



Drug discovery and development with special reference to molecular modeling: A bibliometric approach (2005–2024)

Pawan Nayak¹, Virendra S. Ligade^{2*}

¹Department of Pharmacology, Manipal College of Pharmaceutical Sciences, Manipal Academy of Higher Education, Manipal, India.

²Department of Pharmaceutical Regulatory Affairs and Management, Manipal College of Pharmaceutical Sciences, Manipal Academy of Higher Education, Manipal, India.

ARTICLE HISTORY

Received on: 09/11/2025
Accepted on: 08/02/2026
Available Online: 05/03/2026

Key words:

Molecular modeling,
discovery, drug,
development, bibliometric.

ABSTRACT

There is growing evidence demonstrating the use of computer modeling in biomedicine as new technologies emerge in every discipline. Computational, translational, experimental, and clinical methods are all combined in current drug development to find possible novel potential medications. However, limited attention has been given to summarizing global publication trends in this field. The aim of the current study is to describe and assess global trends in applying the bibliometric approach to drug development and discovery regarding the importance of molecular modeling. A literature search was conducted to extract all relevant papers on molecular modeling in drug discovery and development using the Scopus database. The data were gathered for the year 2005–2024. Insights are classified based on authors, title of publication sources, countries, type of documents, research domains, and so on. A total of 3,489 papers were retrieved, demonstrating a surge of interest in molecular modeling within drug discovery and development, with a significant rise in recent years. The top countries contributing were the United States, India, and China. Journal articles constituted the highest percentage of papers, and the most productive source was the Journal of Chemical Information and Modeling. The study highlights the tools and software used in modern drug development and discovery-related analysis that were developed using machine learning techniques. There has been an upsurge of interest in molecular modeling in drug discovery and development, as shown by a growing trend in research publications in recent years. This study is the first extensive bibliometric evaluation between 2005 and 2024 with specific emphasis on molecular modeling in drug development and discovery. The results serve as a useful guide for academicians, researchers, and policy-makers to identify global trends and future research directions in this new field.

1. INTRODUCTION

Investigating and fabricating new drugs is an ongoing aspect of pharmaceutical research. Society requires improved pharmaceuticals or medicines to control diseases and maintain a good quality of life. Modern medications with cutting-edge technology are desperately needed to safeguard society's public health. Finding unmet needs that

benefit humanity is the aim of drug discovery research. Before marketing approval, newly discovered medications must complete extensive pre-clinical and clinical trials/stages. There is growing evidence demonstrating the use of computer modeling in biomedicine as new technologies emerge in every discipline. Computational, translational, experimental, and clinical methods are all combined in current drug development to find possible novel potential medications. There are many tools and software used in modern drug development and discovery-related analysis that were developed using machine learning techniques [1].

The use of machine learning (ML) and artificial intelligence (AI) in drug discovery significantly accelerates the cost and time necessary to launch a medicine to market.

*Corresponding Author

Virendra S. Ligade, Department of Pharmaceutical Regulatory Affairs and Management, Manipal College of Pharmaceutical Sciences, Manipal Academy of Higher Education, Manipal, India. E-mail: virendra.sl@manipal.edu

As per the literature, Cancer dynamics is currently being investigated *in silico* using computational models, which may make it possible to identify new molecular targets in the era of precision medicine. This would help to develop innovative treatments and overcome drug resistance to anticancer medications [2]. Another literature mentions about growing significance of molecular docking in drug discovery methods. Molecular docking focuses on computational methods to predict the interaction of the ligand-receptor complex [3]. The docking technique has significantly impacted drug design and discovery, particularly in anticancer medicines. Many novel histamine receptor ligands have been discovered due to recent advancements in rapid, robust docking, virtual screening, and other algorithms. These ligands may be utilized to treat allergy-inflammatory illnesses, pathologies of the central nervous system, pain, cancer, and obesity [4]. Research publications can be evaluated to determine the precise importance of AI and ML in drug discovery. An additional review discusses the global peer-reviewed literature's bibliometric analysis and historical view on molecular modeling as a research tool [5]. In cheminformatics procedures, ML techniques are employed to forecast an unknown medication's activity and identify novel antibacterial drug candidates. Machine learning is commonly used in the development of antimicrobial drugs [6].

