Bibliometric analysis of tsRNA based on Pubmed database

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Abstract: Objective: To analyze the development trend and hotspot of tsRNA research based on bibliometrics. *Methods:* The bibliometrics method and PubMed database were used to search tsRNA literature from January 2013 to October 2024, and visualized the research contents and hotspots in this field through R packet based on Medpulse bibliometrics analysis platform. *Results:* a total of 314 studies on tRNA were downloaded after screening. The number of articles on tRNA has been increasing year by year, and the three countries with the most researchers are China, the United States, and Canada. The journal with the most published articles is the International Journal of Molecular Sciences, and the journal with the highest citation per article is Cell. A total of 1,856 authors have studied tRNA, with Chen Qi and Zhang Ying publishing the most articles. *Conclusion:* The research in this field focuses on tumor, diagnosis, biomarkers, miRNA and piRNA. Among them, "tumor", "biomarker" and "miRNA" are important keywords, which provide valuable reference for scholars in this field. It is suggested to actively strengthen international exchanges and cooperation in the future, and use modern sequencing technology to study the mechanism of tsRNA in tumor diagnosis, occurrence and development to achieve higher quality research results.

Key words: Pubmed database; tsRNA; Bibliometric analysis

tRNAs are a group of classical non-coding RNAs that can be cleaved under stress, and their cleaved fragments are a new class of non-small coding Rnas named TrNA-derived small Rnas (tsRNAs)[1,2]. Studies have found that tsRNA is not only abundant, but also has high tissue specificity, and its stability in cells, tissues and peripheral blood is higher than other non-coding small Rnas, and it plays a role in various biological environments [3]. Recently, abnormal expression of tsRNAs has been found in many tumors, including lung cancer, breast cancer, stomach cancer, colorectal cancer, liver cancer, prostate cancer and leukemia [4-6], suggesting that abnormal expression of tsRNA is related to the occurrence and development of tumors.

There was increasing evidence that tsRNAs play a crucial role in human cancer, and tsRNAs can influence the biological behaviors of tumor cells, such as proliferation, apoptosis and metastasis, by regulating protein translation, RNA transcription or post-transcriptional regulation [7,8]. In addition, tsRNAs is widely distributed and stably expressed, which makes it a potential biomarker for early tumor screening, diagnosis and prognosis, and an important target for tumor therapy [9]. Although the biological function of tsRNAs has not been fully elucidated, tsRNAs has a broad application prospect in tumors. Using PubMed database and Medpulse bibliometric analysis platform [10,11], this paper systematically reviewed and analyzed TSRNA-related research literature published from 2010 to 2024, aiming to reveal research trends, hot spots and developments in this field, with a view to providing valuable references for future studies. Promote the development of tsRNA research.

METHOD

1.1 Data Sources:

Literature search was conducted in PubMed database from January 2013 to October 2024, the search language was English, and the literature types were limited to Article and Review article. Specific search methods were as follows: (tsRNA[topic]) OR (tRNA-derived small RNA[topic])) OR (transfer RNA-derived small RNA[topic])) AND

(journal_article[article_type] OR review[article_type])) AND (2013-2024[year]), export data containing a full set of metadata from a PubMed database using the 'PubMed export file' file format.

1.2 Research Methods:

In this study, the Medpulse bibliometrics analysis platform (https://www.medpulse.cn/) was used to visually analyze the research content and hotspots in this field. Mainly USES the R package "bibliometrix" version (holdings) (https://www.bibliometrix.org), build a global delivery network "tsRNA" related literature, Journals, authors, citations, keywords, institutions, countries and co-occurrence networks were selected for data mining and analysis [12]

