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A Bibliometric Perspective on Stable Bacterial Lipases: Research Trends, Scientific Collaboration, and Emerging Directions (2010–2026)

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Abstract

Background: Stable bacterial lipases have become indispensable biocatalysts owing to their exceptional thermostability, catalytic efficiency, and tolerance to harsh industrial environments. Their expanding applications in biocatalysis, biodiesel production, bioremediation, enzyme engineering, and sustainable biotechnology have stimulated substantial scientific interest. However, a comprehensive bibliometric assessment of the intellectual structure, research evolution, and emerging trends in this field remains limited.

Methods: This study presents a comprehensive bibliometric analysis of global research on stable bacterial lipases published between 2010 and 2026. Bibliographic data were retrieved from the Lens.org database using a systematic Boolean search strategy and screened following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) framework. After applying predefined inclusion and exclusion criteria, 499 peer-reviewed journal articles were selected for analysis. Performance analysis and science mapping were conducted using the Bibliometrix/Biblioshiny package in R and VOSviewer (version 1.6.20) to evaluate publication trends, citation patterns, leading journals, authors, institutions, countries, collaboration networks, keyword co-occurrence, co-citation relationships, bibliographic coupling, and thematic evolution.

Results: The dataset comprised 499 journal articles published in 139 sources between 2010 and 2026, involving 2,322 authors with an average of 5.35 co-authors per document. The field exhibited a positive annual publication growth rate of 3.74%, indicating sustained expansion over the study period. The publications accumulated an average of 57.23 citations per document and collectively cited 42,878 references, demonstrating the maturity and scientific influence of the research area. Temporal and thematic analyses revealed increasing attention to enzyme stability, protein engineering, immobilization, biocatalysis, biodegradation, biodiesel production, and environmentally sustainable industrial applications. Network analyses further identified the major research clusters, collaborative patterns, and emerging thematic directions shaping the evolution of the field.

Conclusions: This study provides a comprehensive overview of the global scientific landscape of stable bacterial lipase research from 2010 to 2026. The findings highlight the growth, intellectual foundations, and emerging research priorities of the field while providing

valuable insights for researchers, industrial practitioners, and policymakers seeking to advance enzyme biotechnology and sustainable bioprocess development.

Keywords: Stable bacterial lipases; Bibliometric analysis; Lens.org; VOSviewer; Science mapping.

1. Introduction

Lipases (triacylglycerol acylhydrolases, EC 3.1.1.3) are among the most extensively studied industrial enzymes owing to their ability to catalyze the hydrolysis, esterification, transesterification, alcoholysis, and interesterification of lipid substrates under diverse reaction conditions (Khan et al., 2022; Ali et al., 2023; Sharma et al., 2023; Nag et al., 2023). Their broad substrate specificity, high catalytic efficiency, and stereoselectivity have made them indispensable biocatalysts in numerous industrial sectors, including pharmaceuticals, food processing, detergents, biodiesel production, cosmetics, environmental remediation, and fine chemical synthesis (Hasan et al., 2011; Sharma et al., 2012; Ferreira-Dias et al., 2013). Compared with conventional chemical catalysts, lipases offer several advantages, such as operation under mild reaction conditions, reduced energy requirements, high product selectivity, and compatibility with environmentally sustainable manufacturing processes, making them key components of modern green biotechnology (Borkar et al., 2010; Singh and Mukhopadhyay, 2014; Jaeger and Eggert, 2015; Salihu et al., 2016). Among the various sources of lipases, bacterial lipases have received considerable attention because of their rapid microbial growth, ease of genetic manipulation, short fermentation cycles, and ability to produce extracellular enzymes with desirable catalytic properties (Gupta et al., 2017; Geoffry and Achur, 2018; Sarmah et al., 2019). In particular, stable bacterial lipases, characterized by their thermostability, tolerance to extreme pH, resistance to organic solvents, and long-term operational stability, are increasingly preferred for industrial applications where harsh processing conditions frequently reduce the activity of conventional enzymes (Carr et al., 2023; Zan et al., 2025; Zha and Yan, 2025; Wang et al., 2026). These characteristics enable bacterial lipases to function efficiently in high-temperature bioprocesses, non-aqueous reaction systems, and chemically demanding industrial environments, thereby improving process efficiency, reducing operational costs, and enhancing enzyme reusability.

Growing environmental concerns and the global transition toward sustainable industrial development have further accelerated research on bacterial lipases. These enzymes play a significant role in biodiesel synthesis through transesterification, biodegradation of lipid-rich wastes, wastewater treatment, pharmaceutical intermediate synthesis, food modification, and the production of value-added chemicals (Verma et al., 2020; Yao et al., 2021; Chapman et al., 2021; Sharma et al., 2022). Recent advances in microbial biotechnology, protein engineering, genome mining, metagenomics, synthetic biology, and enzyme immobilization have considerably expanded the discovery and optimization of bacterial lipases with enhanced catalytic performance. Simultaneously, computational approaches, including artificial intelligence (AI)-assisted protein design and machine learning-based enzyme prediction, are opening new opportunities for accelerating enzyme engineering and developing tailor-made biocatalysts for specific industrial applications (Lee et al., 2026; Sutaoney et al., 2026; Majumder et al., 2026).

The rapid expansion of scientific publications over the last decade reflects the increasing importance of stable bacterial lipases in both academic research and industrial biotechnology (Sharma et al., 2024; Dhaka et al., 2024; Wu et al., 2023; Chandra et al., 2024; Dudley et al., 2025). As research becomes increasingly multidisciplinary, encompassing microbiology, molecular biology, structural biology, biochemical engineering, environmental science, and computational biotechnology, understanding the evolution of this knowledge domain becomes essential. Bibliometric analysis provides a quantitative framework for evaluating scientific productivity, collaboration patterns, intellectual structure, and emerging research trends by integrating publication metadata with citation and network analyses (Saka et al., 2010; Dos Santos et al., 2023; Che Hussian and Leong, 2023; Zhang et al., 2024; Neto et al., 2023). Unlike conventional narrative reviews, bibliometric studies objectively identify influential authors, journals, institutions, countries, collaborative networks, research hotspots, and thematic evolution, thereby providing a comprehensive overview of the development of a scientific field.

Although several review articles have summarized the biochemical characteristics and industrial applications of microbial lipases, a comprehensive bibliometric assessment focusing specifically on stable bacterial lipases remains lacking. Previous reviews have primarily emphasized enzyme production, purification, structural characteristics, immobilization strategies, and industrial applications, while comparatively little attention has been devoted to evaluating the global research landscape, scientific collaboration, citation structure, knowledge networks, and emerging research themes. Consequently, researchers

and policymakers currently lack an integrated understanding of how this field has evolved, which research areas dominate the literature, and which scientific directions are likely to shape future developments.

To address this knowledge gap, the present study provides a comprehensive bibliometric analysis of global research on stable bacterial lipases published between 2010 and 2026. Bibliographic records were retrieved from the Lens.org database using a systematic search strategy and screened according to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) framework. Bibliometric performance indicators and science mapping analyses were performed using the Bibliometrix/Biblioshiny package in R and VOSviewer (version 1.6.20). The study evaluates publication growth, citation performance, leading journals, authors, institutions, and countries, while further examining collaboration networks, keyword co-occurrence, co-citation patterns, bibliographic coupling, and thematic evolution. By integrating performance analysis with knowledge mapping, this study provides a comprehensive overview of the intellectual development of stable bacterial lipase research, identifies emerging research priorities, and offers valuable insights for researchers, industrial stakeholders, and policymakers seeking to advance sustainable enzyme biotechnology and industrial biocatalysis (Sales et al., 2023; Verasoundarapandian et al., 2021; Yang et al., 2022; Plaza et al., 2025).

2. Materials and Methods

2.1 Study Design

This study employed a quantitative bibliometric approach to evaluate the global research landscape of stable bacterial lipases published between 2010 and 2026. Bibliometric techniques were used to examine publication growth, citation performance, research productivity, collaboration patterns, intellectual structure, and thematic evolution of the scientific literature. The study was conducted following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA 2020) guidelines to ensure a transparent and reproducible literature screening process (Rethlefsen et al., 2021; Bhaumik et al., 2017).

2.2 Data Source

The bibliographic dataset was retrieved exclusively from the Lens.org scholarly database, an integrated scientific information platform that indexes peer-reviewed literature from multiple publishers and provides comprehensive metadata, citation relationships, patent linkages, and

open-access information. Lens.org was selected because of its broad multidisciplinary coverage, rich bibliographic metadata, and compatibility with bibliometric software for large-scale scientific mapping (Kudryashov et al., 2025; Chigarev, 2022).

2.3 Search Strategy

A comprehensive literature search was conducted in Lens.org to identify publications related to stable bacterial lipases. The search strategy combined terms describing bacterial lipases with terms related to enzyme stability using Boolean operators (Yehui et al., 2024; Chen et al., 2025; Li et al., 2023; Al Zamzami et al., 2025).

The search query was:

(lipase OR lipases OR "microbial lipase")

AND

(bacterial OR bacteria)

AND

(

thermostable

OR thermostability

OR "thermal stability"

OR stable

OR "enzyme stability"

OR "solvent tolerance"

OR "alkaline stability"

OR "organic solvent tolerance"

OR "heat stability"

)

The search was performed on 16 July 2026, and all records published between 2010 and 2026 were considered for further screening.

2.4 Eligibility Criteria and Literature Screening

The retrieved publications were screened using a PRISMA-based workflow. Records were sequentially filtered according to predefined eligibility criteria. Initially, publications were restricted to the period 2010–2026, followed by selection of peer-reviewed journal articles. Subsequent refinement was performed using predefined author keywords associated with bacterial lipases, enzyme stability, biocatalysis, enzyme immobilization, biodegradation, biodiesel production, protein engineering, industrial biotechnology, and related topics. Subject categories relevant to biotechnology, microbiology, biochemistry, catalysis,

environmental engineering, environmental science, pharmaceutical science, ecology, and renewable energy were retained. MeSH-based exclusion criteria were further applied to remove publications primarily associated with humans, animals, gastrointestinal microbiome, pharmaceutical preparations, drug delivery systems, anti-infective agents, plastics, probiotics, antioxidants, and other topics unrelated to industrial bacterial lipases. Following the screening process, 499 journal articles were included for bibliometric analysis. The complete screening procedure is illustrated in **Figure 1**.

