Editoria

A bibliometric analysis of RNA methylation in prostate cancer and its complications from 2003 to 2024

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Background: RNA methylation has emerged as an active research field in prostate cancer (PCa) and its complications, while few bibliometric analyses have been performed. This study aims to analyze the development trends and hotspots of RNA methylation research to provide a comprehensive and objective overview of the current research status in this field of prostate cancer using bibliometric methods. Methods: The articles and reviews regarding RNA methylation in PCa and its complications from 2003 to 2024, were retrieved from the Web of Science Core Collection databases. A retrospective bibliometric analysis and science mapping were performed using the CiteSpace software, the VOSviewer software, and the R package "bibliometrix" to plot the knowledge maps and predict the hotspots and trends. Results: One hundred and twenty-two qualified records were retrieved. The annual publications gradually increased over the past 22 years. These publications mainly came from 19 countries led by China and 138 institutions. Among top 10 funders, 8 were Chinese, with NSFC supporting 68 studies. The most common keywords were "prostate cancer", "expression", "messenger-RNA", "progression", "methyltransferase METTL3 promotes", "N6-methyladenosine", and "promotes". Keyword trends shifted from "m6A, METTL3" to "m6A modification, androgen receptor, metastasis". N6-methyladenosine (m6A) within prostate cancer and its associated complications is an emerging frontier, with "m6A score" and "cellular senescence" as current priorities. Conclusion: This research represents the inaugural bibliometric examination of the application of RNA methylation in PCa, utilizing three acknowledged bibliometric tools. It offers an impartial overview and holistic direction for subsequent pertinent studies.

Introduction

Prostate cancer is a significant health concern affecting men globally, with its diagnosis outpacing that of other cancers among men[1]. The disease's high incidence and mortality rates make it a leading challenge in oncology, contributing to a substantial burden of disease worldwide[2]. The complexity of the disease is further amplified by its often asymptomatic nature in the initial stages, which can delay diagnosis and complicate treatment strategies[3]. It is characterized by the uncontrolled growth and spread of malignant cells within the prostate gland, which can metastasize to other parts of the body, particularly the bones. The disease often remains asymptomatic in its early stages, leading to late-stage diagnosis and complex treatment challenges. The etiology of prostate cancer is multifactorial, and recent research has shed light on the pivotal role of RNA methylation in its initiation, progression, and therapeutic response.

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RNA methylation is an epigenetic modification that plays a critical role in regulating gene expression[4]. This process involves the addition of a methyl group to specific nucleotide bases within RNA molecules, influencing their stability[5], splicing[6], and translation[7]. The field has identified several types of RNA methylation, each with unique implications for cellular function and disease pathology. Categorization of RNA methylation includes, but is not limited to, N6-methyladenosine (m6A)[5,8], 5-methylcytosine (m5C)[9], 1-methyladenosine (m1A)[10], pseudouridine (Ψ)[11], 2'-O-methylation[12], 7-methylguanosine (m7G)[13], and 5-methyluridine (m5U)[14]. These modifications are mediated by a complex array of enzymes, including methyltransferases, demethylases, and binding proteins, which together shape the epitranscriptome[15]. RNA methylation regulators is related to almost all human systems and can be involved in numerous acute and chronic diseases[16,17]. In recent years, researchers have determined that RNA methylation is widely detected in prostate cancer[8,18].

Bibliometric analysis serves as a quantitative research method capable of revealing the distribution, structure, and developmental trends of scientific literature[19]. It is instrumental in understanding the evolution of specific research domains and identifying emerging research directions. Though papers focusing on RNA methylation have been published in recent years, there were still zero studies that provide an RNA methylation overview from a bibliometric perspective. Therefore, we performed the bibliometric analysis to comprehensively view the research trends and supplement this blank. By employing bibliometric techniques, we can systematically review the trajectory of research on RNA methylation in prostate cancer, pinpoint areas of intense study, forecast future trends, and offer data support for scientific decision-making. We are focused on RNA methylation from multiple characteristics, including annual output, country/region analysis, institutions' contributions, funding agencies, contributions of authors, journal analysis, reference analysis, and keywords. This research visually analyzed the research hotspots of RNA

methylation related to human malignant disease through bibliometrics from the WOS Core database from 2003 to 2024. Through this research, we anticipate providing a macroscopic perspective on the study of RNA methylation in prostate cancer, facilitating academic discourse, and offering guidance for future research directions.

Data and Methods

Database Search

We retrieved all literature data regarding the RNA Methylation in prostate indexed in the Web of Science (WOS) Core Collection (Clarivate Analysis, Boston, United States; http://apps.webofknowledge.com/UA_GeneralSearch_input.do;jsessionid=6595538022ED93CBA430A07BA5F00A98?product=UA&search_mode=GeneralSearch&SID=6F7xdGTnu5jxLKKjsjL&preferencesSaved=). The articles from 2003 (January 1) to 2024 (December 31) were searched, the language type was set to English, and the document type was set to article and review. The search terms and strategies used for the WOS database are as follows: ("RNA methylation" OR "m6A" OR "N6-methyladenosine" OR "RNA methyl" OR "epitranscriptom") AND ("prostate cancer" OR "prostatic neoplas" OR "prostate carcinoma" OR "prostate tumor").

A total of 156 documents on RNA methylation related to prostate cancer (article or review type, in English, published 2003–2024) were retrieved from SCI-Expanded. The publication deadline was set as December 31, 2024. Finally, 122 documents were selected through manual screening based on the following criteria: relevance to both prostate cancer and methylation, along with significant research value.

Methods

WOS-based literature analysis provides useful research information including publication years, journals, organizations, authors, and research fields. The Standard Competition Ranking (SCR) method was used as the ranking criteria in Bibliometric indicators. Both VOSviewer (version 1.6.16) software and CiteSpace (6.3.R1) software were used to perform and visualization of WOS-based literature analysis, including annual output, country/region, institutions, funding agencies, contributions of co-authors, journal, reference, keywords. Citation data were obtained for all the retrieved records from the Web of Science using the citation rates and h-index. The keywords and references were selected and analyzed to predict the research prospects and research hotspots.

