

Global Research Trends in Childhood Asthma and the Microbiome: A Bibliometric Analysis of 2000 to 2024

Yanni Chen^{1,*}, Jiaqin Wang^{1,*}, Yueting Lu², Chenfei Song³

¹Department of Traditional Chinese Medicine, Shanghai Baoshan District Youyi Street Community Health Service Center, Shanghai, People's Republic of China; ²Department of Traditional Chinese Medicine, Shanghai Yangpu District Yanji Community Health Service Center, Shanghai, People's Republic of China; ³Department of Pediatric, Shanghai Municipal Hospital of Traditional Chinese Medicine, Shanghai University of Traditional Chinese Medicine, Shanghai, People's Republic of China

*These authors contributed equally to this work

Correspondence: Chenfei Song, Department of Pediatric, Shanghai Municipal Hospital of Traditional Chinese Medicine, Shanghai University of Traditional Chinese Medicine, Shanghai, People's Republic of China, Email 289835808@qq.com; Yueting Lu, Department of Traditional Chinese Medicine, Shanghai Yangpu District Yanji Community Health Service Center, Shanghai, People's Republic of China, Email Lyt18917693819@163.com

Objective: This study systematically maps the global publications on childhood asthma and the microbiome from 2000 to 2024, quantifying publication output, collaboration networks, thematic evolution, and research gaps to guide future basic and translational work.

Methods: On 30 March 2025, the Web of Science Core Collection was searched. English articles and reviews published between 2000 and 2024 were retained, yielding 2,537 records. Annual output was summarised with Microsoft Excel 2021, while VOSviewer 1.6.20, CiteSpace 6.4 R1, Scimago Graphica, and Charticulator were employed to visualise country, institution, author, and journal networks as well as keyword co-occurrence, bursts, and thematic clusters.

Results: Annual publications rose exponentially, peaking at 225 papers in 2022; the United States led in volume (802 papers), citations (48,856), and H-index (105), partnering most closely with the United Kingdom, while China's fast growing output has yet to match Western citation impact. Copenhagen University, Ludwig-Maximilians-Universität Munich, and authors such as Erika von Mutius and Hans Bisgaard occupied central positions in collaboration and co-citation networks. The high frequency and centrality of the keywords "gut microbiota", "early life" and "regulatory T cells" highlight the pivotal role of the early-life gut-lung axis, while keyword burst analysis shows that research has shifted from the hygiene-hypothesis phase toward short-chain fatty acids, multi-omics integration and personalised micro-ecological interventions.

Conclusion: Over the past quarter century, research on childhood asthma and the microbiome has progressed from macro level epidemiology to multi omics mechanism and is now entering a precision medicine phase. Future priorities include longitudinal birth cohort multi omics, targeted restoration of key taxa or metabolites, and expanded participation of low and middle income regions through strengthened international collaboration to reduce the global burden of childhood asthma.

Keywords: childhood asthma, microbiome, gut-lung axis, bibliometric analysis, allergy

Introduction

Childhood asthma is common and imposes a considerable global burden. The WHO estimates that about 300 million people currently live with asthma and projects this number will reach 400 million by 2025.¹ In children, it ranks among the top 20 causes of disability-adjusted life-years worldwide.² Asthma prevalence varies nearly ten-fold across regions, from 2% to 4% in some areas to >30% in others,³ and it is a leading cause of paediatric emergency visits and hospitalisations, limiting daily activities.⁴ Direct and indirect costs absorb 1–2% of health-care budgets in several high-income countries.⁵ Recognising this impact, the WHO and the Global Initiative for Asthma (GINA) have prioritised awareness, evidence-based management and

burden reduction since 1989.⁶ Yet asthma control remains suboptimal in many settings, especially for children whose developing airways and immune systems heighten their susceptibility to environmental triggers.

Growing evidence indicates that early-life microbiota act as modifiable determinants of childhood asthma. Communities in both the gut and the airways shape antigen presentation, T-cell polarisation and epithelial-barrier integrity, thereby maintaining immune homeostasis.^{7,8} Their composition is particularly malleable within the first 1,000 days of life. Early-life loss of *Lachnospira*, *Faecalibacterium*, *Veillonella* and *Rothia* in a Canadian cohort quadrupled school-age asthma risk; reintroducing these taxa into germ-free mice restored short chain fatty acid levels and reduced airway inflammation.^{9,10} Mechanistic investigations support these observations, showing that disturbed gut–lung, exemplified by reduced expansion of regulatory T cells driven by butyrate, together with abnormal early airway colonisation, can induce persistent skewing toward type 2 inflammation.^{11,12} Epidemiological studies reach similar conclusions. Children reared on traditional livestock farms inhale microbe-rich organic dust, develop more diverse gut microbiota, and display up to 50% lower prevalence of asthma and allergy than their urban counterparts.¹³ Taken together, clinical, experimental and population-based data converge on a causal pathway that links early microbial imbalance to later asthma.

Recent work has clarified both the mechanistic and translational links between the microbiome and childhood asthma. Laboratory studies demonstrate that gut-derived metabolites, especially short chain fatty acids, expand regulatory T cells and suppress airway inflammation, while microbial signals fine-tune innate immune pathways that protect the lung.^{14,15} These insights have spurred a diverse set of micro-ecological interventions.¹⁶ Current strategies include probiotic and prebiotic supplementation during pregnancy or early infancy to optimise gut colonisation,¹⁷ direct delivery of microbial metabolites with anti-inflammatory properties,¹⁸ and controlled exposure to farm-associated microbial communities as an immune-training stimulus.¹⁹ Preliminary trials and cohort studies lend support to these approaches; for example, certain probiotic regimens have already reduced wheeze and other respiratory symptoms in infants and toddlers.²⁰ As publications expand rapidly, a systematic, quantitative synthesis is needed to consolidate evidence, identify consistent patterns, and prioritise avenues for translation.

Bibliometric analysis provides a quantitative framework for mapping large bodies of literature. Co-citation, collaboration, and keyword co-occurrence analyses visualise thematic clusters, temporal trends, and research networks, revealing gaps and emerging fronts. A prior study²¹ of the asthma and microbiome interface found that “children” and “childhood asthma” were among the most frequent keywords, indicating that the paediatric population plays a central role in this research space.²² Guided by that observation, the present study concentrates on childhood asthma. The search strategy includes only studies involving children and draws on the Web of science (WOS) database to capture all relevant publications from the field’s origin onward. This approach is intended to generate a comprehensive longitudinal map tailored to paediatric characteristics and research priorities.

Therefore, the present work undertakes a dedicated bibliometric study of childhood asthma and the microbiome. Drawing on all records indexed in the WOS, we will track publication output since the field emerged. This design is expected to (i) portray how research on paediatric asthma–microbiota interactions has grown and shifted over time, (ii) highlight influential authors, institutions and journals, (iii) pinpoint recurring and emerging thematic clusters, and (iv) expose gaps that merit future basic, translational and clinical investigation. By delivering a comprehensive and child-focused landscape, the study aims to guide researchers, clinicians and policy makers toward the most productive directions for reducing the burden of childhood asthma.

Material and Methods

Data Acquisition and Processing

This study was searched in the Web of Science Core Database (WoSCC) on March 30, 2025, using the following search formula: TS=(asthma*) AND TS=(child*) AND TS=(“microbiome” OR “microbiota” OR “flora” OR “microflora” OR microorganism* OR bacteria* OR microbe*) for the years 2000 to 2024. A total of 2,854 articles were obtained. Only English articles and reviews were included in this study, and 317 other types of papers were excluded. These include News Item (n=1), Data Paper (n=1), Retracted Publication (n=2), Correction (n=3), Book Chapters (n=5), and Early Access (n=10), Letter (n=17), Editorial Material (n=58), Meeting Abstract (n=65), Proceeding Paper (n=69), Non-English (n=86). To maintain

a stable, reproducible corpus with a consistent citation window, we excluded “Early Access” records because online-first metadata often change at print publication (reindexing/reassignment), creating duplication risk and inflating late-year counts. There remained 2,537 publications, including 1,817 articles and 720 reviews. Figure 1 shows the specific flow of data acquisition and processing.