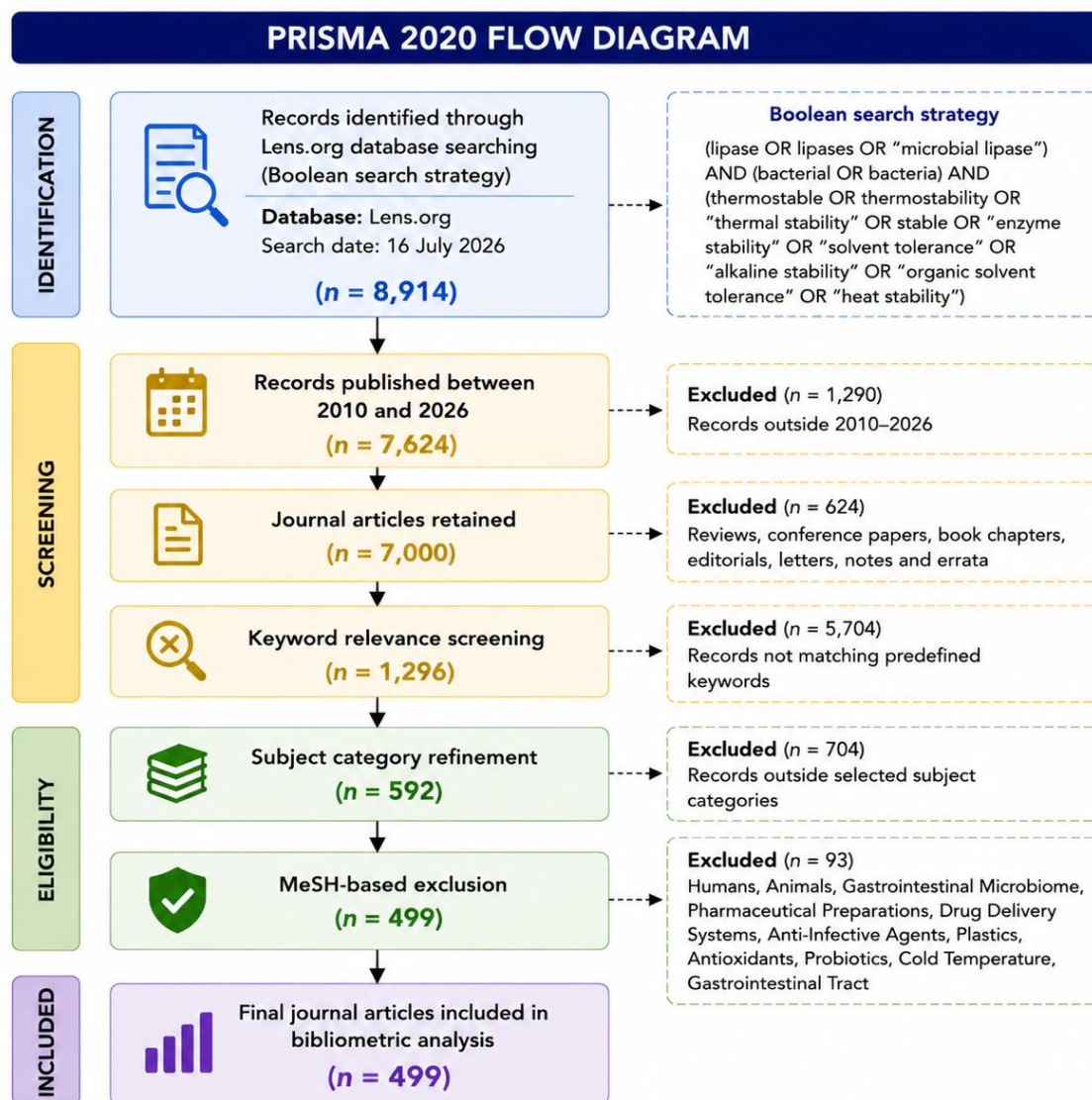


Figure 1. PRISMA 2020 flow diagram illustrating the literature identification, screening, eligibility assessment, and inclusion process for the bibliometric analysis of stable bacterial lipase research. Records were retrieved from the Lens.org database using a predefined Boolean search strategy and sequentially filtered by publication year (2010–2026), document type, keyword relevance, subject categories, and MeSH-based exclusion criteria, resulting in a final dataset of 499 journal articles.

2.5 Data Extraction

Bibliographic metadata were exported from Lens.org and included publication title, authors, publication year, journal, abstract, author keywords, affiliations, country, citation count,

references, digital object identifier (DOI), and other bibliographic information required for scientometric analyses (Xie et al., 2025; Klein et al., 2021; Wei et al., 2021; Zhang et al., 2025). The exported dataset was checked for consistency before analysis.

2.6 Bibliometric Analysis

Descriptive bibliometric indicators were calculated using the Bibliometrix package implemented through the Biblioshiny web interface in R. The analysis included annual scientific production, citation analysis, source productivity, author productivity, country-wise scientific output, collaboration patterns, keyword frequency, thematic evolution, Bradford's Law, Lotka's Law, and historiographic mapping (Yang et al., 2026; Zhao et al., 2025; Zeng et al., 2022; Zheng et al., 2023).

Network visualization analyses were performed using VOSviewer (version 1.6.20) to investigate the intellectual and conceptual structure of the research field. Co-authorship, keyword co-occurrence, co-citation, bibliographic coupling, and collaboration networks were generated using association-strength normalization and visualized as network, overlay, and density maps.(Saka et al., 2010; Dos Santos et al., 2023; Che Hussian and Leong, 2023; Zhang et al., 2024; Neto et al., 2023)

2.7 Bibliometric Indicators

The bibliometric performance of stable bacterial lipase research was evaluated using standard scientometric indicators, including annual publication output, annual publication growth rate, citation performance, average citations per document, average citations per year, source productivity, author productivity, country productivity, collaboration index, keyword occurrence, thematic evolution, and network centrality measures (Wang et al., 2025; Ettadili and Vural, 2025; Cheng et al., 2023; Shettar and Bagewadi, 2025; Abdelwahab et al., 2025). These indicators were used to characterize the scientific development, intellectual structure, and emerging research directions within the field.

2.8 Data Visualization

The bibliometric results were presented using tables, line graphs, bar charts, thematic maps, historiographs, three-field plots, and network visualizations generated from Biblioshiny and VOSviewer (Almeida et al., 2021; Roth et al., 2020; Kahar et al., 2022; Nizar et al., 2025; Klos-Witkowska and Martsenyuk, 2024). These visual representations facilitated the

interpretation of publication trends, collaborative relationships, citation patterns, and thematic structures across the study period.

3. Result and discussion

3.1 Descriptive Bibliometric Characteristics

The bibliometric analysis was conducted on a curated dataset of 499 peer-reviewed journal articles published between 2010 and 2026, retrieved exclusively from the Lens.org scholarly database following a PRISMA-based screening procedure (**Figure 1**). The initial Boolean search identified 8,914 records, which were systematically refined through sequential filtering based on publication year, document type, keyword relevance, subject categories, and MeSH-based exclusion criteria. This rigorous screening ensured that the final dataset represented publications specifically related to stable bacterial lipases and their industrial and biotechnological applications.

The final dataset was published across 139 scientific journals, reflecting the multidisciplinary nature of stable bacterial lipase research, which encompasses microbiology, biotechnology, biochemistry, environmental science, catalysis, pharmaceutical sciences, and biochemical engineering. A total of 2,322 authors contributed to these publications, corresponding to an average of 5.35 authors per document, indicating a strong collaborative research environment. Collectively, the publications cited 42,878 references, demonstrating a well-established knowledge base and the cumulative development of this research domain.

The bibliometric indicators further revealed an annual scientific growth rate of 3.74%, suggesting a sustained expansion of research activity over the study period. Moreover, the publications received an average of 57.23 citations per document, highlighting the considerable scientific influence and visibility of research on stable bacterial lipases. The combination of steady publication growth, extensive citation impact, and high levels of collaboration indicates that the field has matured into an internationally recognized area of enzyme biotechnology with increasing relevance to industrial applications.

These descriptive characteristics demonstrate that research on stable bacterial lipases has evolved into a dynamic and multidisciplinary field supported by extensive scientific collaboration and sustained scholarly interest. The broad distribution of publications across numerous journals and the substantial citation impact emphasizes the importance of stable bacterial lipases in addressing contemporary challenges related to industrial biocatalysis, environmental sustainability, enzyme engineering, and renewable bio-based technologies.

The comprehensive bibliometric profile presented here provides the foundation for subsequent analyses of publication trends, citation patterns, scientific productivity, collaboration networks, and thematic evolution.

Table 1. General bibliometric characteristics of stable bacterial lipase research (2010–2026).

Indicator	Value
Database	Lens.org
Study period	2010–2026
Final publications	499
Document type	Journal articles
Scientific sources (journals)	139
Authors	2,322
Average authors per document	5.35
Total cited references	42,878
Annual scientific growth rate	3.74%
Average citations per document	57.23
Software used	Bibliometrix/Biblioshiny, VOSviewer

3.2 Annual Publication Growth and Research Trends

The temporal distribution of scientific publications demonstrates a sustained expansion of research on stable bacterial lipases between 2010 and 2026 (**Figure 2**). A total of 499 journal articles were published during the study period, revealing a positive annual scientific growth rate of 3.74%. Although research activity remained relatively limited during the early years (2010–2014), publication output increased markedly from 2015 onwards, indicating growing scientific and industrial interest in stable bacterial lipases.

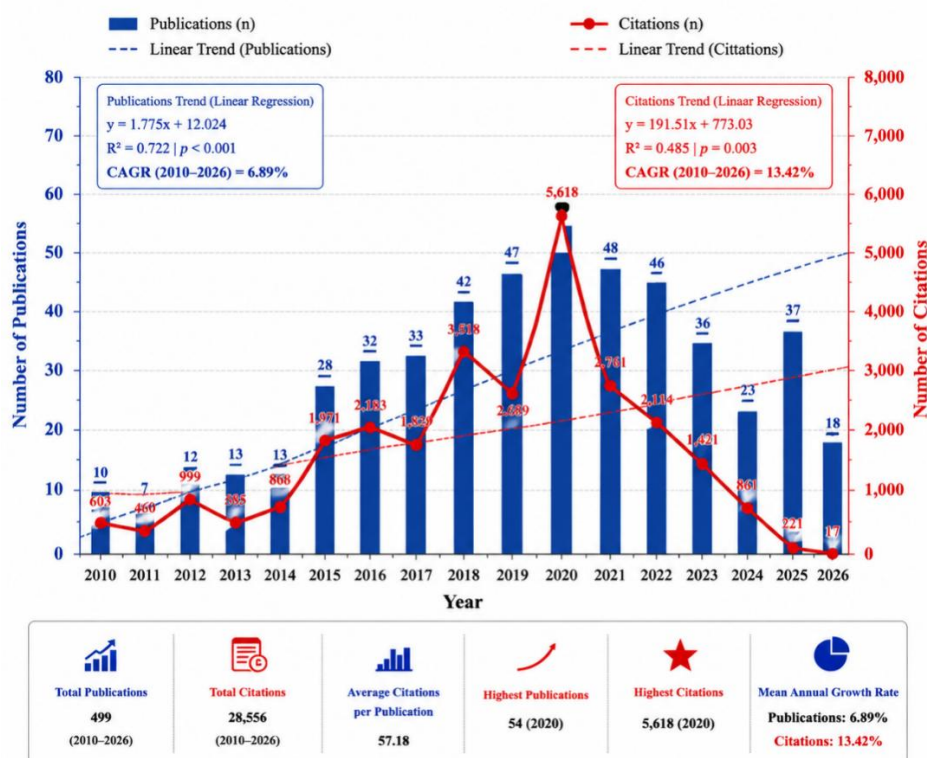
Annual publication output increased from 10 publications in 2010 to 54 publications in 2020, representing the highest research productivity during the study period. The years 2018–2022 constituted the most productive phase, with consistently high publication volumes, reflecting the maturation of the field and its transition from fundamental enzyme discovery toward industrial development and application. Although publication counts appear to decline after 2022, particularly during 2024–2026, this trend should be interpreted cautiously because the most recent years are affected by indexing delays and the incomplete nature of the 2026

publication year. Consequently, the apparent decrease is unlikely to represent a genuine reduction in research activity but rather the progressive indexing of newly published articles. The increasing publication output coincides with the growing recognition of stable bacterial lipases as versatile biocatalysts capable of functioning under extreme physicochemical conditions. Their superior thermal stability, solvent tolerance, and catalytic efficiency have expanded their application in biodiesel production, bioremediation, food processing, pharmaceutical manufacturing, detergent formulation, and other environmentally sustainable industrial processes. Simultaneously, advances in molecular biology, protein engineering, metagenomics, and enzyme immobilization have accelerated the discovery and optimization of bacterial lipases with enhanced catalytic performance, further stimulating research productivity.