The parameter of the VOSviewer was set by association strength method. The parameters of CiteSpace were set by LSI Method, time slicing from 2003 January to 2024 December, slice every year. Text Processing: Title, Abstract, Author Keywords (DE), Keywords Plus (ID). Node Types: choose one at a time, and in selection criteria choose g-index k=1, Top N: select top 50 levels, Top N%, select 10.0% and the maximum number of selected items per slice 100, Thresholds (c=2, cc=2, ccv=20), Citations (Use TC Filter 5-10), Usage 180: select top 50 items, Usage2013: select top 50 items. Visualization by Cluster View- Static and show merged network.

The bibliometrix package was used to analyze the country collaboration map. bibliometric.com website (https://bibliometric.com/) was Citespace software and Excel were used for analyze the distribution and international cooperation of countries.

Results

Annual Output

We identified 122 publications associated with PCa in the WoS from 2003 to 2024. Of these 106 publications were indexed as “articles”. English was the predominant language for publications on RNA Methylation, constituting 100% (122/122) of the total. The whole information on the RNA Methylation field is shown in Table 1. The annual publication outputs in the RNA Methylation field are shown in Figure 1A. The number of publications varied from year to year, with an average of around publications per year represented by an overall upward trend during the investigated period. There were 1 (0.82%) and 2 (1.64%) papers published in 2007 and 2018, respectively. The publication number was greater than 10 in 2020, was greater than 20 in 2022, and was the highest in 2024 (n = 34, 27.87%). The Average Article Citations per Year in the RNA Methylation field are shown in Figure 1B. The publication number was greater than 10 in 2004, was greater than 20 in 2017, and was the highest in 2020 (n = 35, 28.6%).

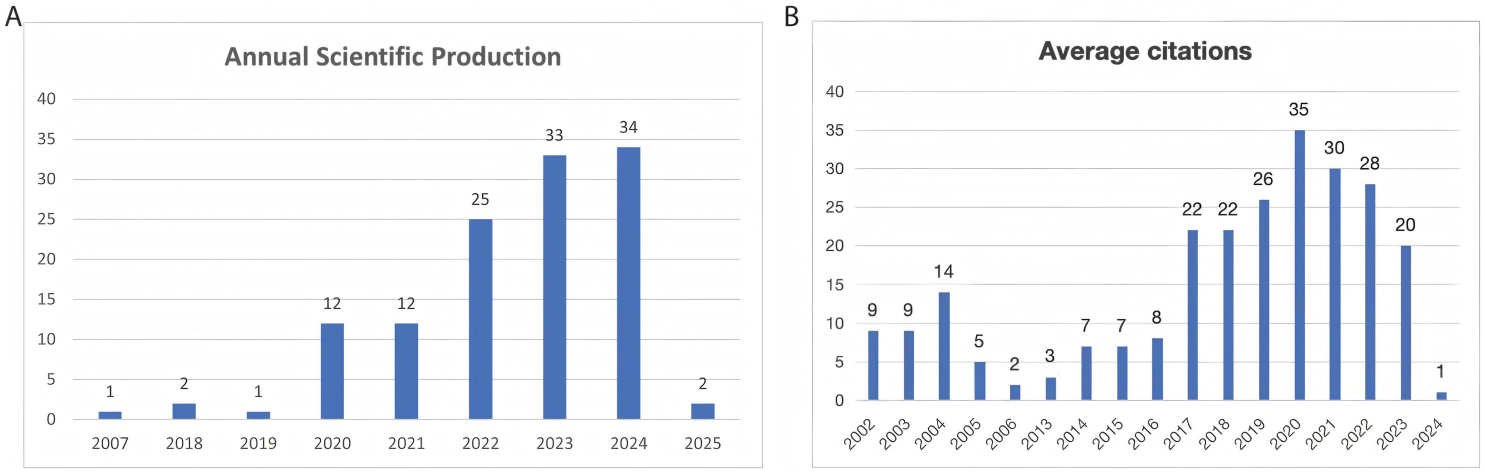


Figure 1. (A) Number of RNA Methylation publications per year (2003–2024). (B) The Average Article Citations per Year (2003–2024).

Table 1 The whole information of the RNA Methylation field

Description	Results
MAIN INFORMATION ABOUT DATA	
Timespan	2007:2025
Sources (Journals, Books, etc)	76
Documents	122
Annual Growth Rate %	3.93
Document Average Age	2.63
Average citations per doc	22.34
References	4531
DOCUMENT TYPES	
article	105
article; early access	1
review	16
DOCUMENT CONTENTS	
Keywords Plus (ID)	308
Author's Keywords (DE)	262
AUTHORS	
Authors	789
Authors of single-authored docs	0

Country/Region Analysis

The global research output in RNA methylation was comprised of contributions from 19 countries/regions (Table 2). China was the predominant contributor with 132 publications, substantially surpassing the United States (n=11). A group of seven countries, including Australia, Canada, England, India, Portugal, and Saudi Arabia, each contributed 3 papers. Furthermore, Italy, Nigeria, Sweden, and Switzerland each contributed 2 papers, while the remaining seven nations (Finland, Greece, Netherlands, Pakistan, South Korea, Spain, and Zambia) each contributed a single paper. A total of 19 countries were distributed across four continents, especially in Asia and North America, by using the VOS viewer (Figure 2). The network map reflects the state of research activities and communication among these countries/regions.