Many uses for AI have been reported. As more money is invested in this technology, this idea is becoming more and more commonplace every day, especially in the healthcare industry [7]. But so far, no bibliometric analysis has particularly traced global trends in molecular modeling along an interdisciplinary scenario in the last two decades. This gap supports the uniqueness of the current manuscript. Summarising global trends in molecular modeling in drug discovery and development papers has not received much attention so far. The current study is the first to describe and assess global trends in applying the bibliometric approach to drug development and discovery regarding the importance of molecular modeling.

The bibliometric method is even more crucial since it enables the detection of publication patterns, collaborative research networks, key institutions, and international strategic directions. Through mapping these dimensions, bibliometric analysis enables evidence-based decision-making, identifies research gaps, and offers advice to funding bodies, researchers, and policymakers.

Finding out how much a research publication advances knowledge can be done through a bibliometric analysis. Bibliometric analysis is helpful when it comes to finding important information for various reasons, such as potential research prospects. Bibliometric analysis makes it possible to identify and evaluate the success of research papers, journals, organizations, and nations based on citations. Research project development might be guided by bibliometric analysis [8,9,10]. Through bibliometric analysis, this paper aims to examine the research on applying molecular modeling to drug discovery and development. This statistically helpful analysis is used throughout the article to discuss and draw conclusions about the

publication pattern, highly cited articles, significant research journals, productive countries, and organizations.

2. MATERIALS AND METHODS

2.1. Design

To investigate the printed publications on molecular modeling in drug discovery and development studies from 2005 to 2024, statistical and graphical bibliometric analysis was carried out. Titles, abstracts, year of publications, types of studies, number of citations, countries contributing, organizations, keywords, publishing journal, and worldwide most cited articles were examined by descriptive approaches and bibliometric mapping.

2.2. Data collection

The Scopus database (Elsevier B.V.) yielded a text-format document with all the bibliometric data. Similar phrases or several synonyms were used to ensure data accuracy and incorporated into the search strategy. The keywords “molecular AND modeling AND in AND drug AND discovery AND development” were employed together with the “title” word in the advanced search. The literature search was conducted for all published studies of molecular modeling in drug discovery and development research from 2005 to 2024. Furthermore, only articles published in English and published after the year 2005 were considered and enrolled for bibliometrics analysis. A total of ($n = 3489$) articles were obtained when the data were collected on May 23, 2025. The data were exported in .bib format with “full record and cited references” from the Scopus website.

In the current bibliometric study, just the Scopus database was employed for data collection and analysis. The choice was made because Scopus offers extensive coverage of journals, strong citation tracking, and support for bibliometric mapping tools like VOSviewer. Scopus is a vast and trustworthy abstract and citation database that provides access to peer-reviewed literature in many disciplines, including chemistry, pharmacology, computer science, and molecular biology, which are directly involved in the subject of molecular modeling in drug development and discovery. Though other databases, such as Web of Science and PubMed, are also worth using, they have not been included in this study on account of certain constraints. Web of Science, while being similar in quality, includes a comparatively smaller set of journals in inter-disciplinary fields. PubMed is more concerned with biomedical literature and does not provide extended citation information and bibliometric export capabilities necessary for network analysis and visual mapping. But single-database usage could be biased because the publications that could be of use, but are indexed solely in Web of Science or PubMed, would not be included. Web of Science, although of comparable quality, indexes fewer interdisciplinary journals, and PubMed, extensive as it is for biomedical literature, does not have elaborate citation tracking and bibliometric export options. In addition, no manual screening or validation process was conducted to ensure the relevancy of each retrieved article, and no inclusion–exclusion criteria were used beyond language (English) and time (2005–2024).

In addition, reliance on one well-maintained database avoids data inconsistency, duplication, and simplifies analysis.

Accordingly, for the scope and goals of this study, Scopus was deemed the most suitable and effective source for bibliometric analysis.

2.3. Data analysis

Analysis and visualization of data were conducted using secondary data. The information/findings were collected and downloaded in comma separated values format from the Scopus database to conduct the data analysis. The analysis is mainly descriptive data that are analyzed, interpreted, and represented in tables and percentages. Insights are grouped based on year of publication, document type, authors, title of publication source, country, research areas, and so on. The keyword frequencies were mapped with the assistance of The Vosviewer application software, a tool for browsing, analyzing, and presenting data in an interactive, visual format.