RESULTS

2.1 Trend analysis of annual publications:

According to the search strategy, a total of 314 relevant literatures were obtained. Overall, the number of publications has increased year by year (Figure 1). Based on the number of published papers, we divide the progress into two stages. In the first phase (2013-2019), there were relatively few publications (less than 20), indicating that research in this area is still in its infancy. The second phase (2020-2024) sees a steady increase in the number of publications. By the end of October 2024, 74 articles have been published. These literatures were cited a total of 2263 times, with an average of 7.21 citations per article, indicating that scholars are paying more and more attention to tsRNA research.
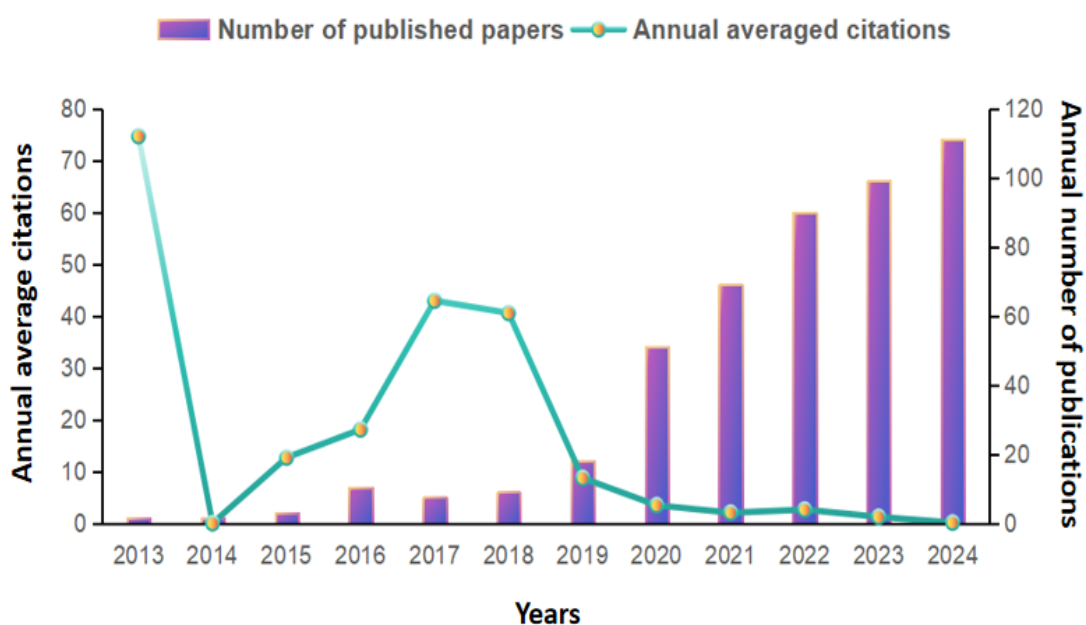