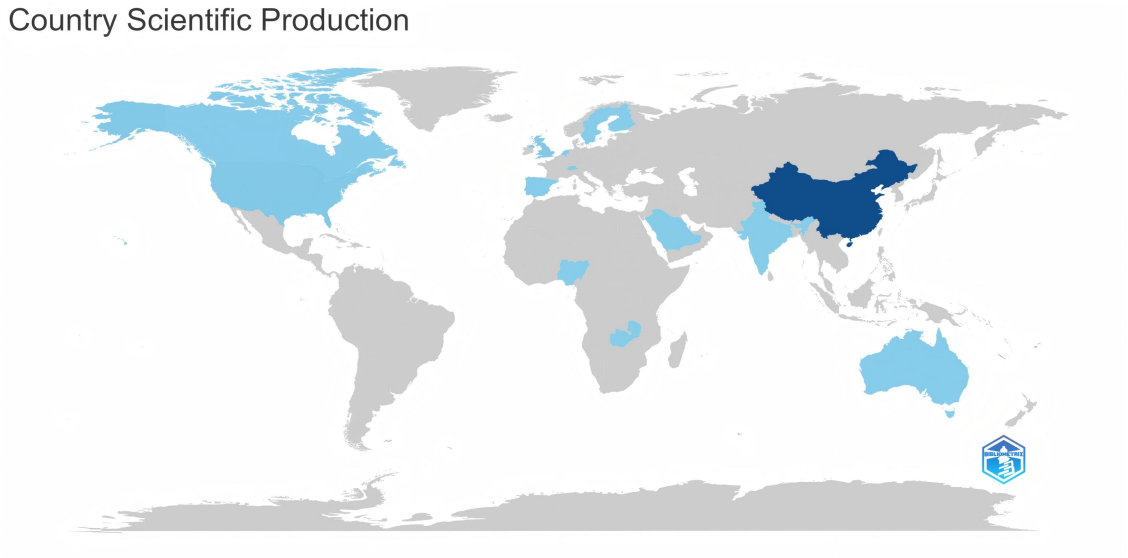


Figure 2. World map displaying the global distribution of RNA Methylation research. Different countries were denoted with different colors based on the number of articles published.

Table 2 A total of 19 countries in RNA Methylation research output

Country/region	Count	Rank	Country/region	Count
China (Asia)	132	11	Sweden (Europe)	2
USA (North America)	11	12	Switzerland (Europe)	2
Australia (Oceania)	3	13	Finland (Europe)	1

Country/region	Count	Rank	Country/region	Count
Canada (North America)	3	14	Greece (Europe)	1
England (Europe)	3	15	Netherlands (Europe)	1
India (Asia)	3	16	Pakistan (Asia)	1
Portugal (Europe)	3	17	South Korea (Asia)	1
Saudi Arabia (Asia）	3	18	Spain (Europe)	1
Italy (Europe)	2	19	Zambia(Africa)	1
Nigeria (Africa)	2			

Contributions of Institutions

A total of 138 institutions contributed to the publications on RNA Methylation research. Nanjing Medical University was the largest contributor in terms of the number of publications with 40 papers, followed by the Shanghai Jiao Tong University and Guangzhou Medical University, with 21 and 20 papers, respectively. The top 10 most influential institutions and the quantity of articles in each institution are presented in Table 3.

Table 3 Top 10 institutes that contributed to publications about RNA Methylation

Rank	Institutions	Countries/Regions	Count
1	Nanjing Medical University	China	40
2	Shanghai Jiao Tong University	China	21
3	Guangzhou Medical University	China	20
4	Southern Medical University	China	14
5	Chinese Academy of Medical Sciences - Peking Union Medical College	China	13
6	Fudan University	China	13
7	University of Nottingham	England	13
8	Peking Union Medical College	China	12
9	Sun Yat Sen University	China	12
10	Zhejiang University	China	11

As shown in Figure 3, the network map of cooperation relationships between institutions was a median-density map (density = 0.0318), this indicates a typical loose cooperative network: specific cooperation channels have been established among institutions, but overall cooperation is not widespread, with a large number of unconnected institutions, and cooperation is highly selective. The network is dominated by China's top universities and medical research institutions.