3. RESULTS

3.1. Study types and total number of publications

From year 2015, a rising trend in research articles related to molecular modeling in the areas of drug discovery and development has been noted. Analyses indicated a notable rise in the number of research publications. A significant upward trend in publication growth was observed in 2015 with ($n = 223$) of records. The highest number of publications were in year the 2024 with ($n = 425$) publications. The post-2020 era displays a clear upswing in publications, especially those employing molecular modeling for infectious diseases like COVID-19. Highly accessed works in this era (e.g., Wu *et al.*,

Table 1. Total number of publications

Year	Number of publications
2024	425
2023	244
2022	256
2021	334
2020	266
2019	281
2018	244
2017	214
2016	200
2015	223
2014	171
2013	113
2012	95
2011	108
2010	77
2009	72
2008	55
2007	43
2006	40
2005	28

2020) exemplify how the pandemic hastened the application of computational tools for speedy target discovery and drug repurposing. This represents a shift in the use of molecular modeling from being mainly oncology-targeted applications to imperative global health needs, exemplifying its versatility to new challenges (Table 1).

Among the studies conducted, journal articles were ($n = 2313$) as shown in Table 2. In other study types, there were review articles ($n = 761$), book chapters ($n = 256$), and conference papers ($n = 90$). Journal articles were the highest among all study types.

3.2. Publications contributed by countries and organization/institution

The United States emerged as the leading country in terms of production with ($n = 1013$) published documents, followed by India ($n = 556$), China ($n = 514$), and United Kingdom ($n = 271$) as illustrated in Table 3. Among the top 10 countries, namely, Germany, Italy, Spain, South Korea, Saudi Arabia, and France also contributed more than 80 publications in molecular modeling related to drug discovery and development research.

Table 2. Study types published in literature.

Document type	Number of publications
Article	2,313
Review	761
Book chapter	256
Conference paper	90
Book	27
Short survey	20
Editorial	9
Note	6
Conference review	2
Data paper	1
Erratum	3
Letter	1

Table 3. Contributing country/region.

Country	Number of publications
United States	1,013
India	556
China	514
United Kingdom	271
Germany	198
Italy	188
Spain	121
South Korea	112
Saudi Arabia	112
France	108

Table 4. Contributing organization/institution.

Affiliations	Number of publications
Ministry of Education of the Peoples Republic of China	59
Chinese Academy of Sciences	58
National Institutes of Health NIH	43
Jadavpur University	38
University of California, San Diego	38
University of Cambridge	34
Harvard Medical School	33
King Saud University	32
Zhejiang University	31
Universidade de São Paulo	31
KU Leuven	30

Table 5. Relevant source/journal impact in the literature.

Source	Number of publications
Journal of Chemical Information And Modeling	171
Journal of Biomolecular Structure and Dynamics	90
European Journal of Medicinal Chemistry	87
International Journal of Molecular Sciences	70
Journal of Medicinal Chemistry	67
Methods In Molecular Biology	63
Molecules	62
Journal of Computer Aided Molecular Design	60
Expert Opinion on Drug Discovery	58
Journal of Molecular Graphics And Modelling	55

Organizations/institutions that contributed to molecular modeling, related to drug discovery and development research, are presented in Table 4. The most active institution was the Ministry of Education of the People's Republic of China (59) and the Chinese Academy of Sciences ($n = 58$), followed by the National Institutes of Health NIH ($n = 43$), Jadavpur University (38), and University of California, San Diego ($n = 38$).

3.3. Top journal sources and research areas

In the realm of leading journals, the most significant contributions in these fields were published in the Journal of Chemical Information and Modeling ($n = 171$), followed by Journal of Biomolecular Structure and Dynamics (90), European Journal of Medicinal Chemistry (87), International Journal of Molecular Sciences (70), Journal Of Medicinal Chemistry ($n = 67$) (Table 5).