Figure 1 Analysis of annual publications and citations

2.2 Distribution of countries and institutions:

Figure 2A lists the top 8 countries with the most tsRNA researchers. Figure 2B shows the collaboration between researchers from different institutions. The institutions with the largest number of tsRNA studies are Central South University (n=46), followed by Sun Yat-sen University (n=28). It is worth noting that among the top 8 institutions with the largest number of publications, Ghent University (Netherlands) has 15 publications, and the other 7 institutions are all in China (Figure 2C). Figure 2D shows that research on tsRNA by different institutions has increased dramatically after 2020.
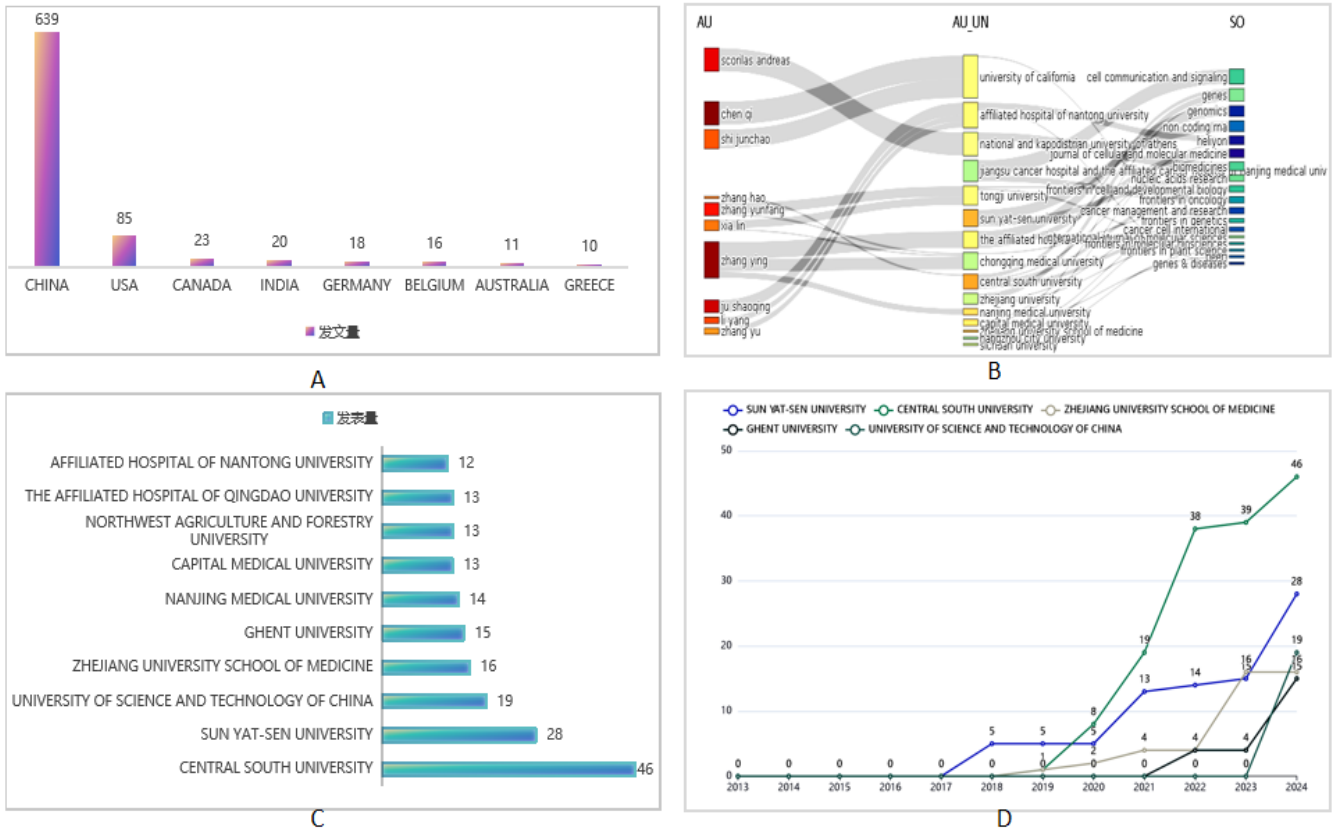
Figure 2 National and institutional distribution of tsRNA research   A: Country map of researchers; B: Three fields; C: Chart of the number of issued documents; D: Output time diagram of mechanism output component

2.3 Periodical Distribution:

Articles related to tsRNA research have been published in a variety of journals, of which the International Journal of Molecular Sciences (n=9) is the most active in the field. This was followed by Genes (n=6) and Nucleic Acids Research (n=6). The output time of these journals has steadily increased after 2018.
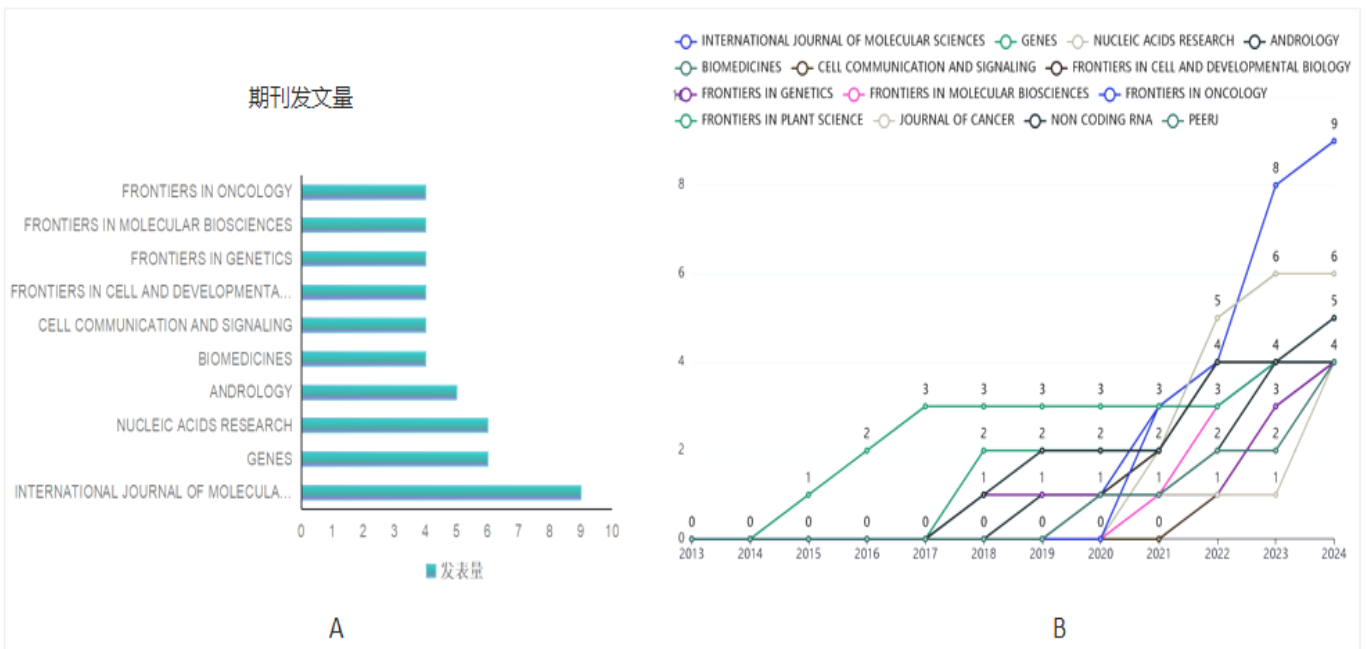