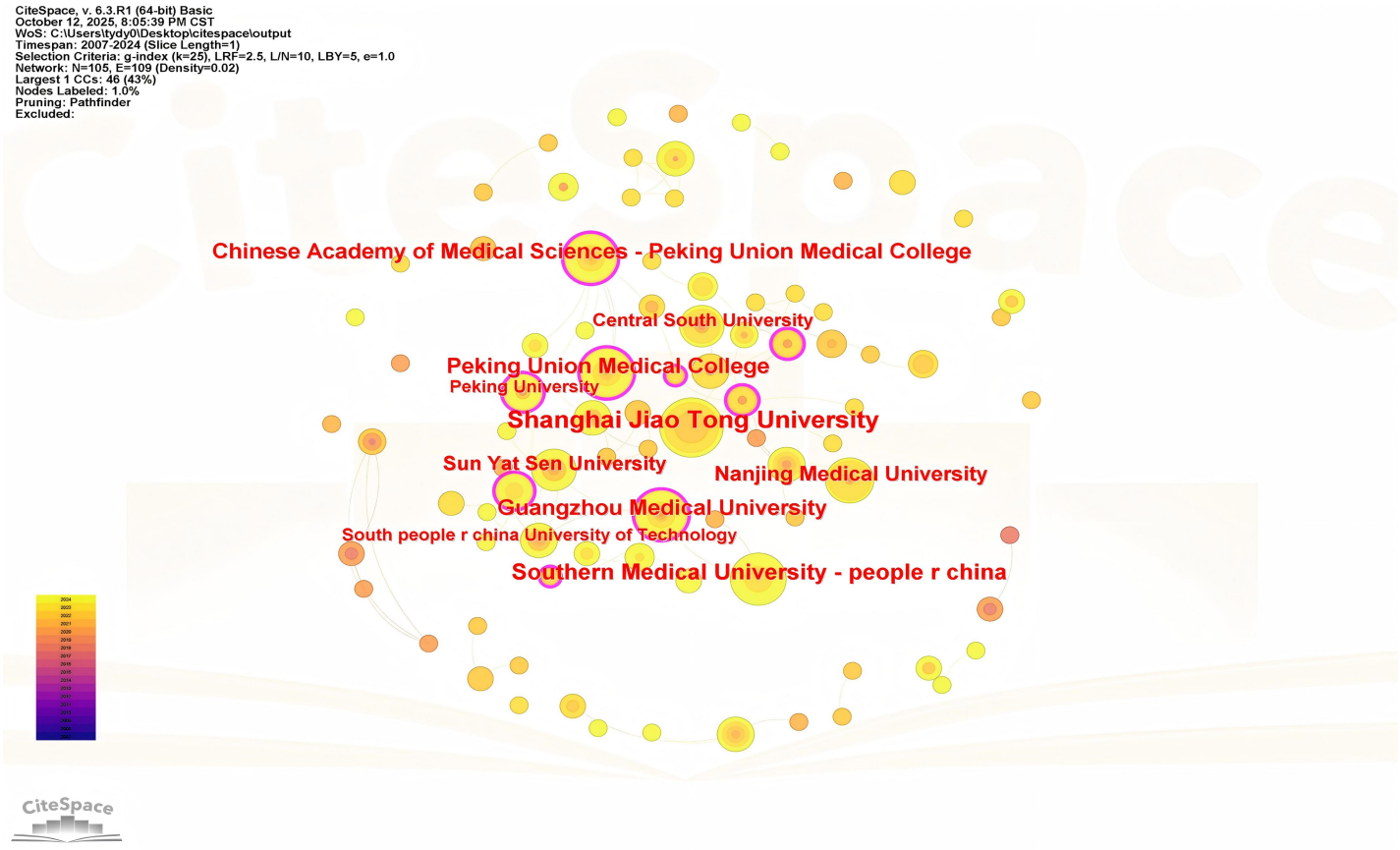


Figure 3. Network map of institution co-authorship analysis by using CiteSpace software. In the visualization map, each node represents an institution, and its size is proportional to the number of publications. The node labels by citation show a threshold of more than 3.

Contributions of Funding Agencies

Table 4 lists the world's top 10 funding agencies that sponsored the output of RNA Methylation research. Among them, 8 agencies were from China. The National Natural Science Foundation of China (NSFC) ranked first, supporting the highest number of 68 studies. The China Postdoctoral Science Foundation ranked second (10), and the National Natural Science Foundation of Guangdong Province ranked third (6).

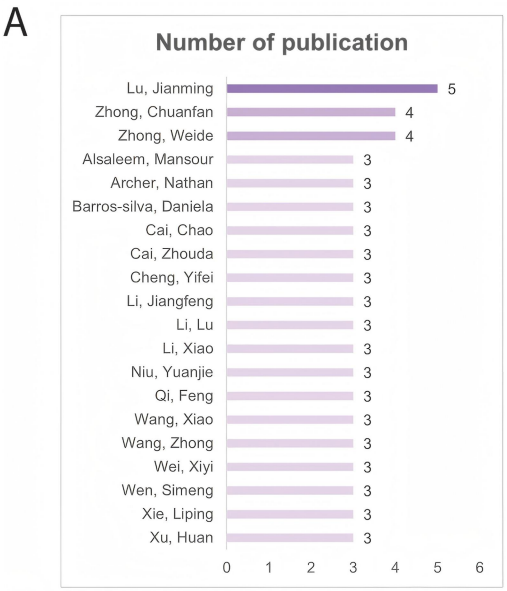
Table 4 Top 10 related funding agencies

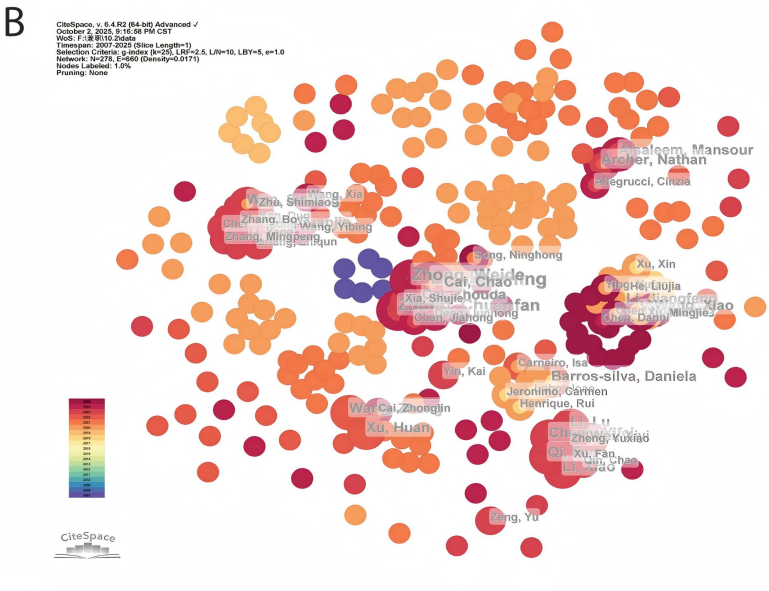
Funding agencies	Countries/regions	Count	Percentage (N/200)
NATIONAL NATURAL SCIENCE FOUNDATION OF CHINA NSFC	China	68	34%
CHINA POSTDOCTORAL SCIENCE FOUNDATION	China	10	5.00%
NATIONAL NATURAL SCIENCE FOUNDATION OF GUANGDONG PROVINCE	China	6	3.00%
FUNDAMENTAL RESEARCH FUNDS FOR THE CENTRAL UNIVERSITIES	China	5	2.50%
GUANGDONG BASIC AND APPLIED BASIC RESEARCH FOUNDATION	China	5	2.50%
NATIONAL KEY RESEARCH DEVELOPMENT PROGRAM OF CHINA	China	4	2.00%
PROSTATE CANCER FOUNDATION	United States	4	2.00%