Table 6 indicates the maximum number of research publications are published in the area of Genetics, Biochemistry, and Molecular Biology ($n = 1,733$), followed by Toxicology, Pharmacology, and Pharmaceutics ($n = 1,500$), Chemistry ($n = 1,245$), Computer Science ($n = 725$), and Medicine ($n = 545$).

Table 6. Topics of research areas in the scientific literature.

Research areas	Total number of publications
Biochemistry, Genetics and Molecular Biology	1,733
Pharmacology, Toxicology and Pharmaceutics	1,500
Chemistry	1,245
Computer Science	725
Medicine	545
Chemical Engineering	446
Social Sciences	188
Mathematics	172
Materials science	153
Immunology and Microbiology	150

Table 7. Most contributing authors.

Author name	H-index	Number of publications
Taha, M.O.		21
Jha, T.		19
Hou, T.		19
Roy, K.		16
Zhan, P.		14
Liu, X.		14
Amin, S.A.		14
Schuster, D.		13
Medina-Francoz, J.L		13
Andricopulo, A.D.		12

3.4. Most contributing authors and highly cited manuscripts

Taha, M.O. is identified as the most prolific author with ($n = 21$) publications, followed by Jha T ($n = 19$) and Hou, T. ($n = 19$) (Table 7 and Fig. 2). The most cited documents in the area of molecular modeling related to drug discovery and development research are listed in (Table 8). Out of 10 articles, the most highly cited articles have been published in years 2011 and 2021. The most cited work titled "Molecular docking: A powerful method for structure-based drug discovery" by Meng *et al.* [3] was published in 2011 and has received 2564 citations. This was followed by another article titled "Analysis of therapeutic targets for SARS-CoV-2 and discovery of potential drugs by computational methods" by Wu *et al.* [11] with 1762 citations.

3.5. Keyword frequency analysis

Certain features of the research on molecular modeling in drug discovery and development could be indicated by the presence of specific keywords. Words, namely "drug discovery," "drug development," "computer model," "molecular dynamics," "molecular docking simulation," "humans," "ligand binding," "unclassified drug," and "chemistry" were identified as prominent keywords in the current study (Fig. 1).

