	18	2.5	11	7	38.9
EGYPT	13	1.8	11	2	15.4
AUSTRALIA	10	1.4	8	2	20
CANADA	9	1.3	4	5	55.6
FRANCE	9	1.3	6	3	33.3
JAPAN	9	1.3	8	1	11.1
POLAND	9	1.3	7	2	22.2
UNITED KINGDOM	9	1.3	7	2	22.2
KOREA	8	1.1	8	0	0
BRAZIL	7	1	6	1	14.3
ROMANIA	7	1	4	3	42.9
TURKEY	6	0.8	5	1	16.7
NETHERLANDS	5	0.7	4	1	20
RUSSIA	5	0.7	4	1	20

Note. SCP: Single Country Publications; MCP: Multiple Country Publications



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