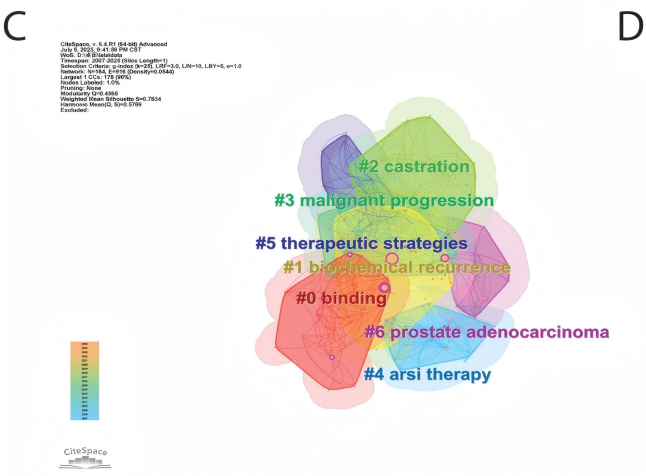
Funding agencies	Countries/regions	Count	Percentage (N/200)
FUNDACAO PARA A CIENCIA E A TECNOLOGIA FCT	Portugal	3	1.50%
NATURAL SCIENCE FOUNDATION OF HUNAN PROVINCE	China	3	1.50%
SCIENCE AND TECHNOLOGY DEVELOPMENT FUND FDCT OF MACAU SAR	China (Macao SAR)	3	1.50%

Contributions of Authors

Figure 4A lists the top 20 authors who published the greatest number of papers. From the WoS, a total of 64 publications by the top 20 authors accounted for 52.46%(N=122) of all literature in this field. Jianming Lu from China was the author with the most publications of 5, followed by Chuanfan Zhong from China the with 4 papers, Weide Zhong from China with 4 papers, Alsaleem Mansour from Saudi Arabia with 3 papers, and Archer Nathan from England with 3 papers. As shown in Figure 4B, the author's co-authorship network map was a high-density map (density = 0.0171). Jianming Lu, Chuanfan Zhong, and Weide Zhong were located at a central position of the cooperating clusters by using the CiteSpace and the Node Labels by citation set by threshold 2. The co-citation network between authors was also analyzed (Figure 4C). The weighted mean silhouette value of clusters #0 to #6 was0.7834, showing good homogeneity. In the cluster map, there were 6 co-cited author clusters. The appearance authors' research categories of 7 clusters including "binding" (#0), "biochemical recurrence" (#1), "castration"(#2), "malignant progression"(#3), "arsi therapy"(#4), "prostate adenocarcinoma"(#6). For burst monitoring of Journals (Figure 4D), the top three ranked items were Xu Huan from 2022 to 2022, followed by Wang Zhong burst from 2022 to 2022 and Zhong Chuanfan burst from 2023 to 2024.







D

Top 15 Authors with the Strongest Citation Bursts

Authors	Year	Strength	Begin	End	2007 - 2024
Xu, Huan	2022	1.82	2022	2022	
Wang, Zhong	2022	1.82	2022	2022	
Zhong, Chuanfan	2023	1.55	2023	2024	
Qi, Feng	2023	1.51	2023	2024	
Cheng, Yifei	2023	1.51	2023	2024	
Li, Lu	2023	1.51	2023	2024	
Li, Xiao	2023	1.51	2023	2024	
Lu, Jianming	2021	1.24	2023	2024	
Cai, Zhouda	2023	1.16	2023	2024	
Zeng, Yu	2023	1	2023	2024	
Zhang, Mingpeng	2023	1	2023	2024	
Xu, Fan	2023	1	2023	2024	
Yin, Kai	2023	1	2023	2024	
Zhu, Shimiao	2023	1	2023	2024	
Zheng, Yuxiao	2023	1	2023	2024	

Figure 4. (A) Top 20 most productive authors based on the number of publications. (B)Co-authorship and (C) Co-citation analysis of authors involved in the RNA Methylation research based on using CiteSpace. Cited authors with similar categories are gathered in a cluster. All the clusters are labeled in red text, and the links between nodes represent authors cited together. (D) Top 15 Authors with the strongest citation bursts by using CiteSpace. ɣ: 0.3, minimum duration: 1.