Figure. 3 Periodical distribution map A: Number of publications in top 10 journals; B: Time chart of journal publication

2.4 Author Distribution:

We analyzed the number of publications between authors and author collaboration (Figure 4) to visualize the strength of the authors' research. In the field of tsRNA research, a total of 1856 authors have contributed. Among the top 10 authors, Chen Qi and Zhang Ying published the most articles (n=6), followed by Chen Lei, Gan Mailin and other 8 authors (n=4) (FIG. 4A). The collaborative network of these authors is shown in Figure 4B, in which Chen Lei, Gan Mailin, and Gu Hao collaborate most closely. These authors are mainly located in China (Figure 4C).
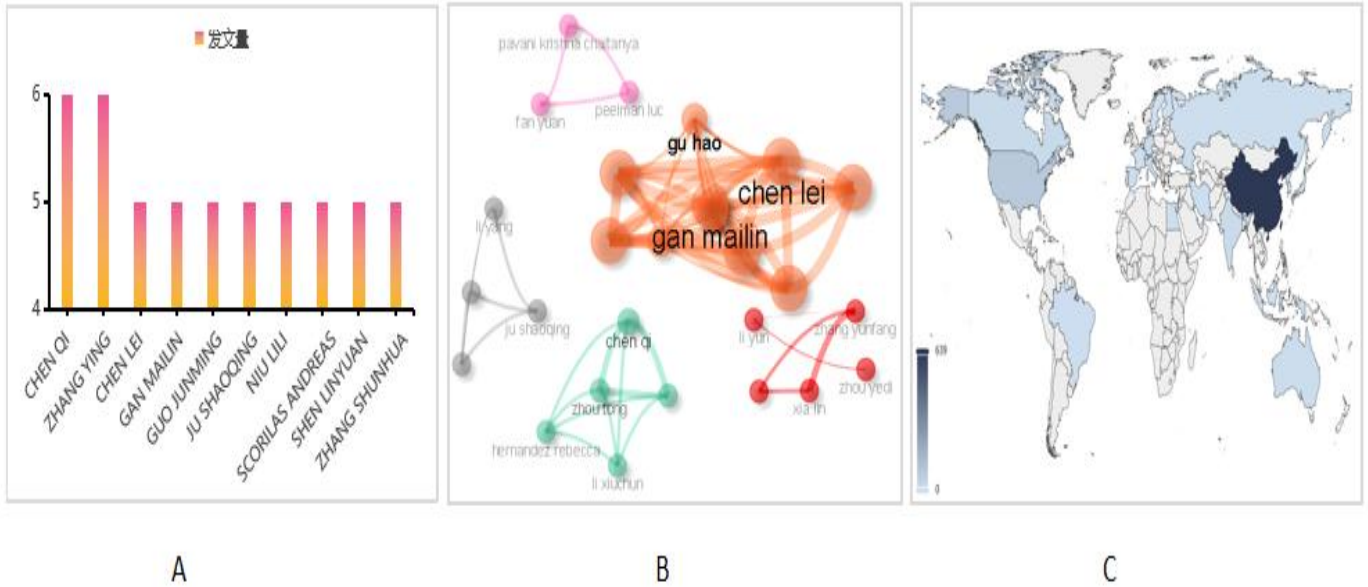