Bibliometric Analysis and Visualization

Bibliometric data were processed and visualised with Microsoft Excel 2021, VOSviewer 1.6.20, CiteSpace 6.4 R1, Scimago Graphica and Charticulator to obtain a comprehensive portrait of the field. Excel summarised annual publication counts from 2000 to 2024, revealing long-term output trends. VOSviewer, developed by van Eck and Waltman,²³ mapped inter-country collaboration, co-authorship, institutional partnerships and journal co-citation. Scimago Graphica depicted yearly output for the most productive countries, whereas Charticulator, an online tool from Microsoft Research (<https://donghaoren.org/charticulator/index.html>), generated chord diagrams that illustrated international collaboration patterns without the need for coding. CiteSpace, created by Chen Chaomei’s team,²⁴ carried out journal dual-map overlays, keyword co-occurrence, reference co-citation and burst-detection analyses, and visualised the resulting networks. We configured CiteSpace with 1-year time slices. Node types included references, author keywords, and countries/institutions. Per-slice node selection used the g-index ($k=25$) with cosine similarity. Networks were pruned with Pathfinder, and clusters were labeled using the log-likelihood ratio (LLR) method. We report Modularity Q and mean silhouette S as map-quality indices and interpret $Q>0.30$ as meaningful modularity and $S>0.50$ as acceptable cohesion ($S>0.70$ strong). Together, these complementary platforms provided integrated quantitative and graphical insights into the structure, evolution and emerging hotspots of research on childhood asthma and the microbiota.

Results

Overview of Research Trends

The temporal distribution of publications offers a clear picture of how research on childhood asthma and the microbiota has evolved. As illustrated in Figure 2, annual output rose gradually between 2000 and 2009, averaging about forty papers per year and surpassing that threshold for the first time in 2003. Production accelerated in 2010 (sixty-eight papers) and crossed one hundred in 2015 (one hundred and twenty-seven), a rise that coincided with wider adoption of high-throughput sequencing and renewed interest in the hygiene-hypothesis framework. From 2016 onward, the field entered a sustained expansion phase with an average annual growth rate of 8.7% and a peak of 225 articles in 2022; although output dipped slightly in 2023 and 2024 (to 167 papers), cumulative publications exceeded 3,500, underscoring continued intellectual and technological momentum. A polynomial fit to the cumulative curve ($R^2 = 0.9968$) confirms the

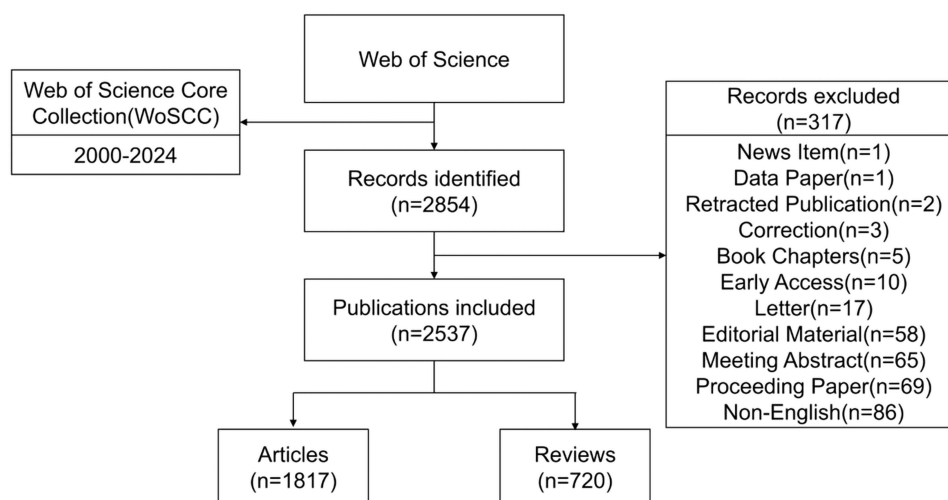


Figure 1 Flowchart for identifying and selecting publications.

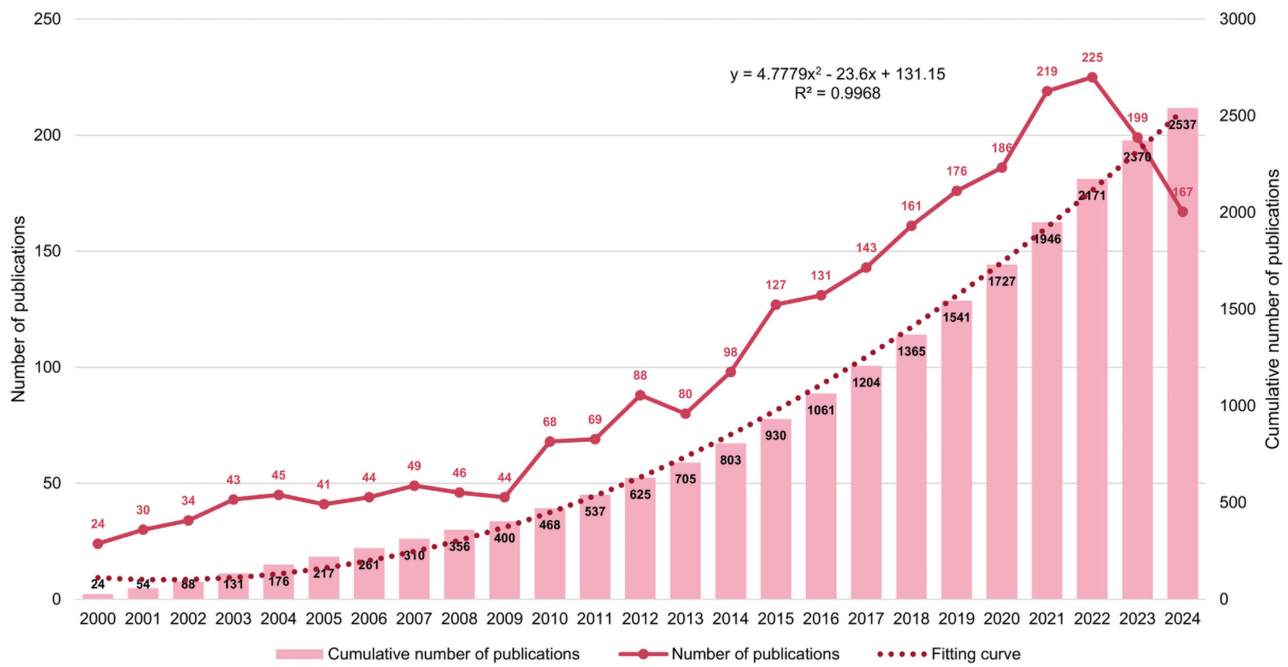


Figure 2 Annual publication volume and research fields.

likelihood of further growth. The corpus analysed comprises 2,537 articles spanning one hundred Web of Science research categories; the most frequent were Immunology (920 articles), Allergy (764), Pediatrics (399), Respiratory System (286) and Microbiology (178), with the full top-twenty list presented in Table 1. As WoSCC categories are assigned at the journal level, cross-disciplinary labels (eg, Construction Building Technology) can appear when journals publish relevant indoor-environment studies.

Country Analysis

A total of 110 countries have published on childhood asthma and the microbiota. As summarised in Table 2, the United States dominates the field with 802 papers, 48,856 citations and an H-index of 105, confirming its pivotal role in basic research, clinical translation and international collaboration. China ranks second in output (305 papers) but lags in impact with 28.7 citations per article and an H-index of 47, suggesting that its expanding volume has not yet translated into high-visibility findings. European countries demonstrate strong quality indicators. The United Kingdom and Germany average 96.3 and 94.9 citations per article, respectively, reflecting long-standing investment in studies. Figure 3A plots annual outputs for the top 10 countries; bubble size indicates the number of publications and bubble color indicates average

Table 1 The Top 20 Research Categories by Number of Publications

Rank	Web of Science Categories	Record Count	Rank	Web of Science Categories	Record Count
1	Immunology	920	11	Medicine Research Experimental	85
2	Allergy	764	12	Nutrition Dietetics	69
3	Pediatrics	399	13	Pharmacology Pharmacy	64
4	Respiratory System	286	14	Biochemistry Molecular Biology	61
5	Microbiology	178	15	Critical Care Medicine	56
6	Medicine General Internal	157	16	Cell Biology	43
7	Public Environmental Occupational Health	134	17	Construction Building Technology	40
8	Multidisciplinary Sciences	121	18	Gastroenterology Hepatology	40
9	Environmental Sciences	109	19	Engineering Environmental	37
10	Infectious Diseases	89	20	Dermatology	34

Table 2 Top 10 Countries in Terms of Publications

Rank	Country	Counts	Citations	Average Citation	H-Index
1	USA	802	48,856	60.92	105
2	China	305	8766	28.74	47
3	United Kingdom	247	23,799	96.35	71
4	Germany	219	20,797	94.96	65
5	Australia	184	9775	53.13	48
6	Italy	159	6665	41.92	42
7	Netherlands	151	13,079	86.62	55
8	Finland	144	11,404	79.19	49
9	Canada	136	14,863	109.29	47
10	Sweden	134	8898	66.40	53

citations per item. [Figure 3B](#) presents a VOSviewer co-authorship network of 32 countries (≥ 20 documents): node size reflects publication counts, link thickness denotes collaboration frequency, and node color indicates collaboration clusters. [Figure 3C](#) shows a chord diagram of bilateral collaborations; the United States forms the densest hub, with its strongest tie to the United Kingdom.