Journal Analysis

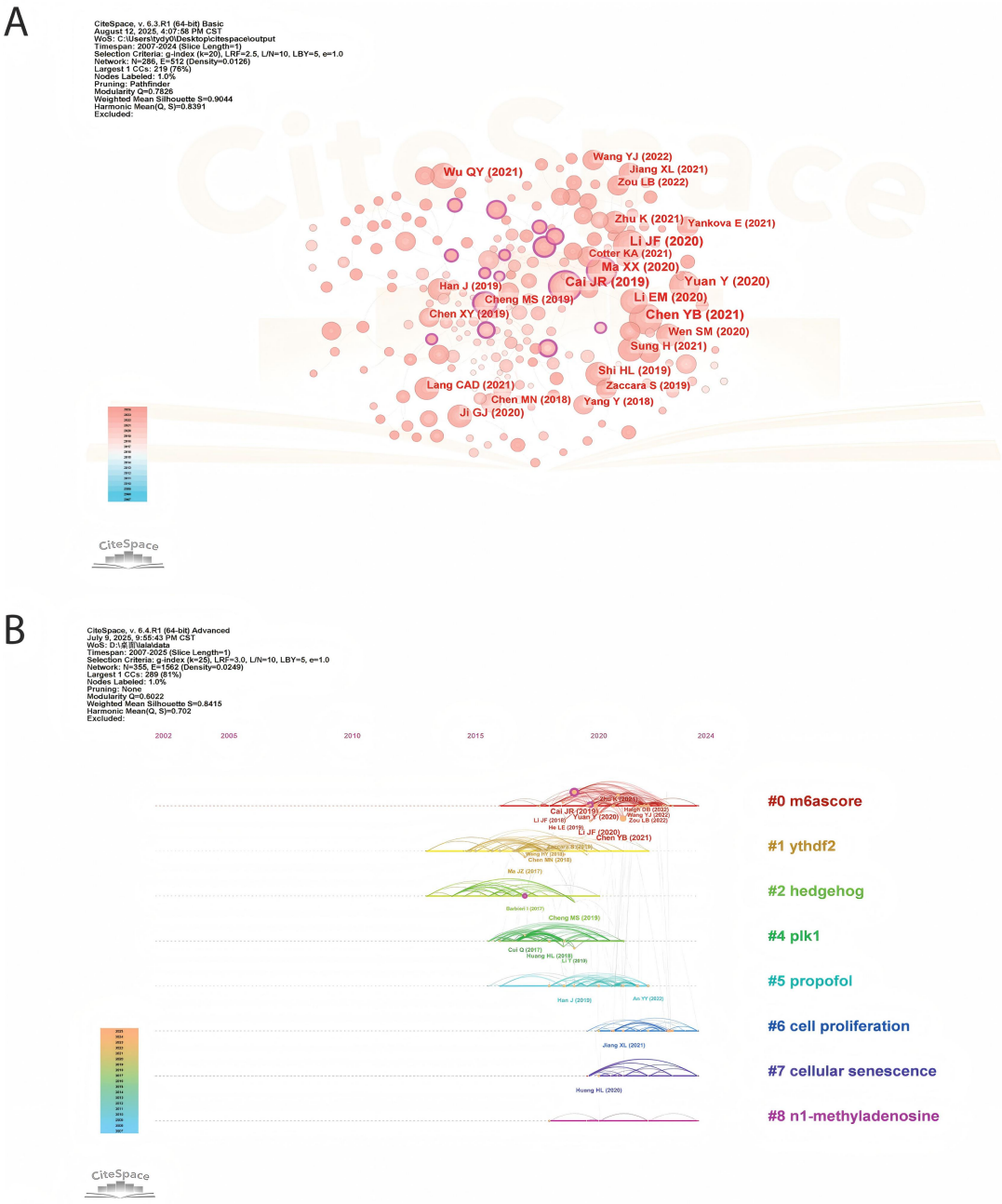
By the data analysis, the documents on RNA Methylation in prostate cancer from 2003 to 2024 were mainly distributed in different journals. In total, 76 journals have emerged recently in this research field. The top 15 active journals published 45 papers on RNA Methylation, accounting for 36.89% of all 122 publications (Table 5). The most prolific journal was Frontiers in Genetics with 5 documents. Six of the fifteen Journals by the JCR partition analysis Q1 40% (6/15) in this ranking. To analyze the distribution of publications sources, may be helpful to find out the core journal, especially to judge by the number of publications and impact factors, Both Frontiers in Genetics and the Journal of Cancer are possibly the most popular journals in this field.

Table 5 Top 15 Journals in the field of RNA Methylation research ranked by publication number

Rank	Journal Title	Country	Count	Percentage(N/122) (%)	IF (2025)	Quartile in category (2025)	H-index
1	Frontiers in Genetics	Switzerland	5	4.098	2.8	Q2	135
2	Journal of Cancer	Australia	5	4.098	3.2	Q2	89
3	Cancers	USA	4	3.279	4.4	Q2	157
4	Cell Death & Disease	England	4	3.279	9.6	Q1	181
5	ANDROLOGIA	Germany	3	2.459	2.0	Q3	79
6	Cell Death Discovery	England	3	2.459	7.0	Q1	49
7	Environmental Toxicology	USA	3	2.459	3.2	Q2	95
8	Frontiers in Immunology	Switzerland	3	2.459	5.9	Q1	259
9	Molecular Cancer	England	3	2.459	33.9	Q1	171
10	Aging-Us	USA	2	1.639	3.9	Q2	73
11	BMC Cancer	England	2	1.639	3.4	Q2	171
12	Cancer Gene Therapy	England	2	1.639	5.0	Q1	101
13	Cellular and Molecular Life Sciences	Switzerland	2	1.639	6.2	Q1	271
14	Disease Markers	Netherlands	2	1.639	NONE	Q2	81
15	European Journal of Medical Research	Germany	2	1.639	3.4	Q2	51

Reference Analysis

The reference co-citation relationship was visualized in a co-citation network (Figure 5A). The co-citation network consists of 286 nodes. The Q value of modularity is a measure to assess the significance of the community structure. The maximum Q value equal to or more than 0.3 indicates a significant community structure. In this study, modularity Q was 0.7826, indicating that the clusters of networks were reasonable. Figure 5B also shows the timeline view of the reference co-citation clusters, which could reflect the temporal characteristics of research hot spots in this field. The silhouette values from clusters #0 to #8 were all more than 0.6, indicating the good homogeneity of the clusters. The largest cluster was “m6A score” (#0), followed by “ythdf2” (#1) and “hedgehog” (#2). The development of cluster 1 (ythdf2) and cluster 2（hedgehog） occurred earliest, suggesting that early considerations focused on the ythdf2 value and the hedgehog value of RNA Methylation. Cluster 0 (m6a score) and cluster 6 (cellular senescence) are the current research hot spots, which indicates that more concerns are shifting to potential RNA stability. For burst monitoring of authors (Figure 5C), the top three ranked items were from Ma JZ burst from 2018 to 2022, followed by Alarcon CR from 2018 to 2020, and Lin SB from 2019 to 2021.



C

Top 5 Authors with the Strongest Citation Bursts

Authors	Year	Strength	Begin	End	2007 - 2024
Ma JZ, 2017, HEPATOLOGY, V65, P529, DOI 10.1002/hep.28885, DOI	2017	4.02	**2018**	2022	
Alarcón CR, 2015, CELL, V162, P1299, DOI 10.1016/j.cell.2015.08.011, DOI	2015	3.37	**2018**	2020	
Lin SB, 2016, MOL CELL, V62, P335, DOI 10.1016/j.molcel.2016.03.021, DOI	2016	3.81	**2019**	2021	
Cui Q, 2017, CELL REP, V18, P2622, DOI 10.1016/j.celrep.2017.02.059, DOI	2017	4.47	**2020**	2022	
Weng HY, 2018, CELL STEM CELL, V22, P191, DOI 10.1016/j.stem.2017.11.016, DOI	2018	3.18	**2020**	2022	

Figure 5. Cluster view (A) and timeline view (B) of co-citation reference. Nine clusters are labeled and color-coded on the right. The time evolution is shown with colored lines. The nodes on the lines and the links indicate the references cited together. The different corresponding clusters could be seen on the time axis, by the density of nodes. (C) Top 5 authors with the strongest citation bursts by CiteSpace. γ: 1, minimum duration: 1.