Analysis of annual citation patterns (**Figure 2**) complements the publication trend by demonstrating the increasing scientific influence of the field. Earlier publications have accumulated substantially higher citation counts because they have had more time to shape subsequent research, whereas recently published articles have naturally received fewer citations due to shorter citation windows. Despite this temporal effect, the consistently increasing publication output combined with strong citation performance indicates that stable bacterial lipase research has evolved into a mature and internationally recognized area of enzyme biotechnology with sustained scientific relevance.

Comparable growth trajectories have been reported in bibliometric studies of industrial enzymes and microbial biotechnology, where increasing research activity has been linked to the global emphasis on sustainable manufacturing, circular bioeconomy strategies, renewable bioresources, and green catalytic technologies. The publication trend observed in the present study therefore reflects not only the scientific advancement of bacterial lipase research but also its expanding role in addressing industrial and environmental challenges through innovative biocatalytic solutions.

Annual Scientific Output and Citation Impact on Stable Bacterial Lipases (2010–2026) (Data Source: Lens.org; n = 499 articles)



Note: CAGR (Compound Annual Growth Rate) computed for the period 2010–2026.

Figure 2. Annual publication output (blue bars) and citation counts (red line) for stable bacterial lipase research from 2010 to 2026 based on the Lens.org database (n = 499). Dashed lines represent linear regression trends, with CAGR (%) indicating the overall growth in publications and citations during the study period.

3.3 Leading Journals and Source Productivity

The analysis of source productivity provides valuable insights into the dissemination patterns of scientific knowledge on stable bacterial lipases. The 499 publications included in this study were distributed across 139 peer-reviewed scientific journals, demonstrating the multidisciplinary nature of the research field and its broad relevance to microbiology, biotechnology, biochemistry, biochemical engineering, environmental science, catalysis, and industrial biotechnology.

The distribution of publications among journals was highly heterogeneous, with a limited number of core journals accounting for a substantial proportion of the total scientific output, while the remaining publications were dispersed across numerous specialized journals. This publication pattern is consistent with Bradford's Law, which states that scientific literature within a research domain tends to concentrate in a relatively small group of highly productive journals followed by progressively larger groups of less productive sources. The Bradford analysis (with fitted model $C(r) = 6.85 + 98.35 \cdot \log(r)$, $R^2 = 0.9942$, Bradford multiplier $k = 4.68$, KS test p-value = 0.995. Zone summary: Zone 1: 5; Zone 2: 25; Zone 3: 109; Total:

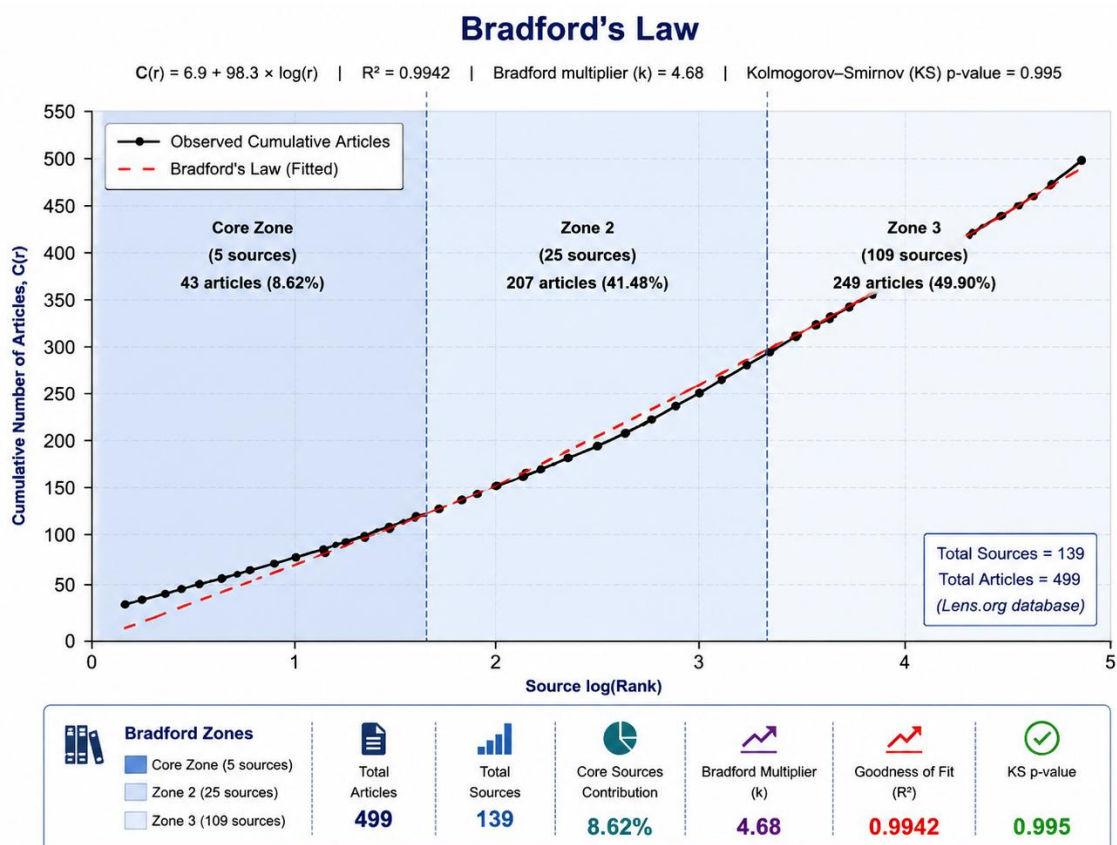
139) (**Figure 3**) clearly identified a core zone of journals that constitute the primary publication outlets for research on stable bacterial lipases.

The predominance of biotechnology- and microbiology-oriented journals among the most productive sources reflects the interdisciplinary character of bacterial lipase research. These journals provide platforms for studies on microbial diversity, enzyme discovery, protein engineering, enzyme immobilization, structural biology, metabolic engineering, and industrial biocatalysis. Their prominence also indicates that research on stable bacterial lipases has evolved beyond fundamental microbiological investigations toward applications in renewable energy, green chemistry, pharmaceutical biotechnology, environmental remediation, and sustainable industrial manufacturing.

Source impact analysis further demonstrated that the leading journals have played a pivotal role in shaping the intellectual development of the field by publishing highly cited and influential studies. These journals have consistently served as major channels for disseminating advances in enzyme characterization, thermostability enhancement, catalytic mechanism elucidation, molecular engineering, and industrial process optimization. Consequently, they continue to influence subsequent research directions and technological innovation in enzyme biotechnology.

The temporal evolution of journal productivity (**Figure 4**) further illustrates the sustained contribution of leading journals throughout the study period. Several journals have maintained continuous publication activity over multiple years, reflecting the increasing scientific maturity of stable bacterial lipase research and the growing demand for innovative enzymatic solutions across diverse industrial sectors.

Overall, the source analysis demonstrates that scientific communication in stable bacterial lipase research is concentrated within a relatively small number of influential journals while simultaneously expanding into a wide range of interdisciplinary publication venues. This pattern highlights the broad scientific interest in stable bacterial lipases and their increasing importance in addressing contemporary challenges in industrial biotechnology and sustainable bioprocess development.



*Bradford's Law describes the exponential scattering of articles across sources:
 a small core of highly productive sources accounts for a large proportion of the literature.*

Figure 3. Bradford's law distribution of journals publishing research on stable bacterial lipases (2010–2026). The distribution identifies 5 core journals, 25 journals in Zone 2, and 109 journals in Zone 3, illustrating the concentration of scientific publications among a limited number of highly productive sources. The solid black curve represents the observed cumulative distribution, while the red dashed line indicates the fitted Bradford model ($R^2 = 0.9942$; Bradford multiplier, $k = 4.68$; KS $p = 0.995$).