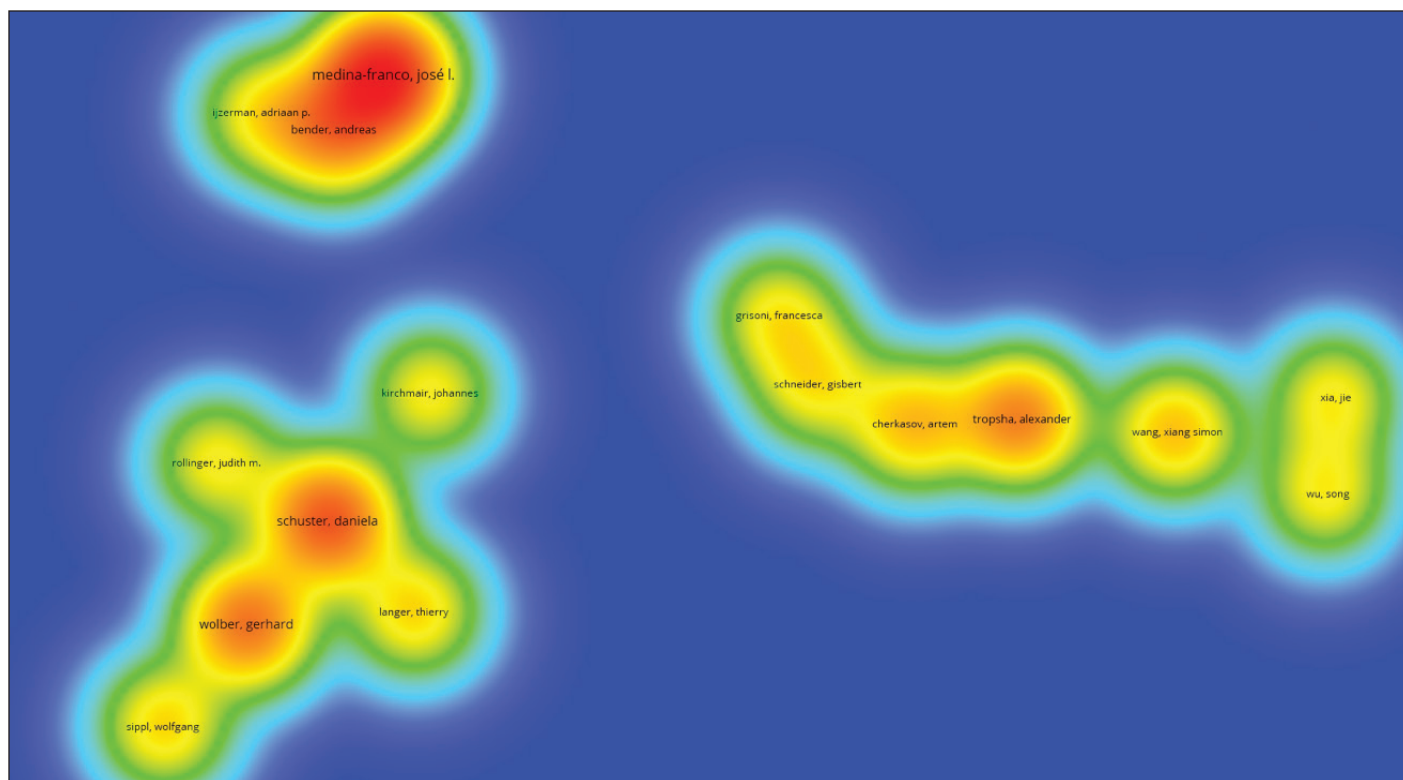


Figure 2. Author density impact analysis.

4. DISCUSSION

Our bibliometric study of Molecular Modeling in Drug Discovery and Development research publications from 2004 to 2023 shows an exponential increase in published evidence. The rise in research publications aligns with the growing popularity of Molecular Modeling for Drug Discovery and research development in general. The study reveals that the developing nations, especially India and China, have become major contributors to molecular modeling studies. India is second on the global list in terms of publication output, an indication of increased investment in computational drug discovery infrastructure and capacity-building programs. This is an important contribution, as it emphasizes that not just developing countries are consumers but also producers of cutting-edge computational research. Their participation also reflects the possibility of more global diversity in collaborations that can close resource gaps and drive innovation across the globe.

Few studies on the significance of AI in drug, discovery and development in different countries have been published so far. These studies have investigated scholarly publication trends by using bibliometric methods. The current study highlighted a few of the latest findings on the significance of Molecular Modeling in Drug Discovery and Development from the literature. The development and discovery of novel medications is an expensive and time-consuming procedure. However, over time, the target-oriented approach achieved notable progress in this field, bringing the golden era of rational planning. In light of this, the growing fields of technological innovation and software development

assist in the rational drug design by cutting costs and time, and computer-aided drug design (CADD) is a good substitute. Significant advancements in various domains, primarily in computational methodologies, have also driven advances in drug design and discovery strategies [12]. Top universities in the field are very productive, as evidenced by their institutional contributions. Although docking and structure-based drug design are still core, recent times have witnessed a progressive transition towards AI and ML strategies. These strategies facilitate virtual screening on a large scale, predictive modeling of molecular interactions, and combination with big data, thus going beyond the conventional domain of docking. Pharmacophore modeling has been more important during the past 10 years and has a variety of uses throughout the drug discovery process [13]. Small molecule drug discovery and development still have a long way to go before deep learning methods are recognized, especially compared to classical ML algorithms. Furthermore, much effort needs to be made to make deep learning more widely used and applied in research settings, such as small molecule medication discovery and research [4]. Despite a few drawbacks, CADD is still in use today and has been the driving force behind numerous advancements in drug development. These techniques will most likely be applied by the following generation of rational designers [5]. The availability of extensive data collection has sparked interest in creating new data mining methods, making machine learning into a dynamic area of research in computer science. Computer-aided drug discovery techniques can make extensive use of machine learning techniques. Drug design employs the most fantastic machine learning techniques supporting biology

modeling in the drug discovery phase [14]. Bioprinting is a highly automated production technology that significantly enhances the throughput of creating 3D *in vitro* models compared to conventional methods, offering improvements in accuracy, resolution, and precision for drug discovery [15]. The ability to modify dose formulations for specific patients, or every individual, is one of the most exciting uses of 3D printing in the pharmaceutical sector; this concept is known as “polypill” [16]. Several elements of varying molecular modeling in the discovery of drug and development are highlighted in the analysis of the current study. Improved research strategies, goals, and resource allocation can be achieved with the help of the study’s findings.