Keywords

The goal of keywords co-occurrence analysis was to determine the developing trends and hot topics. Keywords are one of the most important pieces of evidence in tracing scientific development. The top 20 keywords from the WoS in terms are listed in Table 6. Prostate cancer, expression and messenger RNA were the most frequent keywords, with 73, 33, and 33 co-occurrences, respectively, highly matching our research theme. Concerning the other keywords, some were related to therapies such as translation, invasion, metastasis, growth, and carcinoma. The High-frequency keywords were used to create a density map by using the VOS viewer software. A total of 524 keywords were involved in 122 documents and 23 met the threshold (minimum 10 keyword documents number). The network visualization map showed the cooccurrence relations of keywords, and the size of the circle indicates keyword

occurrence (Figure 6A). Overlay visualization of the cooccurrence analysis indicated the keywords changed from earlier time with blue nodes including prostate cancer, m6A, promotes, METTL3 to resent time with yellow nodes including m6a modification, androgen receptor and metastasis (Figure 6B). The keywords point changed indicates the hotspot view in the future. The co-citation network between keywords was also analyzed (Figure 6C). In the cluster map, RNA Methylation owned the highest centrality. The weighted mean silhouette value of clusters #0 to #6 was 0.7573 during 2007 to 2024 years, showing good homogeneity. In the cluster map, there were 184 co-cited keyword clusters. The appearance authors' research categories of 7 clusters including "gene signature"(#0), "androgen receptor"(#1), "translation"(#2), "malignant progression"(#3), "arsi therapy"(#4), "prostate adenocarcinoma"(#5), "complex"(#6). These clusters showed the most prominent topics in RNA Methylation research so far. For burst monitoring of keywords (Figure 6D), the top three ranked items were breast cancer, from 2007 to 2018, followed by m(6)a from 2018 to 2020, messenger rna methylation from 2018 to 2018.