Author Analysis

A total of 13,229 researchers have contributed to this topic. As shown in [Table 3](#), Erika von Mutius leads with 70 publications, 10,132 citations and an H-index of 44; her landmark farm-effect studies, including the 2002 NEJM paper linking agricultural exposure to lower asthma risk, place her at the centre of the field. Hans Bisgaard (59 papers, 5717 citations) and Charlotte Braun-Fahrlander (28 papers, 5451 citations) follow. Susan Lynch and Jakob Stokholm represent a newer generation, each averaging about 92 citations per paper. The H-index rises with total citations, yet a few seminal papers can markedly elevate individual standing. [Figure 4](#) shows a multi-cluster author collaboration network. The green cluster is centred on Erika von Mutius, whose group shows dense internal links. The red cluster has dual hubs, James E. Gern and Leonard B. Bacharier, and connects numerous North-American collaborators. The yellow cluster, organised around Hans Bisgaard and Jakob Stokholm, maintains frequent interactions with the red cluster. The purple cluster brings together Stuart E. Turvey, Malcolm R. Sears et al, whereas the blue cluster is anchored by Kohei Hasegawa and Carlos A. Camargo Jr. Highly cited scholars occupy cluster cores, and thick inter-cluster links highlight active cross-regional cooperation, suggesting that shared resources and emerging technologies are driving broader global collaboration in this field.

Institutions Analysis

A total of 3,442 institutions have conducted research in this field. [Table 4](#) lists the top 10 organizations by volume. The institution with the highest number of publications was UNIV COPENHAGEN with 89, followed by WASHINGTON UNIV and HARVARD MED SCH with 75 and 73, respectively. In terms of the number of citations per article, UNIV MUNICH has the highest, indicating the highest quality of its published articles. UNIV MUNICH also has the highest H-index, indicating its leading role as an authority in the field. [Figure 5](#) shows the cooperation network diagram of institutions with at least 20 publications, including 58 institutions. It can be seen that the cooperation among institutions is relatively close, which is conducive to the development of this field.

Journals Analysis

Journal analysis confirms the central venues that shape scholarship on childhood asthma and the microbiota. Among the 2,537 articles retrieved, the Journal of Allergy and Clinical Immunology published the largest share with 160 papers, followed by Clinical and Experimental Allergy and Pediatric Allergy and Immunology with 87 and 79 papers, respectively, indicating that researchers in this domain preferentially target specialised allergy and paediatric outlets ([Table 5](#)). Within the same set, Allergy is the highest-ranked periodical by impact factor, while The Lancet tops the cited-

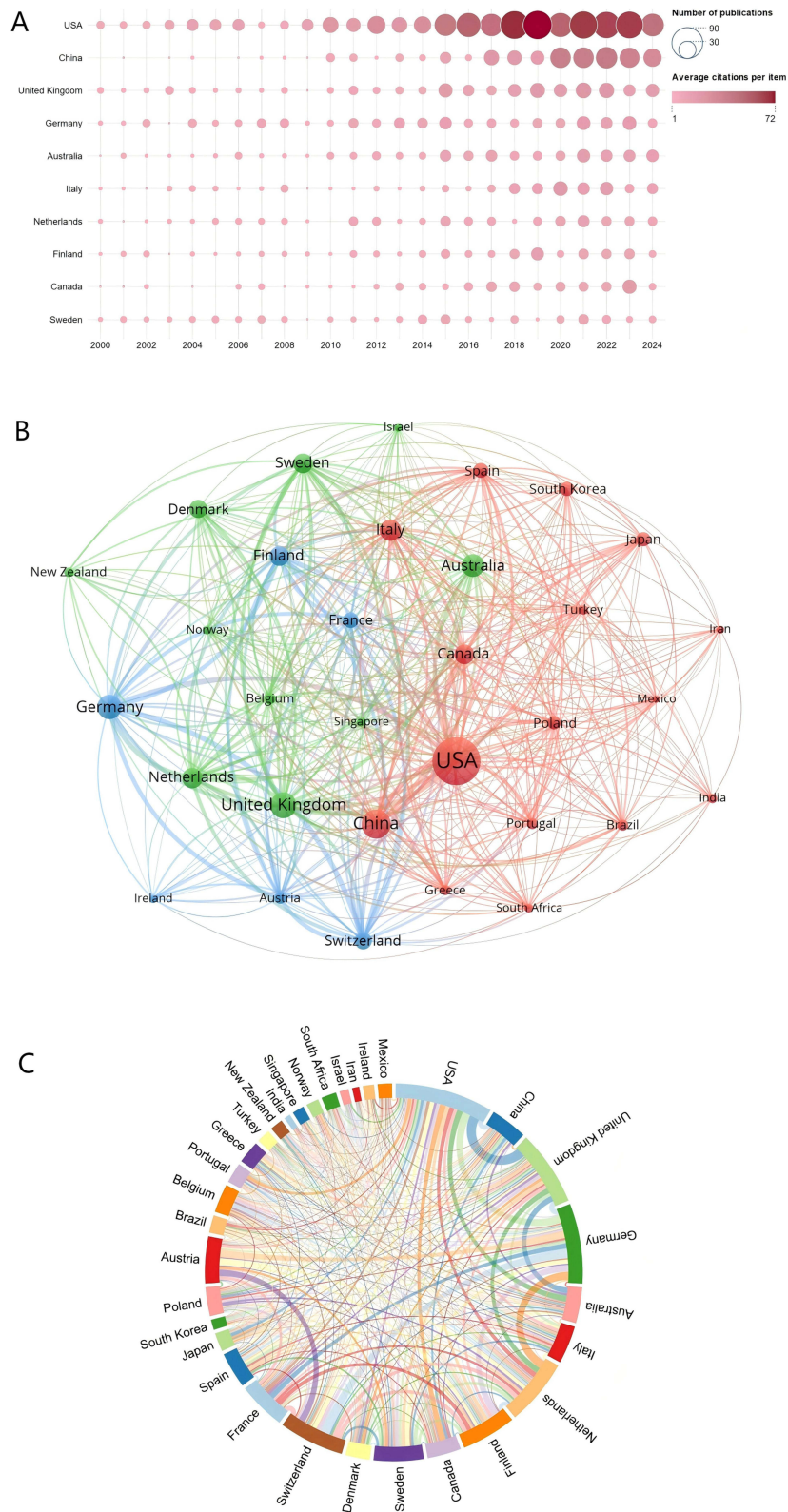


Figure 3 (A) Bubble chart of national output. Bubbles represent country–year records; size: number of publications, color: average citations per item. (B) Map of national cooperation network. Nodes = countries (size = publication count; color = collaboration cluster). Edge thickness = total link strength. (C) Chords of national cooperation. Sectors = countries; ribbon width = collaboration frequency.

Table 3 The Top 10 Authors in Terms of Publications

Rank	Author	Counts	Citations	H-Index
1	Von Mutius, Erika	70	10,132	44
2	Bisgaard, Hans	59	5717	33
3	Stokholm, Jakob	57	4135	29
4	Bonnelykke, Klaus	56	5021	29
5	Chawes, Bo Lund Krogsgaard	53	3352	25
6	Gern, James E.	36	3001	24
7	Lynch, Susan	32	2942	22
8	Bacharier, Leonard B.	30	1717	17
9	Hyvarinen, Anne	29	2033	21
10	Braun-Fahrlander, Charlotte	28	5451	25

journal list despite a smaller output, illustrating the field's reliance on high-profile clinical medicine sources for foundational references. *J Allergy Clin Immunol* leads with 14,199 citations, trailed by the *American Journal of Respiratory and Critical Care Medicine* (4,903) and *Clinical and Experimental Allergy* (4,738). **Figure 6A** displays the co-citation network for 21 journals that have each published at least 20 articles; node size corresponds to output and link thickness to shared citations. The double-map overlay in **Figure 6B** further tracks knowledge flow: citing journals on the left cluster into “Molecular Biology / Genetics” and “Health / Nursing / Medicine”, whereas cited journals on the right concentrate in “Molecular Biology / Immunology” and “Medicine / Clinical”. Among the three principal citation paths, the route linking “Molecular Biology / Genetics” to “Medicine / Clinical” ($z = 7.451$) is the most prominent,