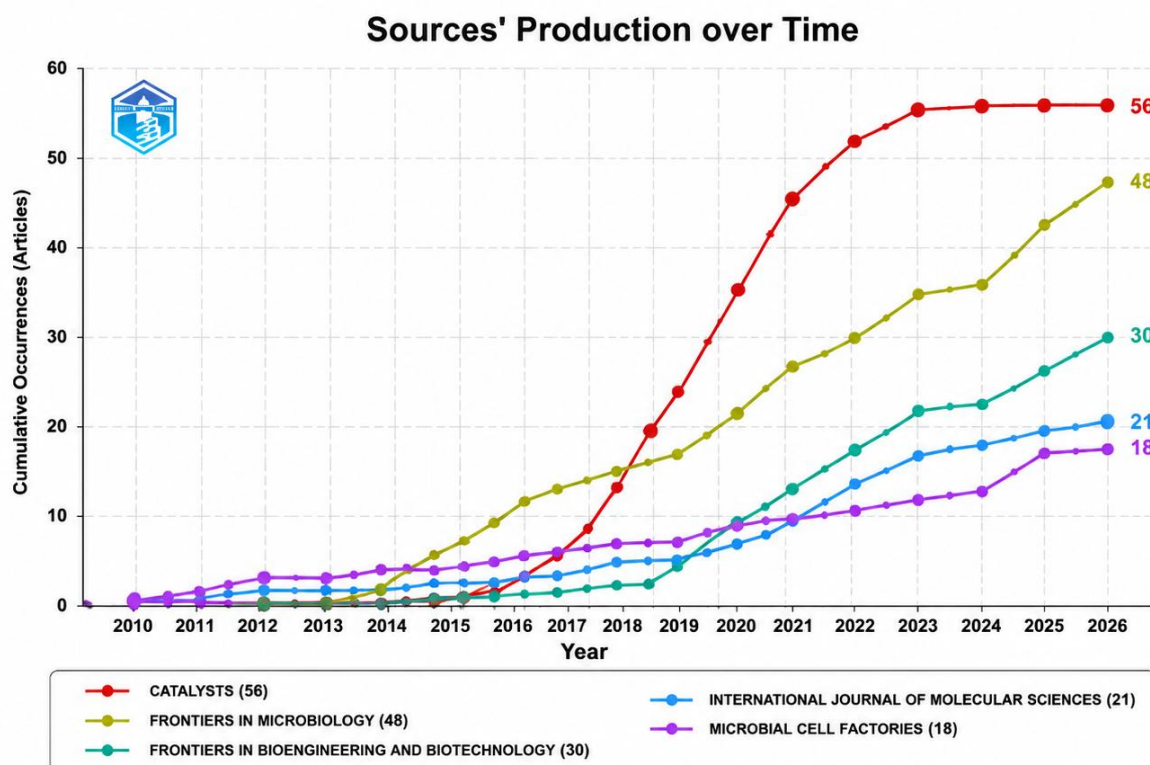


Figure 4. Source production over time illustrating the cumulative publication output of the leading journals in stable bacterial lipase research from 2010 to 2026. Each colored line represents an individual journal, while the values at the right indicate the total number of publications contributed by each source during the study period. The analysis demonstrates a sustained increase in publication activity across the major journals, with *Catalysts* (56 publications) emerging as the most productive source, followed by *Frontiers in Microbiology* (48), *Frontiers in Bioengineering and Biotechnology* (30), *International Journal of Molecular Sciences* (21), and *Microbial Cell Factories* (18). The pronounced acceleration in publication output after 2018 reflects the growing scientific interest in stable bacterial lipases and their applications in enzyme engineering, industrial biotechnology, biocatalysis, and sustainable bioprocesses. The figure highlights the progressive concentration of research within a limited number of high-impact journals, indicating their central role in disseminating advances in the field.

3.4 Author Productivity and Scientific Impact

Author productivity analysis provides valuable insight into the intellectual leadership and collaborative development of stable bacterial lipase research. The bibliometric dataset comprised 2,322 authors contributing to 499 journal articles, with an average of 5.35 authors per publication, indicating that research in this field is predominantly collaborative and multidisciplinary. The increasing complexity of enzyme discovery, molecular characterization, protein engineering, structural biology, and industrial process optimization has encouraged researchers from diverse scientific backgrounds to work collectively, thereby accelerating scientific innovation and technological advancement.

The distribution of scientific productivity among authors exhibited a characteristic bibliometric pattern in which a relatively small number of researchers contributed multiple publications, whereas the majority of authors published only one or a few articles. This distribution closely follows Lotka's Law (using linear regression in log-log space: $\log_{10}(f) =$

$\log_{10}(C) - \beta \cdot \log_{10}(n)$ with result Estimated Beta = 3.5257, Constant C = 0.7393, R-squared = 0.965, KS p-value (theoretical Beta=2) = 0.0149, KS p-value (fitted Beta) = 0.988), demonstrating that scientific productivity is concentrated among a limited group of highly productive investigators while occasional contributors constitute the largest proportion of the research community (**Figure 5**). Such a pattern is commonly observed in mature scientific disciplines and reflects the establishment of specialized research groups with sustained expertise in enzyme biotechnology.

The analysis of the most productive authors identified a core group of researchers who have made substantial contributions to the development of stable bacterial lipase research through continuous publication activity. These authors have played pivotal roles in advancing the understanding of enzyme isolation, molecular characterization, protein engineering, immobilization technologies, thermostability enhancement, catalytic mechanisms, and industrial applications. Their sustained research output has significantly influenced the evolution of the field and has provided the scientific foundation for subsequent investigations.

Scientific impact was further evaluated through local citation analysis, which identifies authors whose publications have exerted the greatest influence within the retrieved dataset. Highly cited authors generally represent pioneers or leading contributors whose studies have established methodological approaches, identified novel bacterial lipases, or introduced innovative enzyme engineering strategies that continue to guide current research. The coexistence of high publication productivity and strong citation performance indicates that these authors have contributed not only a substantial quantity of publications but also research of enduring scientific significance.

Temporal analysis of author productivity (**Figure 6**) reveals the continuous participation of established researchers alongside the emergence of new contributors during recent years. This pattern reflects the dynamic expansion of the research community and demonstrates that stable bacterial lipase research continues to attract investigators from diverse disciplines, including microbiology, biotechnology, biochemical engineering, environmental science, synthetic biology, and protein engineering. The growing diversity of contributors is consistent with the expanding industrial relevance of bacterial lipases in sustainable manufacturing, renewable energy production, waste valorization, pharmaceutical biotechnology, and green biocatalysis.

Overall, the author productivity analysis demonstrates that the scientific development of stable bacterial lipase research has been driven by a relatively small group of influential

researchers supported by extensive collaborative networks. The combination of sustained publication activity, high scientific impact, and increasing participation of emerging researchers suggests that the field has achieved considerable maturity while continuing to evolve through interdisciplinary collaboration and technological innovation.

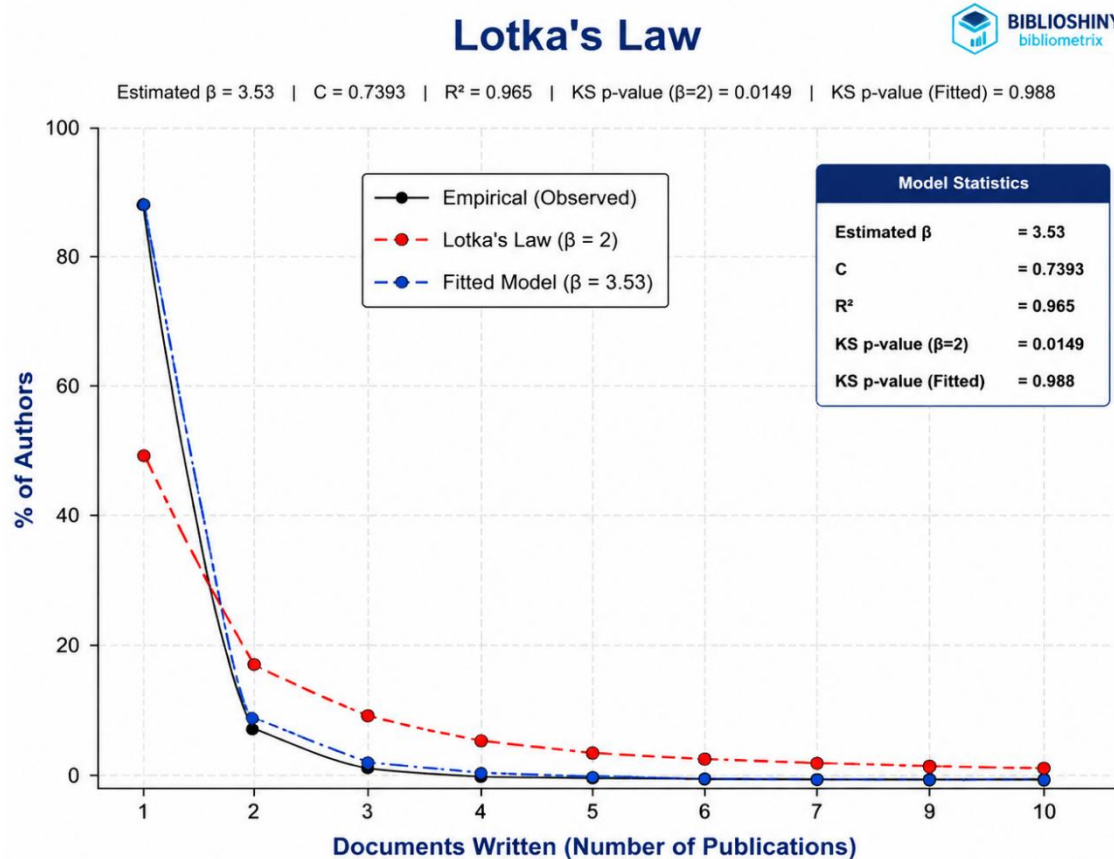


Figure 5. Lotka's Law showing the distribution of author productivity in stable bacterial lipase research (2010–2026).
 The plot displays three curves: Solid black line: the empirical distribution observed in the data;
 Dashed red line: the theoretical Lotka's Law with $\beta = 2$ and Dot-dash blue line: the fitted model using the estimated β .

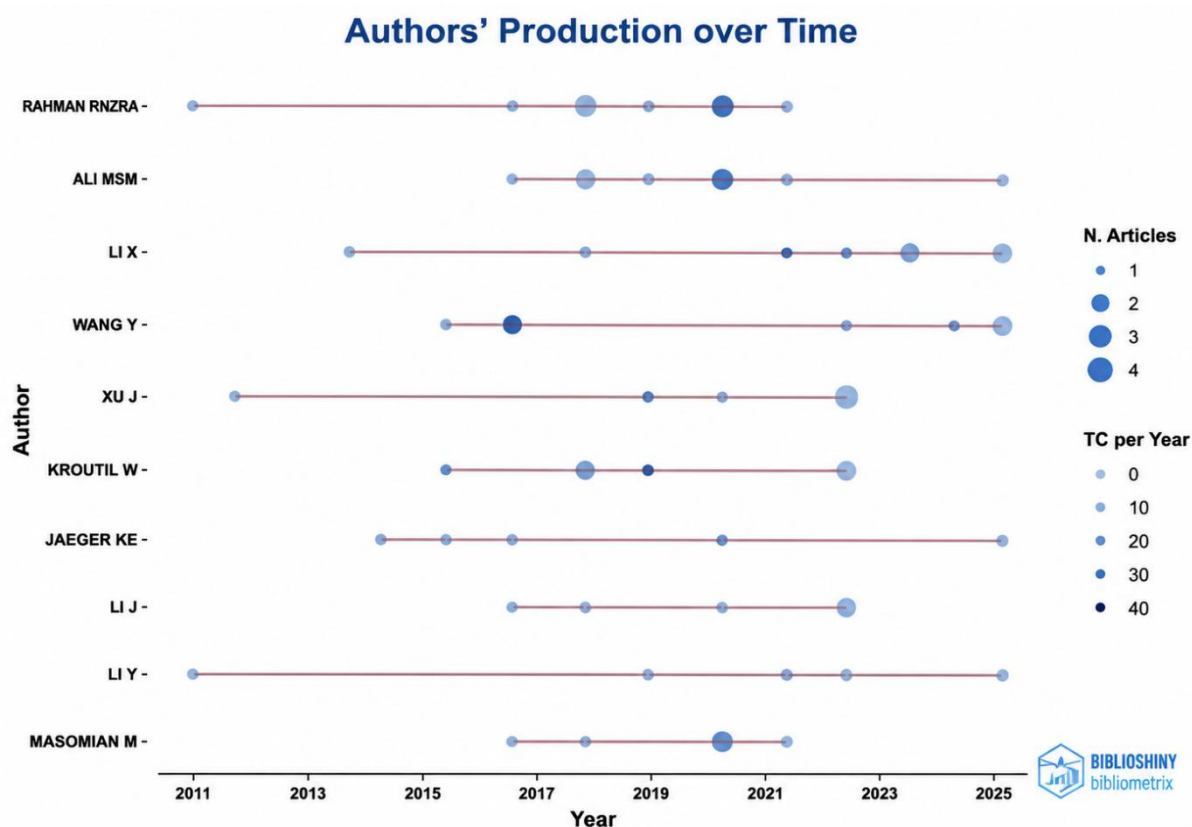


Figure 6. Authors' production over time for the ten most productive researchers in stable bacterial lipase research (2010–2026). Horizontal lines indicate each author's publication period, bubble size represents the number of publications (N. Articles), and bubble colour intensity corresponds to the total citations received per year (TC per Year), illustrating individual publication trajectories and scientific impact over time.