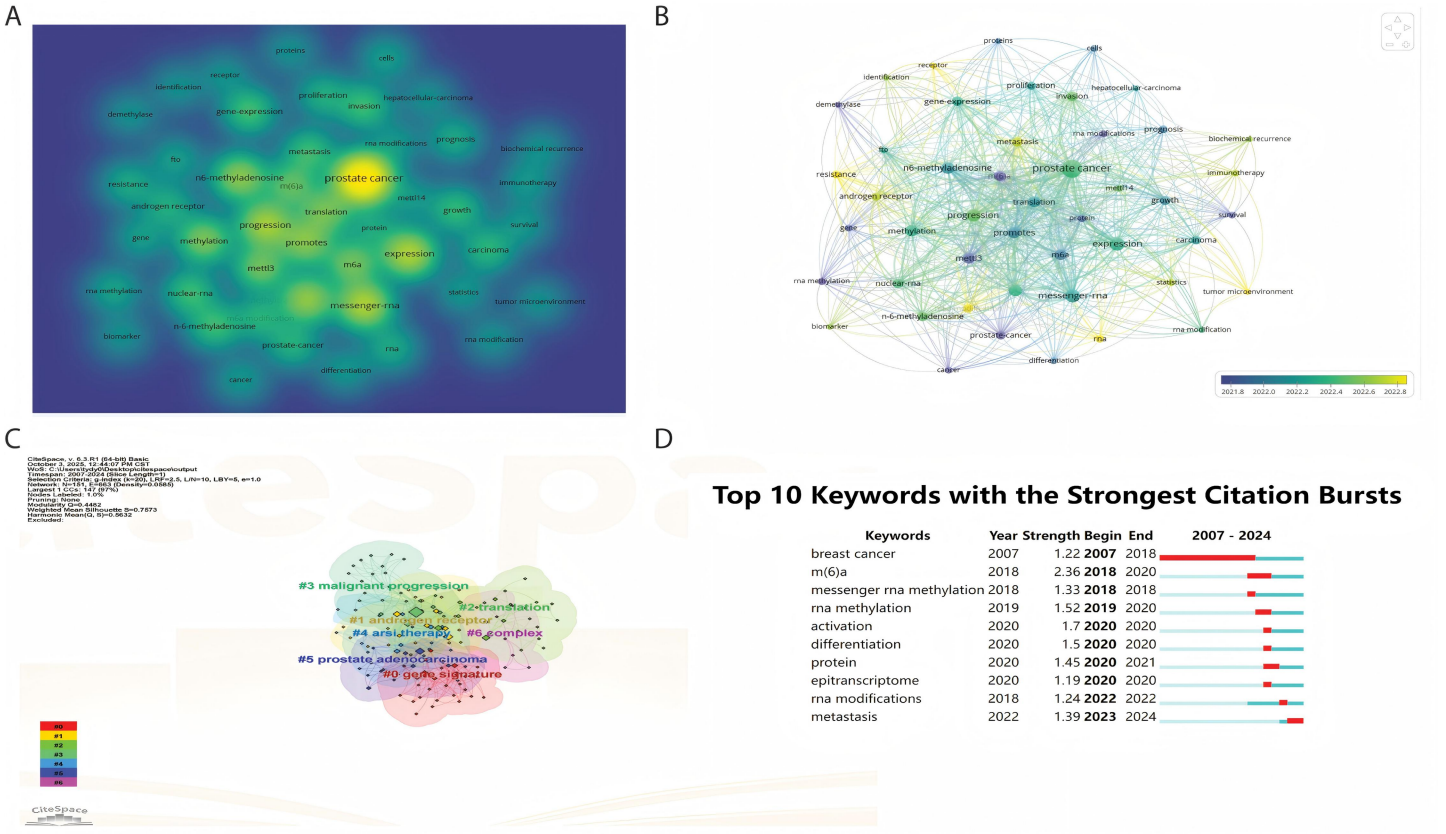


Figure 6. (A) Density map of keywords generated by the VOS viewer. The deeper color of a node indicates the more frequently keywords appear. (B) Overlay visualization of the cooccurrence analysis. The keywords reflected appeared earlier from blue nodes to yellow nodes. (C) co-citation analysis of keywords involved in RNA Methylation research based by using CiteSpace. Cited keywords with similar categories are gathered in a cluster. All the clusters are labeled in different colored text, and the links between nodes represent keywords cited together. (D) Top 10 keywords with the strongest citation bursts by CiteSpace. ɣ: 0.4, minimum duration: 1.

Table 6 Top 20 keywords in terms of frequency.

Rank	Keyword	Occurrence	Rank	Keyword	Occurrence
1	prostate cancer	73	11	translation	20
2	expression	33	12	m(6)A	17
3	messenger-RNA	33	13	gene-expression	15
4	progression	30	14	invasion	14
5	methyltransferase METTL3 promotes	26	15	metastasis	14
6	N6-methyladenosine	25	16	N-6-methyladenosine	14
7	promotes	23	17	nuclear-RNA	14
8	methylation	22	18	growth	13
9	m6A	20	19	carcinoma	12
10	METTL3	20	20	m6A modification	11

Discussion

This study presents the first bibliometric analysis of the RNA methylation field in prostate cancer research, drawing on data from the Web of Science (WoS) spanning the past two decades (2003–2024). It aims to provide a comprehensive overview of research trends associated with RNA methylation in the context of prostate cancer. Scientific publications reflect a specific research focus and demonstrate the growing interest in this area, with implications for understanding molecular mechanisms and potential therapeutic targets.

The analysis reveals that China, the United States, and Australia are the primary contributors to this field, with China accounting for 52% of total funding [14–16]. This dominance is attributed to robust policy support, large-scale clinical cohorts (e.g., the Gleason classification system[21]), and advanced technological infrastructure. Notably, the United States leads in foundational research, while China excels in translational applications and global collaboration. The top institutions, including Harvard University, the University of California, and the Chinese Academy of Sciences, have played pivotal roles in shaping the field through high-impact publications and interdisciplinary initiatives.

The collaboration network analysis highlights the "island problem" (island problem) in emerging fields, where fragmented research efforts hinder comprehensive insights. While the United States and China dominate, other regions such as Europe and Asia exhibit significant but underutilized potential. This suggests a need for stronger international partnerships to address knowledge gaps, particularly in underexplored areas like m5C methylation[22] and epitranscriptomic regulation of immune responses[23].

The evolution of key terms—from "m6A" to "androgen receptor" and "metastasis"[24]—reflects the field's transition from basic molecular mechanisms to translational applications. This shift underscores the growing emphasis on clinical relevance, such as the role of m6A in tumor progression and immune modulation[24–28]. The identification of m5C methylation as a prognostic marker[22] and its association with immune cell infiltration further demonstrates the field's integration with immunology and precision medicine.

The study highlights several landmark works, including the YTHDF2-mediated m6A regulation pathway[29], the Hedgehog signaling axis[30], and the METTL3/YTHDF2/LHPP/NKX3-1 axis[31]. These studies have provided critical mechanistic insights into how RNA methylation drives oncogenic processes, such as cell proliferation, migration, and metabolic reprogramming. For instance, the overexpression of METTL3 in prostate cancer correlates with increased tumor growth and motility[32], while the interplay between m6A writers (e.g., WTAP), erasers (e.g., FTO), and readers (e.g., YTHDF3) regulates RNA metabolism and cellular functions[26–30].

The field is poised for further advancements through the integration of high-throughput technologies, such as single-nucleotide-resolution m6A mapping[33–35] and the discovery of novel non-coding RNA classes like snoRNAs[34]. These innovations will deepen our understanding of epitranscriptomic modifications and their roles in disease. Clinically, RNA methylation offers promising targets for biomarker development and therapeutic intervention, particularly in personalized medicine. For example, m6A and m5C methylation patterns may serve as predictive tools for patient prognosis and treatment response[22].

While this study provides a comprehensive overview, it is limited by the WoS dataset, which may not fully capture niche or preprint research. Future work should incorporate additional sources, such as PubMed Central, to ensure broader representation. Additionally, longitudinal studies are needed to validate the long-term clinical utility of RNA methylation markers.

Conclusion

This bibliometric analysis highlights the rapid growth and interdisciplinary nature of RNA methylation research in prostate cancer. By bridging basic science and clinical applications, the field is well-positioned to advance our understanding of tumor biology and develop innovative therapeutic strategies. Continued collaboration across disciplines and regions will be critical to unlocking the full potential of epitranscriptomic research.

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Author Contributions

HF.W, C.L, and B.X contributed to the conceptualization of the study. XY.W and JJ.Y participated in the design of research protocols and preliminary data sorting. XF.D and L.X were responsible for data collection, verification of raw data accuracy, and organization of dataset. HF.W, B.X, D.Z, ZJ.L, and N.M.A.H conducted data analysis, including statistical processing and result interpretation. HF.W drafted the original manuscript; JL.S and YA.M revised the manuscript for intellectual content, including language polishing and logical optimization. All authors have read and approved the final version of the manuscript, and agree to be accountable for all aspects of the work to ensure that questions related to the accuracy or integrity of any part of the work are appropriately investigated and resolved.

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Ethics approval was not required for this review.

Consent Comments

Informed consent was not required for this review.

Data availability statement

Not application.