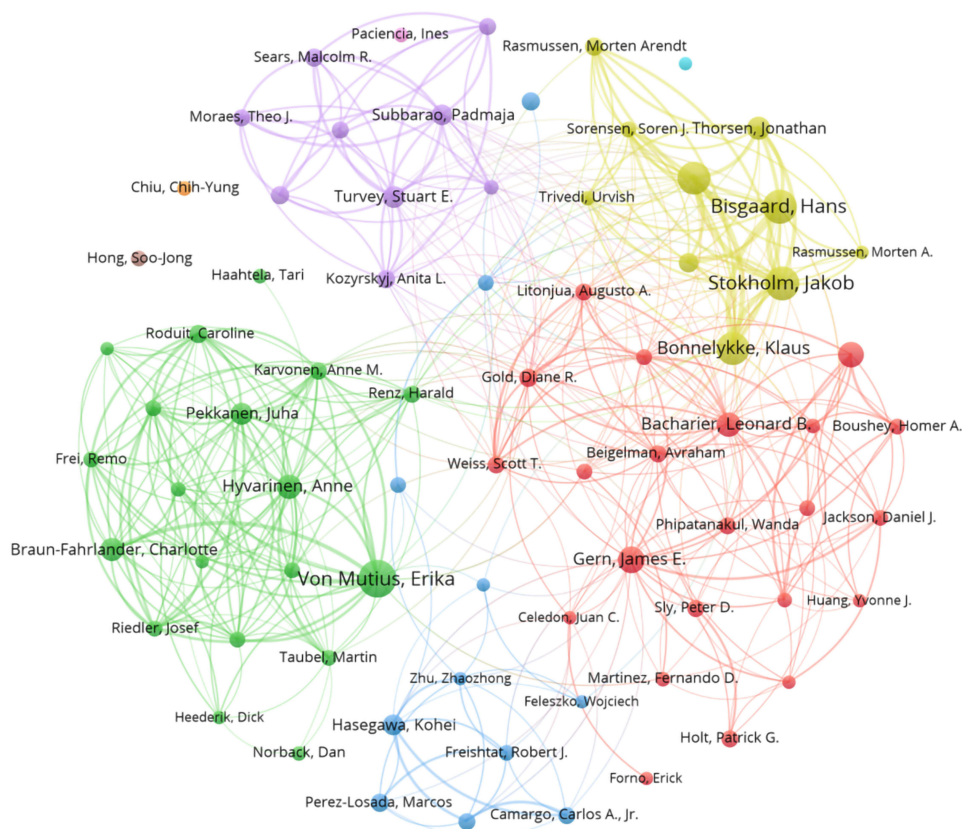
**Figure 4** Author collaboration network.

Table 4 The Top 10 Organizations in the Number of Publications

Rank	Organization	Counts	Citations	H-Index
1	UNIV COPENHAGEN	89	5583	36
2	WASHINGTON UNIV	75	3029	31
3	HARVARD MED SCH	73	3026	32
4	UNIV MUNICH	71	10,116	44
5	KAROLINSKA INST	71	5273	38
6	UNIV WESTERN AUSTRALIA	67	3795	30
7	UNIV HELSINKI	63	5601	33
8	UNIV UTRECHT	58	4559	34
9	UNIV WISCONSIN	52	3703	29
10	UNIV CALIF SAN FRANCISCO	49	3893	28

underscoring a robust translational pipeline that carries basic genetic and molecular insights into clinical applications for childhood asthma.

Keyword Analysis

We retrieved 2,537 publications and extracted 266 keywords, then merged synonyms and removed terms lacking analytical value. In [Figure 7A](#), node size reflects frequency, colours track average publication year, purple rims mark high betweenness centrality (≥ 0.1), and link thickness denotes co-citation strength. The dominant cluster centres on “gut microbiota” (frequency 638, centrality 0.63) and its immunological partners such as “regulatory T cells” and “dendritic cells”, highlighting the pathway by which microbial signals modulate immune tolerance and asthma development. High-frequency terms like “early

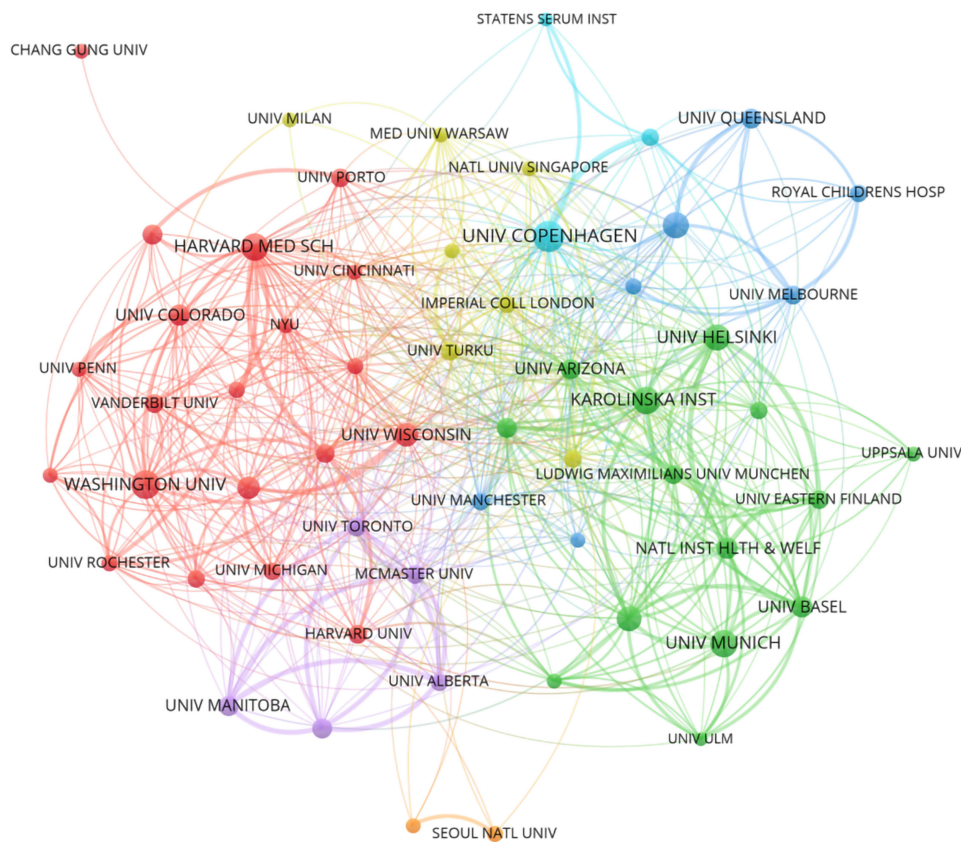


Figure 5 Network map of Organization cooperation.

Table 5 The Top 10 Journals in Publication and the Top 10 Cited Journals in Citation

Rank	Journals	Counts	Country	IF (JCR2023)	Cited Journals	Citations	Country	IF (JCR2023)
1	JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY	160	USA	11.4	J ALLERGY CLIN IMMUN	14199	USA	11.4
2	CLINICAL AND EXPERIMENTAL ALLERGY	87	United Kingdom	6.3	AM J RESP CRIT CARE	4903	USA	19.3
3	PEDIATRIC ALLERGY AND IMMUNOLOGY	79	Denmark	4.3	CLIN EXP ALLERGY	4738	United Kingdom	6.3
4	ALLERGY	78	United Kingdom	12.6	ALLERGY	3761	United Kingdom	12.6
5	PLOS ONE	56	USA	2.9	PLOS ONE	3051	USA	2.9
6	FRONTIERS IN IMMUNOLOGY	48	Switzerland	5.7	NEW ENGL J MED	3017	USA	96.3
7	PEDIATRIC PULMONOLOGY	43	USA	2.7	LANCET	2810	United Kingdom	98.4
8	ANNALS OF ALLERGY ASTHMA & IMMUNOLOGY	42	USA	5.3	EUR RESPIR J	2703	United Kingdom	17
9	CURRENT OPINION IN ALLERGY AND CLINICAL IMMUNOLOGY	38	USA	3	PEDIATRICS	2214	USA	6.2
10	JOURNAL OF ALLERGY AND CLINICAL IMMUNOLOGY-IN PRACTICE	38	Netherlands	8.2	THORAX	2102	United Kingdom	10.8

life” (220), “birth cohort” (47) and “hygiene hypothesis” (93) emphasise the lasting impact of perinatal exposures, while “house dust” (129, centrality 0.60) underscores the importance of indoor microbial antigens. Co-occurrence with “allergic rhinitis”, “eczema” and “food allergy” suggests that dysbiosis may drive multi-organ allergic phenotypes through shared Th2-IgE pathways; the prominence of “sensitization” (centrality 0.53) and “respiratory tract infections” (58) further links microbial interactions to allergen priming. Although “probiotics” appear with moderate frequency (106), their low centrality (0.10) and weak ties to “randomized controlled trials” (152) indicate that clinical evidence remains preliminary. The relative absence of emerging terms such as “virome” and “metabolomics” points to future opportunities for deeper functional profiling of the paediatric microbiome.