3.5 Institutional Productivity and Research Contributions

Institutional productivity analysis provides valuable insight into the organizational structure of global research on stable bacterial lipases and identifies the major research centers driving scientific innovation in this field. The bibliometric dataset demonstrates that research on stable bacterial lipases is distributed across a wide range of universities, research institutes, and industrial organizations, reflecting the multidisciplinary and application-oriented nature of enzyme biotechnology (Figure 7). These institutions have played pivotal roles in advancing fundamental research on bacterial lipases while simultaneously promoting their translation into industrial biotechnology, environmental remediation, renewable energy production, and pharmaceutical applications.

The most productive institutions exhibited sustained publication activity throughout the study period, indicating the establishment of specialized research groups dedicated to microbial enzyme discovery, molecular characterization, protein engineering, enzyme immobilization, and industrial biocatalysis. Continuous contributions from these institutions have significantly enhanced the understanding of enzyme structure–function relationships,

thermostability mechanisms, catalytic efficiency, and process optimization under industrial conditions. Their long-term research efforts have also facilitated the development of robust bacterial lipases with improved operational stability for applications in biodiesel synthesis, wastewater treatment, food processing, detergent formulations, and other environmentally sustainable technologies.

Institutional productivity further reflects the concentration of scientific expertise within established research laboratories possessing advanced facilities for microbiology, molecular biology, structural biology, biochemical engineering, and computational enzyme design. The presence of internationally recognized institutions among the leading contributors suggests that stable bacterial lipase research is increasingly supported by interdisciplinary collaborations integrating experimental biology, bioinformatics, protein engineering, and industrial process development. Such collaborative environments have accelerated the discovery of novel bacterial lipases and the optimization of their physicochemical properties for commercial applications.

The geographical distribution of leading institutions also highlights the global expansion of enzyme biotechnology research. Universities and research organizations from Asia, Europe, and other scientifically active regions have contributed substantially to the growth of the field, reflecting increasing investments in sustainable biotechnology and bio-based industrial processes. The concentration of productive institutions within countries possessing strong biotechnology infrastructure further demonstrates the importance of institutional capacity, research funding, and international collaboration in driving scientific productivity and technological innovation.

Overall, the institutional productivity analysis indicates that scientific progress in stable bacterial lipase research has been largely driven by a relatively small number of highly productive research organizations supported by extensive national and international collaborations. These institutions continue to shape the intellectual development of the field through sustained scientific output, technological innovation, and interdisciplinary research, thereby contributing to the growing industrial relevance of stable bacterial lipases.

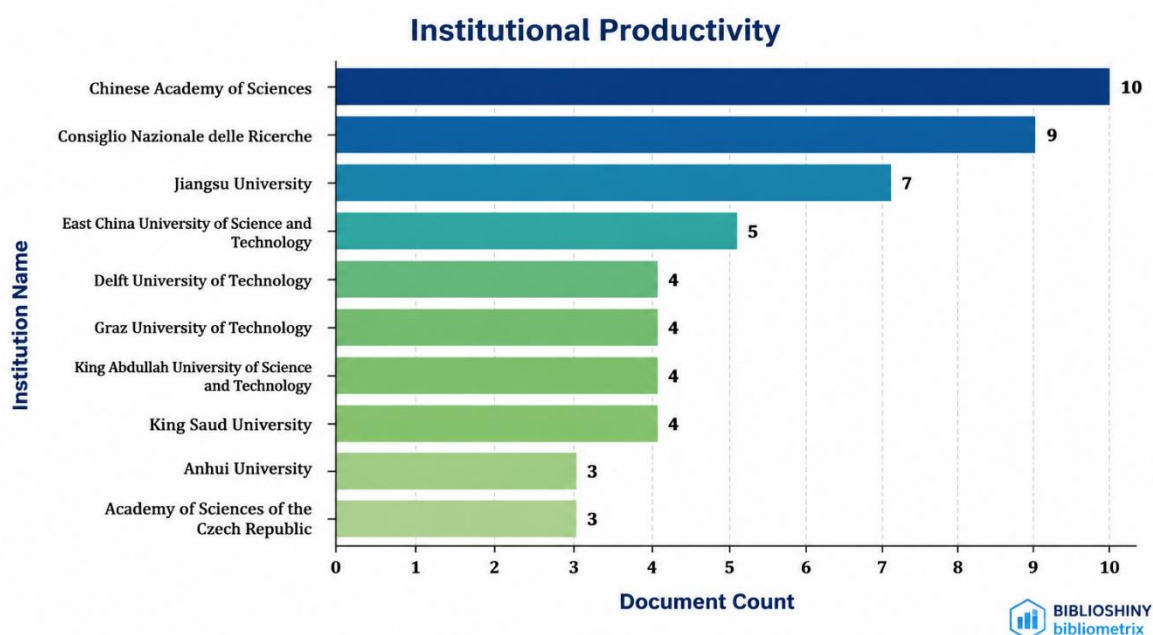


Figure 7. Institutional productivity showing the leading research organizations contributing to stable bacterial lipase research between 2010 and 2026.

3.6 Country-wise Scientific Contributions

The geographical distribution of scientific publications provides important insights into the global development of stable bacterial lipase research and identifies the countries that have made the greatest contributions to this field. Analysis of country productivity revealed that research on stable bacterial lipases is conducted across a broad international landscape, reflecting the growing recognition of bacterial lipases as versatile biocatalysts for industrial biotechnology, environmental sustainability, and renewable bio-based industries. The widespread participation of countries from Asia, Europe, North America, and South America demonstrates the global importance of enzyme biotechnology in addressing contemporary scientific and industrial challenges.

The leading countries exhibited sustained scientific productivity throughout the study period and collectively accounted for a substantial proportion of the total publications included in the bibliometric dataset. These countries have established strong research infrastructures in microbiology, molecular biotechnology, biochemical engineering, and protein engineering, enabling continuous advances in bacterial lipase discovery, enzyme characterization, molecular modification, and industrial process development. Their scientific contributions have significantly expanded the knowledge base of stable bacterial lipases and facilitated the translation of laboratory discoveries into practical industrial applications.

Temporal analysis of country productivity (**Figure 8**) demonstrates that several countries have maintained continuous research activity over the study period, while emerging economies have shown a marked increase in publication output during the last decade. This pattern reflects increasing global investment in sustainable biotechnology, renewable energy, circular bioeconomy strategies, and environmentally friendly manufacturing technologies. The expansion of scientific output from developing countries also indicates improved research capacity, increased international collaboration, and greater access to advanced molecular and computational technologies for enzyme engineering.

The observed geographical distribution further highlights the importance of international scientific collaboration in accelerating research progress. Collaborative partnerships among countries have enabled the sharing of expertise, advanced analytical facilities, microbial resources, and interdisciplinary knowledge, thereby promoting innovation in enzyme biotechnology. Such collaborations have contributed to the development of bacterial lipases with enhanced thermostability, catalytic efficiency, solvent tolerance, and industrial applicability, supporting diverse sectors including biodiesel production, wastewater treatment, food biotechnology, pharmaceuticals, and green chemistry.

Overall, the country-wise analysis demonstrates that stable bacterial lipase research has evolved into a globally collaborative scientific discipline. The concentration of publications in scientifically advanced countries, together with the increasing participation of emerging research nations, reflects the expanding international interest in sustainable enzyme technologies and the growing importance of bacterial lipases as environmentally friendly biocatalysts for future industrial applications.

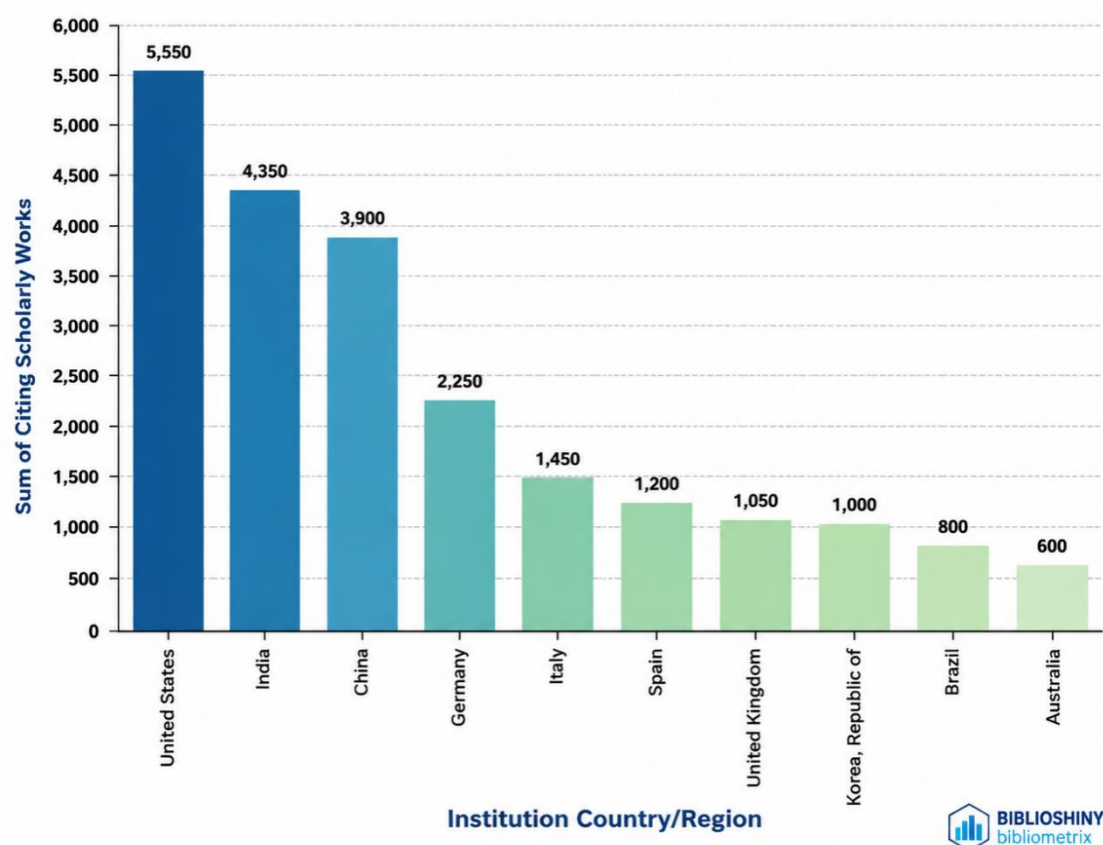


Figure 8. Geographical distribution of research impact measured by the total number of citing scholarly works (2010–2026).