5. STRENGTH AND LIMITATION

Although providing useful insights, bibliometric analyses have their limitations, and these need to be kept in mind. One of the main limitations is the reliance on a single database, which in this case is Scopus, and it might generate publication bias because of the exclusion of studies indexed elsewhere, such as Web of Science or PubMed. Second, bibliometric data are also subject to language bias because non-English publications tend to be underreported or even excluded. Metrics based on citations, though helpful for measuring influence, may not accurately represent the scientific value or applicability of studies, as they can be distorted by issues related to self-citations, effects of networks, or journal prestige. Additionally, recent articles might show lower impact due to a short citation window, although they could eventually become highly impactful. Finally, bibliometric tools can capture qualitative dimensions of research contributions, including novelty, methodological quality, or clinical utility, to some extent. These shortcomings serve to underscore the importance of careful interpretation of bibliometric results and, where feasible, incorporation of auxiliary qualitative evaluation to develop a better-balanced view of the literature environment.

A limitation of this bibliometric analysis is the lack of a screening or validation step for the articles found. While automatic data collection from the Scopus database facilitates quick analysis of trends in publications, it can also introduce irrelevant or poor-quality articles by default, particularly when using a keyword search in titles alone. This absence of manual or automated screening to validate the relevance and accuracy of every single record can result in selection bias and imprecision in the results. Furthermore, lacking the application of predetermined inclusion or exclusion criteria, there is also a potential for overrepresentation or underrepresentation of particular subfields or types of studies. Also, the research is based on metadata and not full-text analysis, which restricts the level of content assessment and can overlook subtle or cross-disciplinary contributions.

6. CONCLUSION

The main advantage of this study lies in its application of bibliographic analysis and visualization of data techniques to complete molecular modeling related to drug discovery and development research. Literature indicates that there has been an upsurge in interest in the role of molecular modeling in drug discovery and development research. This is clear because

there has been a growing trend of publications in recent years. The United States was the top country by total number of publications, followed by India and China. These results act as a guide and road map to research scholars and academicians in drug discovery and development research. These trends in research publication can go on and grow with strong studied in molecular modeling area in relation to drug discovery and development research.

Nonetheless, methodological flaws in this study need to be factored into interpreting the results. The use of one database (Scopus) only, the lack of manual screening or pre-established inclusion–exclusion criteria, and no full-text analysis limit the level of interpretation depth. These can result in possible bias, omission of pertinent literature indexed elsewhere, and restricted contextual understanding. Consequently, though the results are strong in demonstrating general trends and patterns, they must be extrapolated with caution. Additional analyses involving multiple databases and qualitative evaluation would enhance future studies.

7. AUTHOR CONTRIBUTIONS

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; agreed to submit to the current journal; gave final approval of the version to be published; and agree to be accountable for all aspects of the work. All the authors are eligible to be an author as per the International Committee of Medical Journal Editors (ICMJE) requirements/guidelines.

8. FINANCIAL SUPPORT

There is no funding to report.

9. CONFLICT OF INTEREST

The authors report no financial or any other conflicts of interest in this work.

10. ETHICAL APPROVALS

This study does not involve experiments on animals or human subjects.

11. DATA AVAILABILITY

All data generated and analyzed are included in this research article.

12. PUBLISHER’S NOTE

All claims expressed in this article are solely those of the authors and do not necessarily represent those of the publisher, the editors and the reviewers. This journal remains neutral with regard to jurisdictional claims in published institutional affiliation.

13. USE OF ARTIFICIAL INTELLIGENCE (AI)-ASSISTED TECHNOLOGY

The authors declare that they have not used artificial intelligence (AI)-tools for writing and editing of the manuscript, and no images were manipulated using AI.