Figure 7B displays ten keyword clusters (#0–#9) derived with CiteSpace (Q = 0.812, S = 0.970), confirming a clear and reliable structure. #0 Probiotics addresses how short-term supplementation modifies gut colonisation and immune tone; #1 Childhood Asthma links indoor microbial exposure (house dust) with regulatory-T-cell pathways that shape paediatric asthma risk; #2 Atopy merges eczema, food allergy and dysbiosis, pointing to a shared Th2-IgE axis across allergic diseases; #4 Early Life stresses the lasting imprint of prenatal and early-life environments, nutrition and maternal microbial transfer on immune programming; #6 Allergic Thinitis (one-airway theory) highlights overlapping inflammatory circuits between rhinitis and asthma; and #7 Antibiotic suggests that early antibiotic use, by depleting short chain fatty acids, may precipitate wheeze, though mechanistic data remain limited. Collectively, these themes centre on the early-life microbiome–immune axis and its modulation by environment, diet and therapeutics.

Keyword burst analysis (Figure 8) charts how research priorities have shifted over time. Early bursts (2000–2010) centred on epidemiological links between asthma and co-existing allergic diseases, with “allergic rhinitis”, “allergic disease” and “endotoxin” signalling intense interest in household-dust exposures and immuno-sensitisation. From 2007 to 2015 the “hygiene hypothesis” rose to prominence as high-throughput sequencing redirected attention toward the microbiome; concurrent bursts for “randomised controlled trials”, “probiotics”, “caesarean section” and “breast-feeding” marked first forays into clinical translation and the long-term impact of early-life colonisation. During the multi-omics phase (2013–2020) emphasis shifted from community composition to function, evidenced by bursts in “microbiome”, “birth cohort” and “regulatory T cells”, which together highlighted longitudinal designs and tolerance pathways. The most recent period (2021–2024) features high-intensity bursts for “dysbiosis”, “short chain fatty acids” and persistent attention to “food allergy”, underscoring a precision-medicine agenda focused on metabolic mediators and the gut–lung–allergy axis.

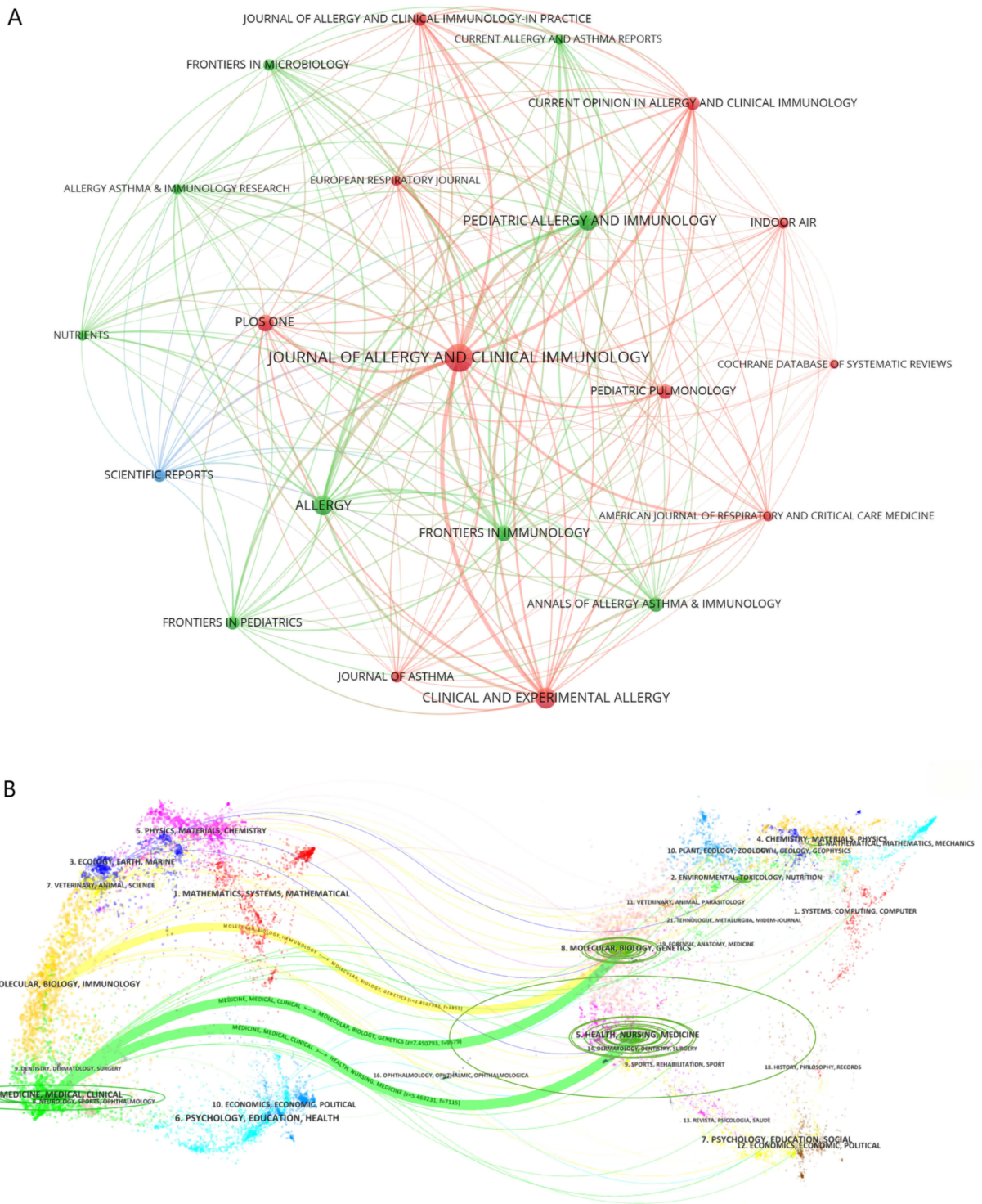


Figure 6 (A) Journal co-citation network. Nodes = journals (size = co-citation count; color = cluster). Edges = link strength (co-citation frequency). **(B)** The dual-map overlay of journals. Left = citing fields; right = cited fields. Colored paths trace citation flows (thickness = frequency).

Reference Co-Citation Analysis

The co-citation network shown in [Figure 9A](#). The largest node represents the landmark paper by Arrieta et al, 2015,¹⁰ cited 117 times. Working within the Canadian CHILD birth cohort, Arrieta et al showed that transient loss of four gut genera (Faecalibacterium, Lachnospira, Veillonella and Rothia) in the first 100 days predicted later asthma, and that

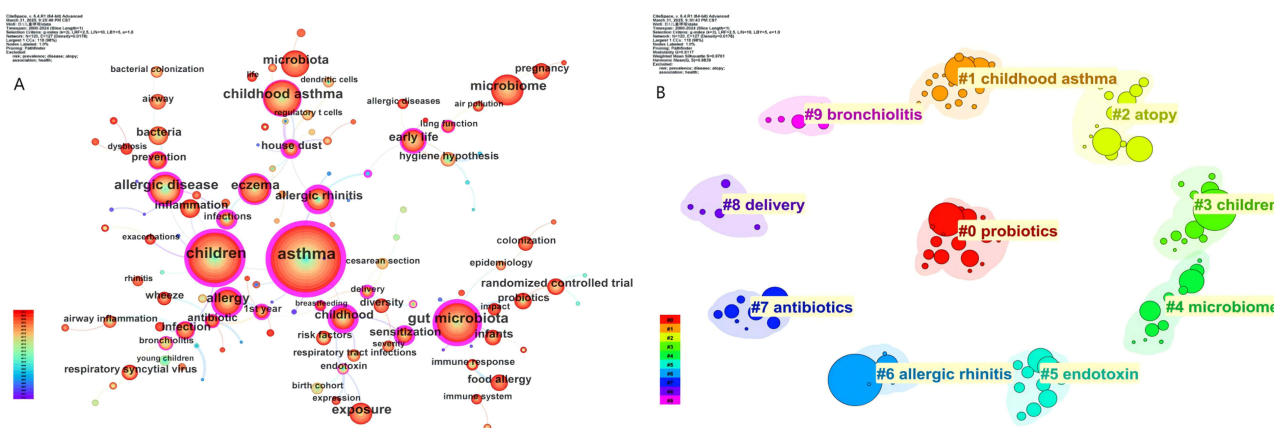


Figure 7 (A) Keyword co-occurrence network. Nodes = keywords (size = occurrence). Ring/edge colors encode time: cooler hues indicate earlier years; warmer hues indicate more recent years. Edges = co-occurrence links. **(B)** Keyword clustering. Same network grouped by topics. Color: cluster (labels with IDs). Node size: occurrence.

reintroducing these taxa into germ-free mice reduced airway inflammation, thereby establishing a causal gut–lung axis and pinpointing an early therapeutic window. Log-likelihood-ratio clustering of the same reference set yielded 20 robust clusters ($Q = 0.787$, $S = 0.901$), visualised in Figure 9B. The largest groups include #0 Nasal Microbiota, #1 Allergy Development, #2 Systematic Review, #3 Antibiotic Use and #4 Dust Endotoxin, highlighting work on airway microbial communities, longitudinal allergy trajectories and environmental triggers.