A   B   C

Figure 4 Author distribution mapA: Top 10 published authors; B: Author collaboration network diagram; C: Author collaboration map

2.5 Co-occurrence of theme words:

The analysis of keywords can provide a hot spot for the research in this field. Table 5 shows the 12 keywords with the highest frequency and the strongest centrality. The most frequent words were tsRNA (n = 93) and biomarker (n = 33). These words are all related to the subject term we are searching for. In addition, Diagnose (n = 15) and Cancer (n =14) occur frequently, indicating that scholars in the field are mainly concerned about the diagnostic and marker potential of tsRNA in tumors
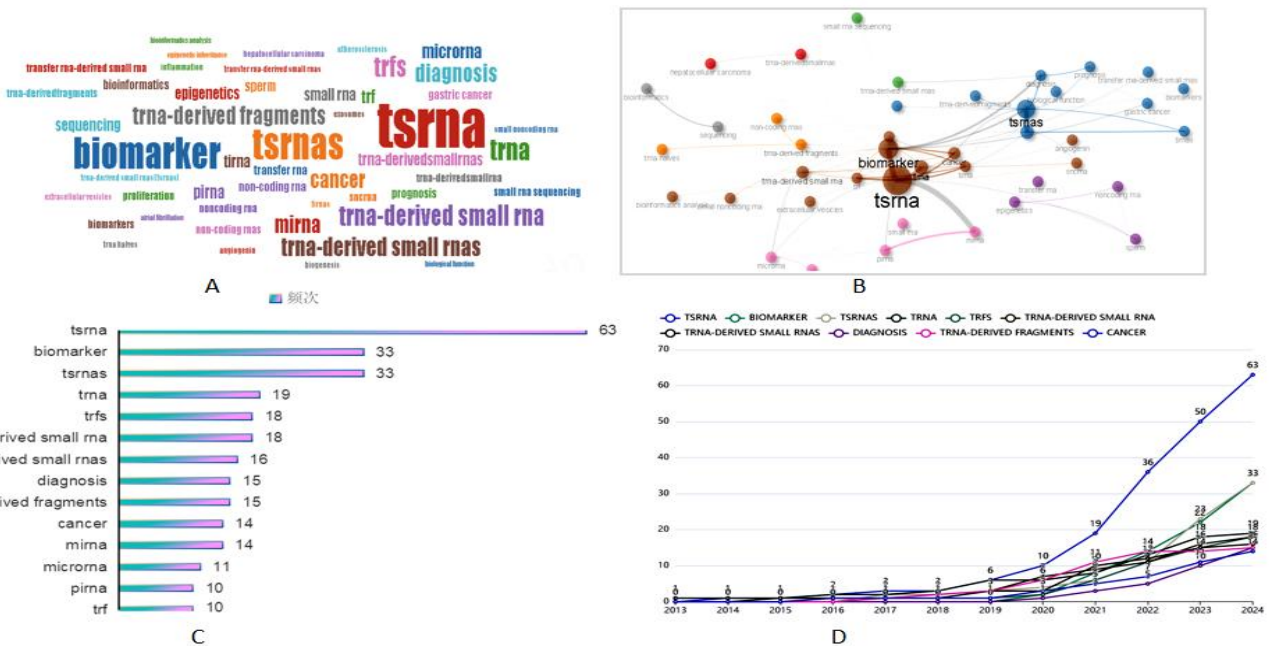

A   B

C   D

Figure 5 Co-occurrence of subject wordsA: keyword cloud map; B: keyword co-occurrence network diagram; C: Figure of occurrence frequency of subject words; D: Annual change chart of theme word frequency

2.6 High scores and highly cited articles:

We analyzed literature with high scores and articles with high citations, as shown in Figure 6. Schorn Andrea J (n=195) is the article with the most citations. This was followed by Li Siqi (n=146), Shen Yinjing (n=114) and Unterholzner Leonie (n=112). The paper published with the highest impact factor was Schorn Andrea J's LR-Retrotransposon Control by tRNA-Derived Small RNAs (IF=45.5), Followed by Sunyang Ying (IF=40.8), Xiong Qunli (IF=29.5).