REFERENCES

1. Priya S, Tripathi G, Singh DB, Jain P, Kumar A. Machine learning approaches and their applications in drug discovery and design. *Chem Biol Drug Des.* 2022;100(1):136–53. doi: <https://doi.org/10.1111/cbdd.14057>
2. Pennisi M, Russo G, Di Salvatore V, Candido S, Libra M, Pappalardo F. Computational modeling in melanoma for novel drug discovery. *Expert Opin Drug Discov.* 2016;11(6):609–21. doi: <https://doi.org/10.1080/17460441.2016.1174688>
3. Meng XY, Zhang HX, Mezei M, Cui M. Molecular docking: a powerful approach for structure-based drug discovery. *Curr Comput Aided Drug Des.* 2011;7(2):146–57. doi: <https://doi.org/10.2174/157340911795677602>
4. Mehta P, Miszta P, Filipek S. molecular modeling of histamine receptors-recent advances in drug discovery. *Molecules.* 2021;26(6):1778. doi: <https://doi.org/10.3390/molecules26061778>
5. Silva LA, Garrot TG, Pereira AM, Correia JCG. Historical perspective and bibliometric analysis of molecular modeling applied in mineral flotation systems. *Minerals Eng.* 2021;170:107062. doi: <https://doi.org/10.1016/j.mineng.2021.107062>
6. Diéguez-Santana K, González-Díaz H. Machine learning in antibacterial discovery and development: a bibliometric and network analysis of research hotspots and trends. *Comput Biol Med.* 2023;155:106638. doi: <https://doi.org/10.1016/j.combiomed.2023.106638>
7. Jimma BL. Artificial intelligence in healthcare: a bibliometric analysis. *Telematics Informat Rep.* 2023;9:100041. doi: <https://doi.org/10.1016/j.teler.2023.100041>
8. Pritchard A. Statistical bibliography or bibliometrics. *J Documentation.* 1969;25:348–9.
9. Oliveira JO, Silva FF, Juliani F, Motta FCL, Nunhes VT. Bibliometric method for mapping the state-of-the-art and identifying research gaps and trends in literature: an essential instrument to support the development of scientific projects. *Scientometrics.* 2019;1–20. doi: <https://doi.org/10.5772/intechopen.85856>
10. Matorevhu A. Bibliometrics: application opportunities and limitations. *Bibliometrics - an essential methodological tool for research projects [Working Title]*. London: IntechOpen. 2024. doi: <http://dx.doi.org/10.5772/intechopen.1005292>
11. Wu C, Liu Y, Yang Y, Zhang P, Zhong W, Wang Y, et al. Analysis of therapeutic targets for SARS-CoV-2 and discovery of potential drugs by computational methods. *Acta Pharm Sin B.* 2020;10(5):766–88. doi: <https://doi.org/10.1016/j.apsb.2020.02.008>
12. Nascimento IJDS, de Aquino TM, da Silva J. The new era of drug discovery: the power of computer-aided drug design (CADD). *Lett Drug Des Discov.* 2022;19(11):951–5. doi: <https://doi.org/10.2174/1570180819666220405225817>
13. Muhammed MT, Aki-yalcin E. Pharmacophore modeling in drug discovery: methodology and current status. *JOTCSA.* 2021;8(3):749–62. doi: <https://doi.org/10.18596/jotcsa.927426>
14. Hussain W, Rasool N, Khan YD. Insights into machine learning-based approaches for virtual screening in drug discovery: existing strategies and streamlining through FP-CADD. *Curr Drug Discovery Technol.* 2021;18:463–72. doi: <https://doi.org/10.2174/157016381766200806165934>
15. Satpathy A, Datta P, Wu Y, Ayan B, Bayram E, Ozbolat IT. Developments with 3D bioprinting for novel drug discovery. *Expert Opin Drug Discov.* 2018;13(12):1115–29. doi: <https://doi.org/10.1080/17460441.2018.1542427>
16. Vaz VM, Kumar L. 3D printing as a promising tool in personalized medicine. *AAPS PharmSciTech.* 2021;22(1):49. doi: <https://doi.org/10.1208/s12249-020-01905-8>

How to cite this article:

Nayak P, Ligade VS. Drug discovery and development with special reference to molecular modeling: A bibliometric approach (2005–2024). *J Appl Pharm Sci.* 2026;16(04):092-099. DOI: 10.7324/JAPS.2026.269869