Figure 10 shows the top 25 references with the strong citation bursts. An initial validation stage (2000–2006) in which farm-based epidemiology confirmed the “hygiene hypothesis”, a diversity-association stage (2009–2016) catalyzed by high-throughput 16S/metagenomic sequencing and exemplified by Ege et al’s 2011 NEJM study linking environmental microbial diversity to lower asthma risk,²⁵ and a mechanism-to-precision stage (2014–2024) marked by multi-omics, animal models, and landmark papers (eg, Arrieta 2015, Teo 2015, Stockholm 2018) that elucidated the gut-lung axis and immune-metabolic pathways.^{10,26,27} Hotspots now center on multi-omics birth cohorts, immunoprotective metabolite mapping, and AI-driven personalized probiotic/postbiotic or phage trials.

Discussion

General Information

Over the past two decades, global scholarship on the nexus between asthma and the microbiome has expanded rapidly, with annual publication counts rising each year. The United States sits at the center of this growth, leading in both output and total citations, clear markers of its research capacity and scholarly influence. The landscape, however, is increasingly multipolar. China’s publication volume has surged, and the United Kingdom, Germany, Denmark and other European nations, together with the United States, constitute the backbone of an extensive international collaboration network. Network analyses reveal especially tight partnerships between the United States and the United Kingdom and strong intra-European links. Multinational projects have catalyzed landmark discoveries, such as the GABRIELA study, which showed that children exposed to microbiome-rich farm environments have lower asthma prevalence.²⁸ This shows the scientific dividends of cross-border cooperation.

At the institutional and author levels, leading contributors remain concentrated in well-funded centres across North America and Europe. In the United States, teams such as that of Susan V. Lynch at the University of California have published influential work in journals like *Nature Medicine* and *JACI* since 2010, clarifying how neonatal gut and airway microbiota shape asthma risk.²⁹ In Denmark, Hans Bisgaard’s Copenhagen cohort studies linked newborn airway colonization patterns to later childhood asthma.³⁰ Parallel progress in Canada, exemplified by B. B. Finlay and collaborators within the CHILD cohort, revealed that early life gut-microbiome diversity and metabolic profiles predict subsequent asthma development.^{10,31} The dense co-authorship networks forged by these teams have produced many highly cited papers, reinforcing a leadership pattern shared by North America and Europe while also highlighting Asia’s

Top 25 Keywords with the Strongest Citation Bursts

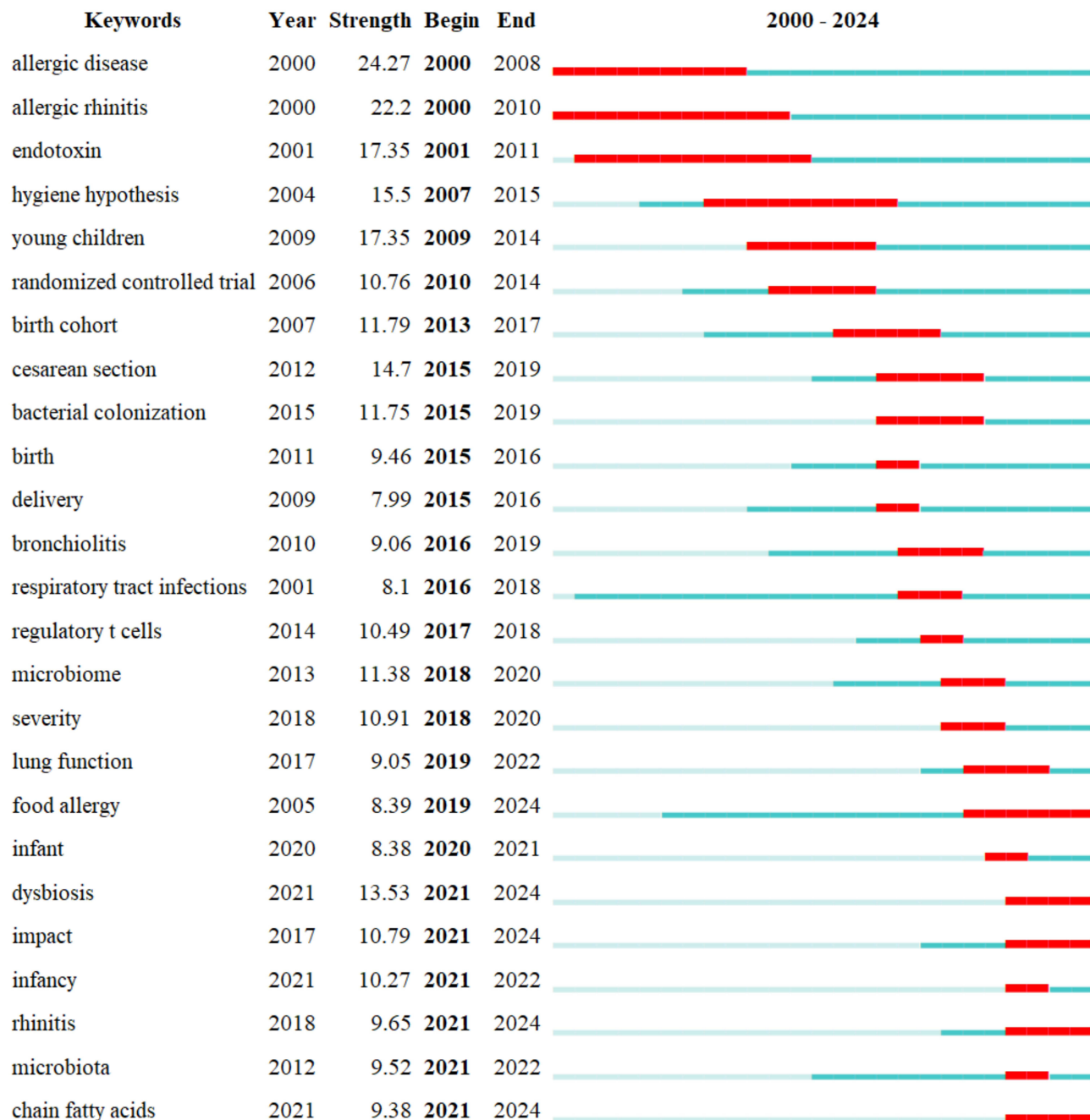


Figure 8 The keywords with the strong citation bursts.

rapid ascent. Together, these transnational and cross-institutional collaborations have laid a solid foundation for deeper mechanistic insights into the microbiome's role in asthma pathogenesis and for future advances in prevention and therapy worldwide.

Research Hotspots and Theme Evolution

Bibliometric mapping identifies “microbiota/microbiome” as the dominant keyword cluster that has linked asthma research across the entire study period.³² Work in both gut and airway compartments now converges on the idea that

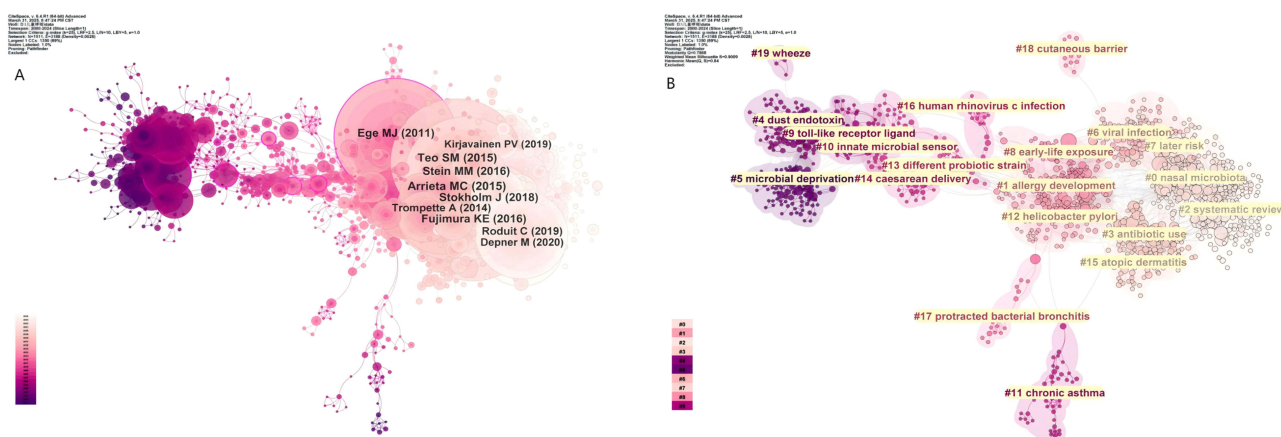


Figure 9 (A) Co-citation of references; **(B)** Reference clustering.