Note: The figure shows the top 10 countries/regions ranked by the total citations received for publications in stable bacterial lipase research.

3.7 Co-authorship Analysis

Co-authorship analysis was conducted to evaluate the collaborative structure of global research on stable bacterial lipases and to identify the extent of scientific cooperation among researchers. Scientific collaboration is an important indicator of knowledge exchange, interdisciplinary integration, and research maturity, particularly in biotechnology, where advances often require expertise from microbiology, molecular biology, protein engineering, biochemical engineering, and environmental sciences. The co-authorship network was constructed using VOSviewer (version 1.6.20) based on the bibliographic records retrieved from the Lens.org database.

The bibliometric dataset comprised 2,305 authors, of which 139 authors met the minimum threshold of two publications and two citations for inclusion in the network analysis. The resulting collaboration network consisted of three clusters, containing nine authors in the largest connected component, with 14 collaborative links and a total link strength (TLS) of 15 (**Figure 9**). The different clusters represent distinct research communities formed through

repeated collaborations among authors working on complementary aspects of stable bacterial lipases, including enzyme isolation, molecular characterization, protein engineering, immobilization techniques, and industrial applications.

The collaboration network indicates that research in this field is driven by several specialized research groups rather than a single highly interconnected international network. Most collaborative relationships were concentrated within institutional or regional research teams, suggesting that investigators preferentially collaborate with established partners sharing similar research interests and experimental expertise. Although the presence of multiple clusters demonstrates active scientific cooperation, the relatively small largest connected component and modest total link strength indicate that global collaboration among research groups remains limited. This fragmented collaboration pattern is characteristic of emerging and highly specialized research domains, where expertise is distributed among independent laboratories focusing on different scientific and technological aspects of enzyme biotechnology.

The increasing industrial demand for thermostable bacterial lipases in biodiesel production, environmental bioremediation, pharmaceutical manufacturing, food biotechnology, detergent formulations, and green chemistry is expected to promote broader international collaboration in the coming years. Expanding collaborative networks between microbiologists, structural biologists, computational scientists, biochemical engineers, and industrial researchers could accelerate the discovery of novel bacterial lipases, facilitate protein engineering strategies, and improve the translation of laboratory findings into commercial biocatalytic processes. Strengthening interdisciplinary and multinational collaborations will therefore be essential for advancing stable bacterial lipase research and addressing future challenges in sustainable industrial biotechnology.

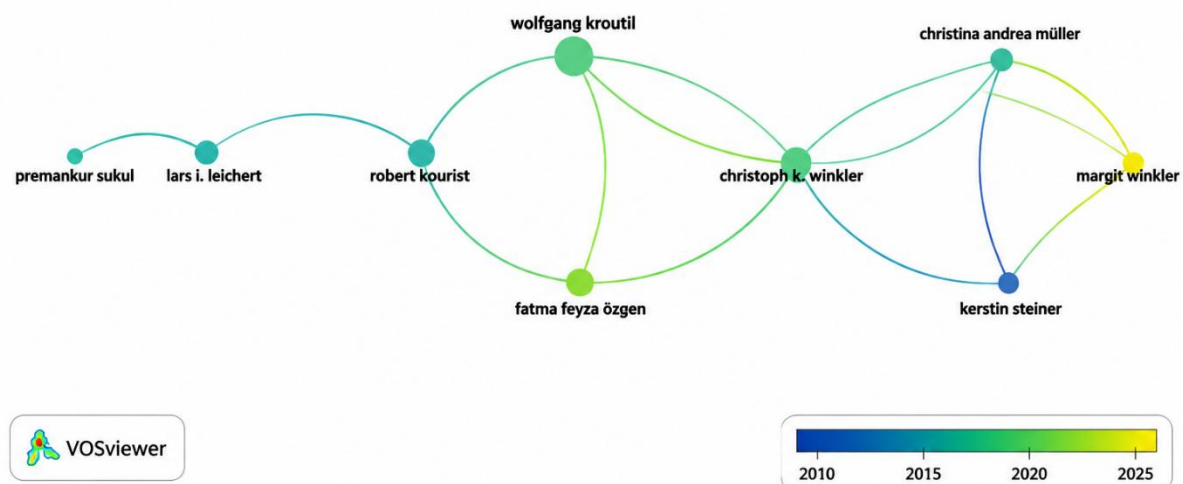


Figure 9. Author co-authorship network of stable bacterial lipase research generated using VOSviewer. Node size represents author productivity, link thickness indicates collaboration strength, and colors denote collaborative clusters. The color gradient reflects the average publication year of the author's documents (2010–2025).

3.8 Keyword Co-occurrence and Research Hotspots

Keyword co-occurrence analysis was performed to identify the conceptual structure, major research themes, and emerging hotspots in stable bacterial lipase research. Author keywords reflect the primary scientific focus of individual studies and provide valuable insights into the evolution of research priorities within a given discipline. The co-occurrence network was generated using VOSviewer (version 1.6.20) based on author-supplied keywords extracted from the bibliographic dataset.

A total of 2,827 author keywords were identified across the 499 publications included in the study. Applying a minimum occurrence threshold of five, 65 keywords qualified for network construction. The resulting network comprised seven distinct clusters, interconnected through 389 links with a total link strength (TLS) of 638 (**Figure 10**). The high degree of connectivity among keywords indicates that research on stable bacterial lipases is conceptually well integrated, with strong relationships among studies focusing on enzyme discovery, molecular engineering, industrial applications, and sustainable biotechnology.

The identified keyword clusters represent the principal research domains that have shaped the field during the study period. One cluster is centered on lipase, bacteria, enzyme, and microbiology, highlighting the continued emphasis on the isolation, screening, and characterization of bacterial lipases. Another major cluster is associated with biocatalysis,

protein engineering, enzyme immobilization, and catalysis, reflecting efforts to enhance enzyme stability, catalytic efficiency, and industrial applicability through molecular and biochemical engineering approaches. Additional clusters emphasize biodiesel production, transesterification, biofuel, and renewable energy, demonstrating the increasing application of stable bacterial lipases in sustainable energy production. Keywords related to biodegradation, waste management, wastewater treatment, and environmental biotechnology further indicate the growing importance of bacterial lipases in environmental remediation and circular bioeconomy initiatives.

Overlay visualization and temporal keyword analysis revealed a progressive shift in research priorities over the study period. Earlier investigations predominantly focused on enzyme isolation, biochemical characterization, and optimization of catalytic conditions, whereas more recent studies increasingly emphasize protein engineering, enzyme immobilization, extremophilic microorganisms, industrial biocatalysis, organic solvent tolerance, and sustainable bioprocesses. This transition reflects the evolution of stable bacterial lipase research from fundamental microbiological investigations toward advanced biotechnological applications addressing industrial efficiency and environmental sustainability.

The dense interconnections observed among keyword clusters indicate that modern research on stable bacterial lipases is inherently multidisciplinary, integrating microbiology, molecular biology, biochemistry, protein engineering, chemical engineering, and environmental sciences. The emergence of keywords associated with sustainable biotechnology, renewable bioresources, and industrial enzyme engineering further demonstrates that future research is increasingly directed toward developing robust biocatalysts capable of operating under harsh industrial conditions while supporting environmentally friendly manufacturing processes. Collectively, the keyword co-occurrence analysis highlights the expanding scientific scope of stable bacterial lipase research and identifies the principal thematic areas that are expected to drive future innovation in enzyme biotechnology.

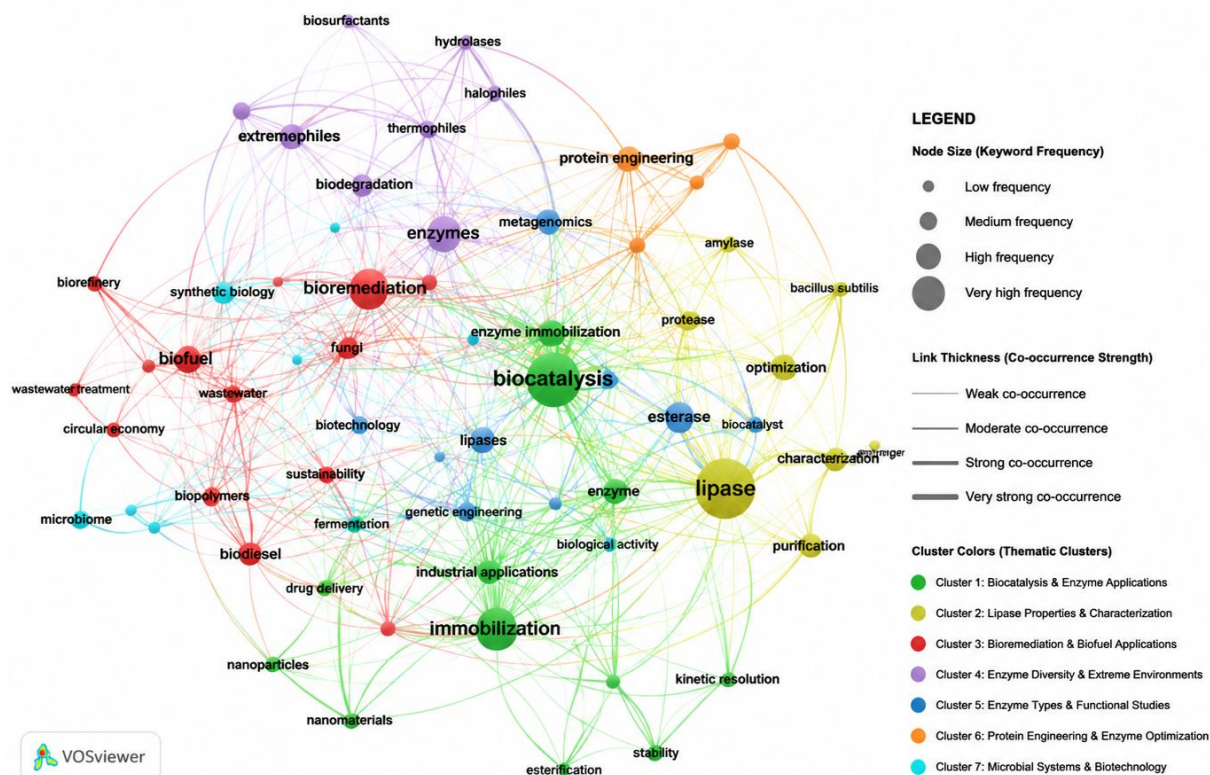


Figure 10. Keyword co-occurrence network generated using VOSviewer illustrating the thematic structure of stable bacterial lipase research published between 2010 and 2026. Node size represents keyword occurrence frequency, link thickness indicates the strength of co-occurrence between keywords, and colors denote distinct thematic clusters. Major research themes include lipase characterization, biocatalysis, enzyme immobilization, protein engineering, bioremediation, biofuel production, extremophiles, and industrial biotechnology, highlighting the interdisciplinary evolution of the field.