高被引文献

GREEN DARRELL, 2016,	34
OBERBAUER VERA, 2018,	36
CHEN HUI, 2019,	42
ROMPALA GREGORY R, 2018,	49
ZHANG XUDONG, 2016,	59
GEBERT DANIEL, 2017,	60
UNTERHOLZNER LEONIE, 2013,	112
SHEN YIJING, 2018,	114
LI SIQI, 2018,	146
SCHORN ANDREA J, 2017,	195

Table 1 Statistical table of top 10 articles with high scores

Title	Ahthors	Journal	IF	Citated
LTR-Retrotransposon Control by tRNA-Derived Small RNAs	Schorn, Andrea J	Cell	45.5	195
tRF-Gln-CTG-026 ameliorates liver injury by alleviating global protein synthesis	Ying Sunyang	Signal Transduction and Targeted Therapy	40.8	6
Small RNA modifications: regulatory molecules and potential applications	Xiong Qunli	Journal of Hematology & Oncology	29.5	8
tRNA-derived small RNAs in human cancers: roles, mechanisms, and clinical application	Zhou Manli	Molecular Cancer	27.7	0
Aging-induced tRNAGlu-derived fragment impairs glutamate biosynthesis by targeting mitochondrial translation-dependent cristae organization	Li Dingfeng	Cell Metabolism	27.7	2

DISCUSSION

In general, the amount of literature on tsRNA research is increasing year by year. From 2013 to 2019, the literature on tsRNA is relatively small, and the research in this field is still in the early stage, possibly because many scholars believe that tsRNA is only the lysate of tRNA and has no actual biological function. From 2020 to the present, the number of papers published each year has increased rapidly and steadily, indicating that more and more scholars realize that tsRNA plays an important role in many diseases, including a variety of tumors, and are beginning to pay attention to this field. In terms of the number of publications, China has published a large number of articles, many of which are of high quality, indicating that domestic research in the field of tsRNA has also kept up with the world's leading edge. There are few exchanges and cooperation between domestic institutions, and even less cooperation with the international community. In the future, we should strengthen international exchanges and cooperation to obtain faster and more high-quality research results.

In terms of research institutions, most of them are limited to domestic cooperation, with less international cooperation, which is not conducive to long-term academic development. However, we note that Central South University and Sun Yat-sen University, which have a large number of published papers, do not cooperate with other institutions, which may hinder the development of research in this field. Therefore, in

the future, we should strengthen institutional and international exchanges and cooperation to efficiently obtain more high-quality research results and promote the development of TSRNA-related research. From a Journal perspective, the International Journal of Molecular Sciences has the most publications (n=9) and is the most active journal in the field, This was followed by Genes (n=6) and Nucleic Acids Research (n=6). The analysis results indicated that current studies mainly focused on basic studies and few clinical studies.

In terms of authors, Chen Qi and Zhang Ying were the most prolific, publishing six articles, the main contribution of which was to explore tsRNA's regulation of gene transcription and modification functions in disease. However, Schorn Andrea J (n=195), whose work "LTR-Retrotransposon Control by tRNA-Derived Small RNAs" published in Cell in 2017 [13], has been cited the most frequently. This study revealed that tsRNA retrotransposon is a highly conserved mechanism for controlling the biological function of transposon migration that escapes epigenetic inhibition, and confirmed that tsRNA regulates reverse transcription, providing a reliable basis for the study of tsRNA, and its influence in this field is extremely prominent.

Aluable literature can have a significant academic impact on research in the field. Through the analysis of keywords, the most frequently researched topics in this field can be summarized. In this study, we screened the 12 keywords with the highest frequency and centrality. In addition to TSRNA-related words, Biomarker, Diagnose, Cancer, miRNA, and piRNA appear very frequently, which indicates that biomarkers and tumor diagnosis have become key areas of tsRNA research. It may also regulate the occurrence and development of disease through interaction with miRNA or piRNA [14-16].

This study is the first to conduct a bibliometric analysis of the tsRNA field and provide an objective and comprehensive summary of the field. However, there are also shortcomings. First of all, only the literature published in English pubmed database was searched, and some articles in other databases were ignored, which leads to certain selection bias and incomplete literature.

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