Top 25 References with the Strongest Citation Bursts

References	Year	Strength	Begin	End	2000 - 2024
Björkstén B, 1999, CLIN EXP ALLERGY, V29, P342, DOI 10.1046/j.1365-2222.1999.00560.x, DOI	1999	18.94	2000	2004	
Matricardi PM, 2000, BMJ-BRIT MED J, V320, P412, DOI 10.1136/bmj.320.7232.412, DOI	2000	18.28	2000	2005	
Kalliomäki M, 2001, LANCET, V357, P1076, DOI 10.1016/S0140-6736(00)04259-8, DOI	2001	21.77	2001	2006	
von Mutius E, 2000, CLIN EXP ALLERGY, V30, P1230	2000	18.24	2001	2005	
Von Ehrenstein OS, 2000, CLIN EXP ALLERGY, V30, P187, DOI 10.1046/j.1365-2222.2000.00801.x, DOI	2000	18.24	2001	2005	
Riedler J, 2001, LANCET, V358, P1129, DOI 10.1016/S0140-6736(01)06252-3, DOI	2001	23.09	2002	2006	
Braun-Fahrlander C, 2002, NEW ENGL J MED, V347, P869, DOI 10.1056/NEJMoa020057, DOI	2002	26.41	2003	2007	
Bisgaard H, 2007, NEW ENGL J MED, V357, P1487, DOI 10.1056/NEJMoa052632, DOI	2007	23.78	2009	2012	
Ege MJ, 2011, NEW ENGL J MED, V364, P701, DOI 10.1056/NEJMoa1007302, DOI	2011	45.57	2011	2016	
Hilty M, 2010, PLOS ONE, V5, P0, DOI 10.1371/journal.pone.0008578, DOI	2010	26.12	2011	2015	
Dominguez-Bello MG, 2010, P NATL ACAD SCI USA, V107, P11971, DOI 10.1073/pnas.1002601107, DOI	2010	20.35	2011	2015	
Bisgaard H, 2011, J ALLERGY CLIN IMMUN, V128, P646, DOI 10.1016/j.jaci.2011.04.060, DOI	2011	19.67	2012	2016	
Trompette A, 2014, NAT MED, V20, P159, DOI 10.1038/nm.3444, DOI	2014	24.71	2014	2019	
Abrahamson TR, 2014, CLIN EXP ALLERGY, V44, P842, DOI 10.1111/cea.12253, DOI	2014	20.16	2014	2019	
Lynch SV, 2014, J ALLERGY CLIN IMMUN, V134, P593, DOI 10.1016/j.jaci.2014.04.018, DOI	2014	18.65	2015	2019	
Arrieta MC, 2015, SCI TRANSL MED, V7, P0, DOI 10.1126/scitranslmed.aab2271, DOI	2015	42.46	2016	2020	
Teo SM, 2015, CELL HOST MICROBE, V17, P704, DOI 10.1016/j.chom.2015.03.008, DOI	2015	37.68	2016	2020	
Schuijjs MJ, 2015, SCIENCE, V349, P1106, DOI 10.1126/science.aac6623, DOI	2015	18	2016	2020	
Fujimura KE, 2016, NAT MED, V22, P1187, DOI 10.1038/nm.4176, DOI	2016	32.2	2017	2021	
Stein MM, 2016, NEW ENGL J MED, V375, P411, DOI 10.1056/NEJMoa1508749, DOI	2016	31.86	2017	2021	
Stokholm J, 2018, NAT COMMUN, V9, P0, DOI 10.1038/s41467-017-02573-2, DOI	2018	29.57	2019	2024	
Roduit C, 2019, ALLERGY, V74, P799, DOI 10.1111/all.13660, DOI	2019	23.94	2020	2024	
Depner M, 2020, NAT MED, V26, P1766, DOI 10.1038/s41591-020-1095-x, DOI	2020	27.56	2021	2024	
Barcik W, 2020, IMMUNITY, V52, P241, DOI 10.1016/j.immuni.2020.01.007, DOI	2020	21.76	2021	2024	
Patrick DM, 2020, LANCET RESP MED, V8, P1094, DOI 10.1016/S2213-2600(20)30052-7, DOI	2020	19.33	2022	2024	

Figure 10 References with the strong citation bursts.

dysbiosis heightens asthma susceptibility. Landmark datasets substantiate this trajectory. Infant-cohort studies show that early deviations in gut bacterial composition predict later asthma,¹⁰ whereas sequencing of bronchial samples reveals a microbial community in established asthma that differs sharply from healthy airways.³³ Mechanistic syntheses, most notably Lynch's review in Nature Reviews Microbiology, describe bidirectional crosstalk along the axis connecting the gut and lungs.³⁴ Perturbations such as an abnormal Firmicutes-to-Bacteroidetes ratio reduce short-chain fatty-acid (SCFA) output and skew immune-cell differentiation, thereby increasing risk.³⁵ Parallel profiling of stable asthma links airway microbial signatures to inflammatory phenotypes and variable responses to steroids and antibiotics;³⁶

Edwards et al further catalogue how specific microbes influence asthma onset, course and prevention.³⁷ These studies account for the persistent keyword bursts for “microbiome/microbiota” and the dominance of the corresponding clusters in our maps.

A second keyword cluster centred on immunopathology, captured by terms like “allergy”, “inflammation”, and “immunity”, traces growing interest in how microbial metabolites reshape host defence. SCFAs produced by dietary-fibre fermentation calibrate regulatory and effector responses and dampen allergic airway inflammation.^{38,39} These small molecules now anchor a broader agenda that extends beyond taxonomic shifts to functional outputs, positioning the gut microbiota as a hub for communication among the gut, liver and brain and for systemic homeostasis.⁴⁰ Consequently, the discourse has moved from cataloguing “who is there” to asking “what are they doing” and “how can we intervene.”

A third hotspot bridges epidemiology and mechanism through terms such as “risk”, “exposure”, “farm”, “pets”, and “antibiotics.” Strong evidence indicates that broad microbial encounters in early life foster immune maturation and reduce allergy and asthma incidence.^{29,41} Current priorities include defining effective microbial exposure, quantifying its dose–response relationship, and clarifying how lifestyle factors shape colonisation trajectories in children.³¹ These questions intersect with broader disease models in inflammatory bowel disease, obesity and other non-communicable conditions, many of which were first explored through classic in-vitro culture studies.⁴²

Chronologically, the field has shifted from macro-level observation to micro-level mechanism. Early-2000s work, framed by the hygiene hypothesis,^{43–45} relied on epidemiological links between family size, infections and allergy. Around 2010, high-throughput 16S rRNA sequencing overturned the “sterile lung” assumption,^{46–48} prompting a wave of studies that connected microbial metabolites to immune regulation.^{49–51} Since 2015, longitudinal birth cohorts and multi-omics platforms have driven an integrative phase. Future breakthroughs are expected from targeted restoration of key taxa or metabolites to prevent asthma,⁵² deeper analysis of interactions among host genetics, immune development and the microbiome to identify high-risk subpopulations and personalise interventions,³⁶ and panoramic mapping of the gut–lung axis by combining metagenomics, metabolomics and other omics layers.⁵³ Syntheses sharpen the early-life and functional picture: infant-gut enrichment of *Bifidobacterium*, *Faecalibacterium*, and *Roseburia* predicts lower asthma risk, whereas certain *Bacteroides* patterns and fungal signals (eg, *Malassezia*) predict higher risk; SCFA reviews consolidate the butyrate pathway’s anti-inflammatory role. In parallel, airway-microbiome profiles now track with exacerbation risk and steroid responsiveness, while “farm-effect” surrogates and multi-omics point to actionable mechanisms beyond taxonomy.