3.9 Co-citation Analysis

Co-citation analysis was performed to investigate the intellectual structure and foundational knowledge base of stable bacterial lipase research. Co-citation occurs when two publications are cited together by subsequent studies, indicating their conceptual or methodological relationship. Consequently, co-citation networks provide valuable insights into the influential publications, authors, and research themes that have shaped the evolution of a scientific discipline. The analysis was conducted using VOSviewer (version 1.6.20) to visualize the relationships among frequently co-cited references within the bibliometric dataset.

The co-citation network revealed a well-defined intellectual structure composed of several interconnected clusters, each representing a distinct area of scientific specialization (**Figure 11**). These clusters were formed through repeated citation of seminal publications focusing on bacterial lipase discovery, enzyme purification, biochemical characterization, molecular cloning, protein engineering, enzyme immobilization, and industrial applications. The close relationships among the clusters demonstrate that stable bacterial lipase research has evolved

through the integration of multiple scientific disciplines, including microbiology, molecular biology, biochemistry, structural biology, biochemical engineering, and environmental biotechnology.

The largest co-citation clusters were dominated by highly influential studies that established the fundamental principles of bacterial lipase research. These landmark publications have served as essential references for subsequent investigations by providing methodologies for enzyme screening, purification, structural characterization, catalytic mechanism analysis, and stability enhancement. Their persistent co-citation over time indicates their continued relevance in supporting current research on enzyme engineering and industrial biocatalysis. The network also illustrates how classical studies remain closely linked with more recent publications, reflecting the cumulative development of scientific knowledge in this field.

The distribution of co-citation clusters further demonstrates the gradual transition of research priorities from fundamental enzyme characterization toward application-oriented investigations. Early influential studies primarily focused on the isolation and biochemical characterization of bacterial lipases, whereas more recent highly co-cited publications emphasize protein engineering, immobilization technologies, computational enzyme design, solvent tolerance, thermostability enhancement, and sustainable industrial applications. This shift reflects the growing demand for robust biocatalysts capable of operating efficiently under harsh industrial conditions.

The interconnected nature of the co-citation network indicates that stable bacterial lipase research has developed a strong intellectual foundation supported by a relatively cohesive body of scientific literature. Rather than evolving through isolated research themes, the field has progressed by continuously integrating advances in microbial biotechnology, enzyme engineering, structural biology, and industrial biotechnology. Such integration has facilitated the development of innovative strategies for improving enzyme performance and expanding industrial applications.

Overall, the co-citation analysis demonstrates that the scientific advancement of stable bacterial lipase research has been guided by a core group of highly influential publications that continue to shape contemporary research directions. The persistence of these foundational studies within the co-citation network highlights their importance in establishing the theoretical and methodological framework upon which current investigations and future technological developments are built.

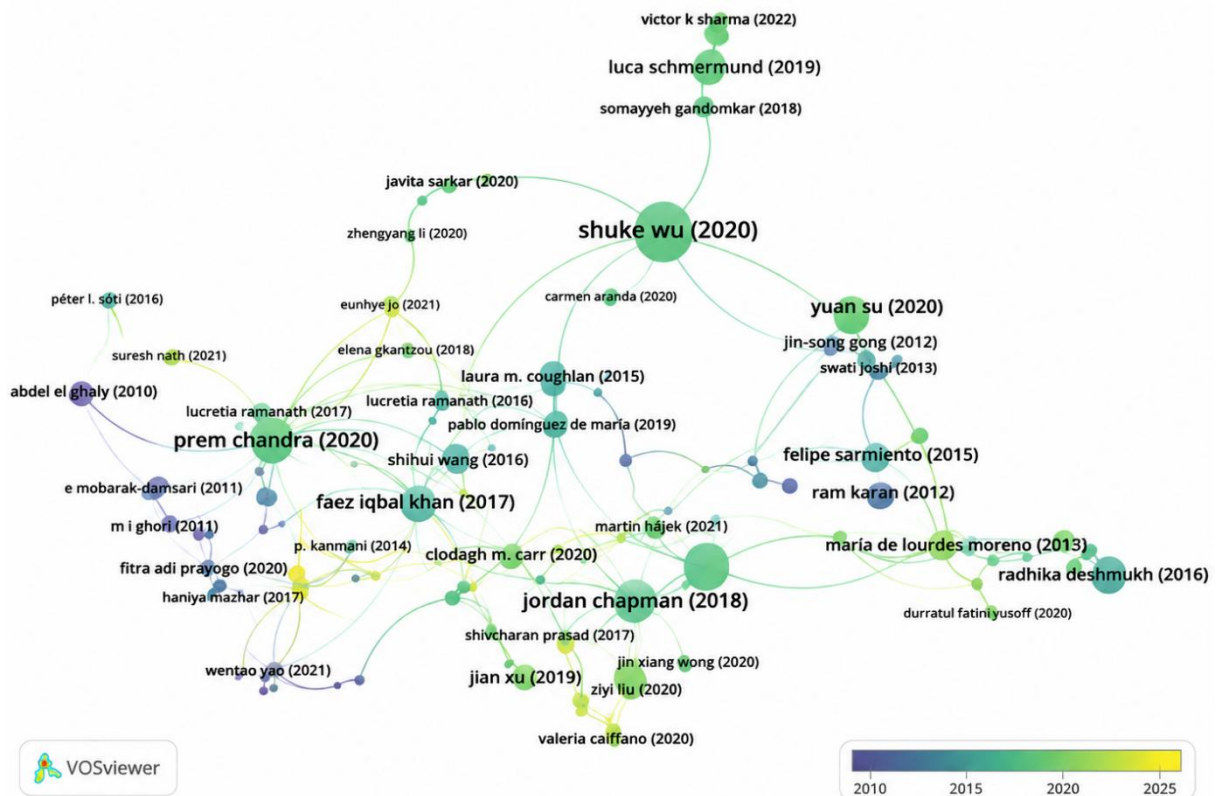


Figure 11. Co-citation network of publications related to stable bacterial lipases generated using VOSviewer. Nodes represent cited references, node size corresponds to citation frequency, link thickness indicates co-citation strength, and colors represent distinct intellectual clusters.

3.10 Bibliographic Coupling

Bibliographic coupling analysis was performed to investigate the contemporary intellectual relationships among publications in stable bacterial lipase research. Unlike co-citation analysis, which reflects the historical knowledge base of a research field, bibliographic coupling identifies documents that share common references and therefore represent current research directions and thematic convergence. The analysis was conducted using VOSviewer (version 1.6.20) to visualize the similarity among publications based on their shared bibliographic references.

The bibliographic coupling network demonstrated a highly interconnected research structure, indicating strong thematic relationships among contemporary publications. Of the 499 journal articles included in the dataset, 390 documents satisfied the threshold for network construction. The resulting network comprised 10 thematic clusters, interconnected through 8,606 links with a total link strength (TLS) of 16,666 (**Figure 12**). The large number of links and high total link strength indicate substantial overlap in the literature cited by individual studies, reflecting a well-established and cohesive scientific domain.

The identified clusters represent major contemporary research directions within stable bacterial lipase research. Publications grouped within the same cluster frequently shared references related to enzyme screening, bacterial diversity, molecular characterization, protein engineering, immobilization technologies, catalytic mechanisms, structural biology, and industrial bioprocess optimization. Additional clusters emphasized applications of bacterial lipases in biodiesel production, environmental bioremediation, waste valorization, pharmaceutical biotechnology, and green chemistry, illustrating the broad industrial relevance of these enzymes. The close interconnection among clusters suggests that these research themes are complementary rather than isolated, collectively contributing to the advancement of enzyme biotechnology.

The high degree of bibliographic coupling further indicates that recent investigations increasingly build upon a common body of scientific literature. This convergence reflects the growing maturity of the field, where advances in genomics, metagenomics, computational biology, protein engineering, and biochemical engineering are integrated to improve enzyme stability, catalytic performance, and industrial applicability. The extensive sharing of references among publications also demonstrates that contemporary research is becoming progressively interdisciplinary, combining experimental and computational approaches to address challenges associated with enzyme discovery, optimization, and commercialization.

Overall, the bibliographic coupling analysis highlights a cohesive and rapidly evolving research landscape in which investigators draw upon a shared scientific foundation while exploring diverse industrial applications of stable bacterial lipases. The strong coupling relationships observed among publications indicate that future research is likely to continue integrating molecular engineering, sustainable bioprocess development, and advanced biotechnological approaches to produce highly efficient bacterial lipases capable of meeting the increasing demands of modern industrial biotechnology.

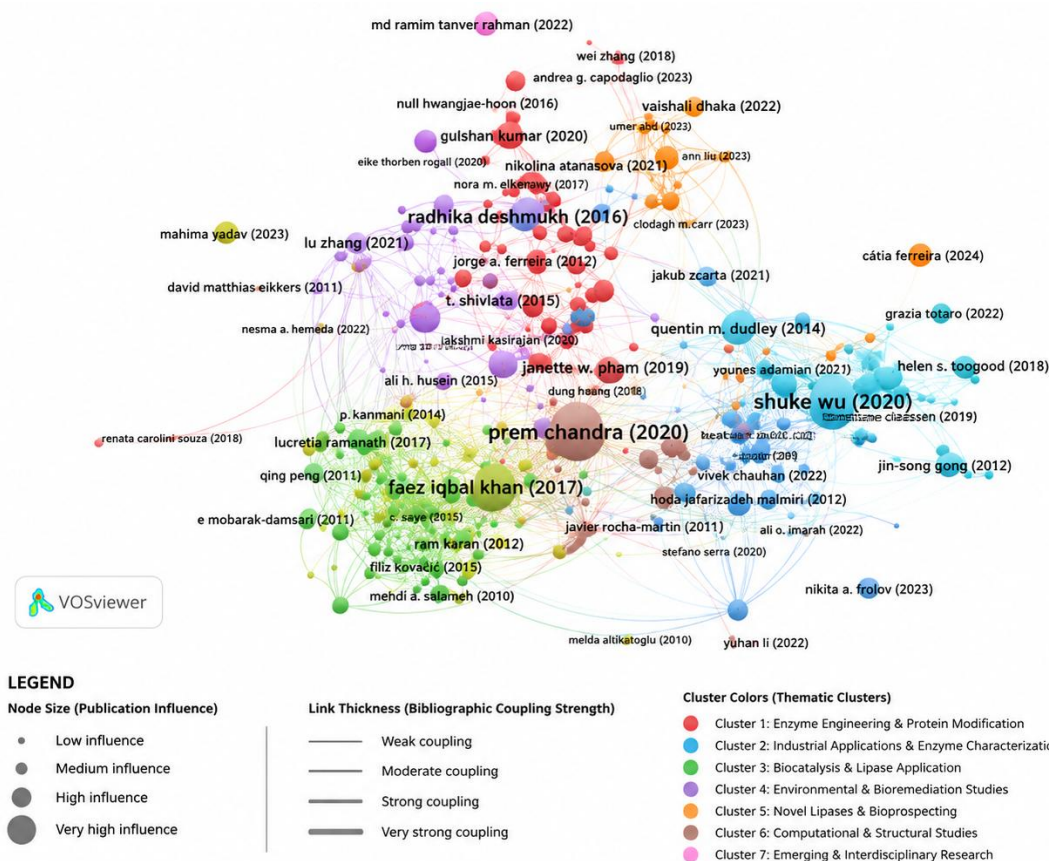


Figure 12. Bibliographic coupling network of publications on stable bacterial lipases generated using VOSviewer. Nodes represent individual publications, node size corresponds to publication influence within the network, link thickness indicates the strength of bibliographic coupling, and colors represent thematic clusters.

3.11 Thematic Evolution

Thematic evolution analysis was performed to examine the conceptual development of stable bacterial lipase research and to identify shifts in research priorities throughout the study period. Unlike performance indicators, thematic analysis reveals how scientific themes emerge, mature, and diversify, thereby providing insights into the intellectual progression of a research field. The analysis was conducted using the Bibliometrix package (Biblioshiny) through thematic mapping, trend topic analysis, co-word networks, and factorial analysis to characterize the evolution of the conceptual structure of stable bacterial lipase research.

The thematic map identified several interconnected research domains representing different stages of scientific development (**Figure 13**). Core themes were primarily associated with bacterial lipases, enzyme stability, biocatalysis, and microbial biotechnology, indicating that these topics constitute the conceptual foundation of the research field. Their high centrality reflects strong connections with other research areas, while their density suggests that these themes have undergone substantial scientific development over the past decade.

As the field matured, research progressively expanded from fundamental studies of enzyme isolation, purification, and biochemical characterization toward advanced investigations involving protein engineering, enzyme immobilization, structural biology, and industrial bioprocess optimization. These themes have become increasingly interconnected as researchers seek to improve catalytic efficiency, thermal stability, solvent tolerance, and operational robustness for industrial applications. The integration of molecular biology, computational approaches, and biochemical engineering has further accelerated the development of engineered bacterial lipases with enhanced functional properties.

Trend topic analysis revealed a noticeable transition in research emphasis over time. Earlier studies were dominated by investigations of lipase production, microbial screening, and enzyme characterization, whereas more recent publications increasingly focus on extremophilic microorganisms, protein engineering, enzyme immobilization, organic solvent tolerance, biocatalysis, biodiesel production, and sustainable biotechnology. This transition reflects the growing industrial demand for highly stable enzymes capable of operating under harsh processing conditions while supporting environmentally sustainable manufacturing technologies.

The factorial analysis and co-word network further demonstrated that the conceptual structure of the field has become progressively more integrated. Research themes that were previously investigated independently are now closely associated through multidisciplinary studies combining microbiology, molecular genetics, structural biology, biochemical engineering, computational enzyme design, and environmental biotechnology. This convergence indicates that stable bacterial lipase research is evolving toward comprehensive biotechnological solutions rather than isolated investigations of enzyme properties.

The observed thematic evolution also reflects broader global scientific priorities emphasizing renewable bioresources, circular bioeconomy strategies, waste valorization, and green industrial processes. Emerging themes associated with artificial intelligence-assisted enzyme engineering, genome mining, metagenomics, synthetic biology, and machine learning-guided protein design are expected to play increasingly important roles in future research. These approaches have the potential to accelerate the discovery of novel bacterial lipases, improve predictive enzyme engineering, and facilitate the development of next-generation biocatalysts tailored for specific industrial applications.

Overall, the thematic evolution analysis demonstrates that stable bacterial lipase research has progressed from a predominantly descriptive discipline toward an advanced, multidisciplinary field focused on engineering robust biocatalysts for sustainable industrial

biotechnology. The integration of emerging computational technologies with experimental enzyme engineering is likely to define the next phase of scientific development, creating new opportunities for innovation in pharmaceutical manufacturing, environmental remediation, renewable energy production, food biotechnology, and other bio-based industries.



Figure 13. Thematic map illustrating the conceptual structure and evolution of stable bacterial lipase research based on co-word analysis generated using Biblioshiny.

3.12 Emerging Research Directions and Future Perspectives

The comprehensive bibliometric analysis demonstrates that research on stable bacterial lipases has evolved into a mature and multidisciplinary scientific domain with steadily increasing global interest. The integration of performance analysis, collaboration networks, citation patterns, thematic mapping, and conceptual structure provides a comprehensive understanding of the historical development and current status of this research field. The consistent growth in publication output, increasing citation impact, expanding international collaborations, and diversification of research themes collectively indicate that stable bacterial lipases have become one of the most promising classes of industrial biocatalysts for sustainable biotechnology.

The thematic evolution and keyword analyses reveal a clear transition from fundamental investigations of bacterial isolation, enzyme purification, and biochemical characterization toward application-oriented research emphasizing protein engineering, enzyme immobilization, industrial biocatalysis, renewable biofuels, environmental remediation, and sustainable manufacturing. This shift reflects the increasing industrial demand for enzymes capable of maintaining high catalytic efficiency under elevated temperatures, extreme pH conditions, and organic solvent-rich environments. Consequently, future research is expected to focus increasingly on developing robust bacterial lipases with improved operational stability, substrate specificity, and catalytic performance for large-scale industrial applications.

Recent advances in molecular biology and computational biotechnology are expected to further transform bacterial lipase research. Technologies such as genome mining, metagenomic sequencing, directed evolution, rational protein engineering, and synthetic biology are enabling the discovery and optimization of novel enzymes from previously unexplored microbial resources. In parallel, the integration of artificial intelligence (AI) and machine learning (ML) into enzyme engineering is creating new opportunities for predicting protein structures, identifying beneficial amino acid substitutions, designing thermostable variants, and accelerating enzyme optimization while reducing experimental time and cost. These computational approaches are likely to become integral components of next-generation enzyme discovery and industrial biocatalyst development.

The collaboration analysis also highlights opportunities for strengthening international scientific partnerships. Although productive research clusters have been established, collaboration remains concentrated within relatively small research communities. Expanding multidisciplinary and multinational collaborations among microbiologists, structural biologists, computational scientists, biochemical engineers, and industrial researchers will facilitate technology transfer, resource sharing, and the development of standardized methodologies. Such collaborative efforts are expected to accelerate innovation and improve the translation of laboratory discoveries into commercially viable bioprocesses.

From an industrial perspective, stable bacterial lipases are expected to play an increasingly important role in advancing the circular bioeconomy by enabling environmentally sustainable manufacturing processes with reduced energy consumption and lower environmental impact. Their expanding applications in pharmaceutical synthesis, biodiesel production, food processing, detergent formulation, polymer synthesis, bioremediation, wastewater treatment, and waste valorization demonstrate their potential to replace conventional chemical catalysts

with efficient, renewable, and environmentally benign biocatalysts. Future research should therefore prioritize enzyme stability under industrial conditions, process integration, scalable production systems, and techno-economic evaluation to facilitate commercial implementation.

Despite the significant progress identified in this bibliometric study, several challenges remain. Research activity is still concentrated in a limited number of countries and institutions, while collaborations among geographically diverse research groups remain relatively limited. In addition, relatively few studies integrate experimental enzyme characterization with computational modeling, systems biology, and industrial process optimization. Addressing these limitations through interdisciplinary research frameworks and international collaborations will be essential for sustaining scientific progress and expanding the practical applications of bacterial lipases.

Overall, the findings of this bibliometric study indicate that stable bacterial lipase research is entering a new phase characterized by the convergence of enzyme biotechnology, computational biology, artificial intelligence, and sustainable industrial development. Continued advances in these complementary disciplines are expected to drive the discovery of highly efficient bacterial lipases and support their widespread application across biotechnology, pharmaceutical manufacturing, environmental engineering, renewable energy production, and other bio-based industries.

4. Conclusion

This study presents a comprehensive bibliometric assessment of global research on stable bacterial lipases published between 2010 and 2026, based on 499 peer-reviewed journal articles retrieved from the Lens.org database. By integrating bibliometric performance indicators with science mapping techniques using Bibliometrix/Biblioshiny and VOSviewer, the study provides a detailed overview of the scientific development, intellectual structure, collaborative networks, and thematic evolution of this rapidly expanding research field.

The findings demonstrate that research on stable bacterial lipases has experienced sustained growth over the past decade, accompanied by increasing scientific impact and extensive international participation. The progressive rise in publication output, citation performance, and multidisciplinary collaborations reflects the growing importance of bacterial lipases as robust industrial biocatalysts. Source, author, institutional, and country analyses identified the major contributors driving scientific advancement, while co-authorship, co-citation, keyword

co-occurrence, and bibliographic coupling analyses revealed a well-established knowledge network supported by closely interconnected research communities. Thematic evolution further demonstrated a clear transition from fundamental studies on enzyme isolation and biochemical characterization toward advanced research focusing on protein engineering, enzyme immobilization, industrial biocatalysis, environmental sustainability, renewable biofuels, and circular bioeconomy applications.

This bibliometric investigation also highlights several emerging trends that are expected to shape future research. Advances in genome mining, metagenomics, synthetic biology, directed evolution, and rational protein engineering are expanding the discovery and optimization of novel bacterial lipases with enhanced catalytic properties. Furthermore, the integration of artificial intelligence, machine learning, and computational protein design into enzyme engineering is creating new opportunities for accelerating enzyme discovery, improving predictive molecular engineering, and developing highly efficient biocatalysts tailored for specific industrial processes.

Despite the significant progress achieved, the study identifies opportunities to strengthen international collaboration, expand research participation across underrepresented regions, and enhance interdisciplinary integration between microbiology, structural biology, computational sciences, and biochemical engineering. Addressing these challenges will facilitate the translation of laboratory discoveries into scalable industrial technologies and promote the broader commercial utilization of stable bacterial lipases.

Overall, this study provides a comprehensive bibliometric benchmark for stable bacterial lipase research and establishes a valuable knowledge framework for researchers, industrial stakeholders, and policymakers. The findings not only summarize the historical development and current scientific landscape of the field but also identify future research priorities that will contribute to the advancement of sustainable enzyme biotechnology, green industrial processes, pharmaceutical manufacturing, environmental remediation, and renewable bio-based industries.

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