Taken together, the mechanistic and epidemiologic strands outlined above, linking dysbiosis to immune calibration, SCFA-mediated signalling along the gut–lung axis, and early-life exposure effects, delineate a pragmatic intervention space. Near-term, early-life antibiotic stewardship, breastfeeding promotion with delivery-mode-aware counselling, dietary fibre/prebiotic strategies to enhance SCFA tone, targeted strain-specific probiotics/postbiotics in defined high-risk infants, and indoor air-quality/allergen control appear the most implementable, albeit with heterogeneous evidence and generally modest effect sizes. Emerging, less standardised options include tailored synbiotics, farm-inspired microbial exposure surrogates, bacterial lysates or immunomodulators, and airway microbiota biotherapeutics; paediatric FMT remains experimental. Priorities include phenotype stratified trials, robust dose response and timing, strain and formulation standardisation, and agreed core outcomes.

Influential Literature and Research-Paradigm Transformation

Early theoretical development in the asthma–microbiome field was anchored by the hygiene hypothesis, first articulated at the end of the last century and refined in Strachan’s seminal work.^{47,54} Landmark cohort studies then tested this hypothesis in real-world settings. For example, Bisgaard et al reported in *The New England Journal of Medicine* that newborn airway colonisation by *Streptococcus pneumoniae* or *Staphylococcus aureus* predicted a markedly higher risk of asthma later in childhood.^{29,31} These data moved the discourse beyond broad epidemiological correlations toward specific microbial clues that could underpin causality, signalling a transition from macro-level observation to mechanistic enquiry.

Around 2010, the field underwent a decisive paradigm shift catalysed by next-generation sequencing and systems-biology tools. Hilty et al applied 16S rRNA profiling to reveal a dysregulated airway microbiota in asthmatic patients, overturning the long-held assumption that healthy lungs are sterile.^{36,55,56} Subsequent studies linked distinct airway bacterial patterns to airway hyperresponsiveness, inflammatory phenotypes and disease severity, including work that

dissected the microbiome of severe asthma.⁵⁷ Complementary gut-focused investigations, such as the Canadian CHILD cohort, combined metagenomics and metabolomics to show that depletion of butyrate-producing taxa like *Faecalibacterium* elevates asthma risk while illuminating how microbial catabolites modulate host immunity.^{10,58} Together, these findings established “microbial metabolites regulating host immunity” as a core research paradigm and created a dense, highly cited knowledge network spanning hypothesis, epidemiology and mechanism. This progression is reflected in our burst-term chronology and cluster evolution, which highlight the gut–lung axis, multi-omics integration, and microecological interventions as emergent foci. These landmark contributions also inform current priorities, including restoration of protective taxa and metabolites, stratification of high-risk children, and integration of multi-omics approaches for target discovery.

Citation-burst analysis now highlights literature that is driving a second shift, from mechanistic insight to translational application. Recent highly cited papers concentrate on the gut–lung axis, multi-omics integration and microecological interventions, reflecting the transformative impact of high-throughput sequencing, metagenomics and other omics platforms.^{58–60} Researchers can now characterise complex communities in situ, probe metabolite pathways and model host–microbe interactions with unprecedented resolution. These advances are steering the field toward microbiome-based prevention and precision medicine. Future priorities include restoring key taxa or metabolites to prevent asthma, mapping host genetic and immune interactions to stratify high-risk individuals and deploying integrated omics to discover therapeutic targets.^{53,54,61} The evolution from empirical observation to mechanistic explanation and on to clinical translation illustrates a mature research paradigm poised to deliver microbiota-guided strategies for asthma management.

Recent evidence, including China-based indoor exposome/microbiota work¹³ and global multi-omics advances,^{53,58–60} alongside airway-microbiome phenotyping studies,^{55,56} supports integrating exposome–microbiome analytics into risk stratification and prevention in China.

Limitations

This study has several limitations that merit consideration. Firstly, reliance on a single source (WoSCC) may introduce coverage and ascertainment bias due to differences in journal inclusion and indexing across WoSCC, PubMed, Scopus, and Embase. Database choice can shift publication counts, rankings, and network metrics, so future work should triangulate multiple databases with de-duplication and pre-specified sensitivity analyses. Secondly, our term selection, centred on “asthma”, “child”, and “microbiome/microbiota”, may miss studies emphasising dysbiosis, microbial metabolites, or airway colonisation that do not explicitly use “microbiome”. This keyword dependency introduces subjectivity and could underestimate the field’s breadth. Thirdly, restricting the search to English-language publications creates linguistic bias that could mask important contributions from non-English-speaking regions. Fourthly, bibliometric indicators such as publication counts and citation frequencies, while useful for mapping productivity and influence, do not directly gauge methodological rigour or clinical relevance and can be inflated by self-citation or topic popularity. Fifth, asthma has multiple interacting etiologies (genetic, immunodevelopmental, environmental/occupational, socio-economic, comorbidities, medications); because our search included only studies of the gut/respiratory microbiome, the findings should be interpreted within this context and may reflect residual confounding from unmeasured co-exposures. Future work should integrate genetic and exposome-wide factors. Finally, because the asthma–microbiome field is advancing rapidly, the very newest studies were not yet indexed at the March 30, 2025 cut-off, so hotspots and trends may soon evolve. Even so, by integrating complementary visual-analytics platforms and examining two-and-a-half decades of output, this work still provides a robust, panoramic baseline that clarifies global collaboration patterns, illuminates emergent thematic clusters and pinpoints priority directions for future mechanistic and translational research.

Conclusion

This bibliometric analysis maps 25 years of scholarship at the intersection of childhood asthma and the microbiome. From an early, hygiene-hypothesis phase focused on farm exposures, the field has progressed to molecularly defined gut–lung crosstalk and is now entering a translational era of precision probiotics, postbiotics and environment-based immune training. The United States, several European nations and, increasingly, China dominate output, while author and

institution networks reveal a tight core of long-standing collaborations that drive high-impact discoveries. Keyword evolution and reference burst analyses converge on functional microbiome profiling as the present research frontier.

Ethics and Dissemination

Ethical approval is not required for this secondary data analysis. The results will be peer-reviewed and intended for publication.

Acknowledgments

We thank all participants in this study and WOS for providing data support.

Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work.

Funding

This study was funded by the Shanghai Baoshan District Medical Key Specialty Class B: Community Integrated Chinese and Western Medicine Paediatrics Construction (BSZK-2023-BZ09), Shanghai Baoshan District Science and Technology Commission (24-E-84), Shanghai Baoshan District Health Commission Excellent Youth (Yucai) Program (BSWSYC- 2024-24), Shanghai Municipal Health Commission (SQZBZK-23-28).

Disclosure

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

References

- Enilari O, Sinha S. The Global Impact of Asthma in Adult Populations. *Ann Glob Health.* 2019;85(1):2. doi:10.5334/aogh.2412
- Zhang D, Zheng J. The Burden of Childhood Asthma by Age Group, 1990-2019: a Systematic Analysis of Global Burden of Disease 2019 Data. *Front Pediatr.* 2022;10:823399. doi:10.3389/fped.2022.823399
- Asher MI, García-Marcos L, Pearce NE, Strachan DP. Trends in worldwide asthma prevalence. *Eur Respir J.* 2020;56(6):2002094. doi:10.1183/13993003.02094-2020
- Liu Y, Zhao Y, Liu F, Liu L. Effects of Physical Exercises on Pulmonary Rehabilitation, Exercise Capacity, and Quality of Life in Children with Asthma: a Meta-Analysis. *Evid Based Complement Alternat Med.* 2021;2021:5104102. doi:10.1155/2021/5104102
- Sullivan PW, Ghushchyan VH, Campbell JD, Globe G, Bender B, Magid DJ. Measuring the cost of poor asthma control and exacerbations. *J Asthma.* 2017;54(1):24–31. doi:10.1080/02770903.2016.1194430
- Masoli M, Fabian D, Holt S, Beasley R. Global Initiative for Asthma (GINA) Program. The global burden of asthma: executive summary of the GINA Dissemination Committee report. *Allergy.* 2004;59(5):469–478. doi:10.1111/j.1398-9995.2004.00526.x
- Ciabattini A, Olivieri R, Lazzeri E, Medagliani D. Role of the Microbiota in the Modulation of Vaccine Immune Responses. *Front Microbiol.* 2019;10:1305. doi:10.3389/fmicb.2019.01305
- Peterson CT, Sharma V, Elmén L, Peterson SN. Immune homeostasis, dysbiosis and therapeutic modulation of the gut microbiota. *Clin Exp Immunol.* 2015;179(3):363–377. doi:10.1111/cei.12474
- Yoo JY, Groer M, Dutra SVO, Sarkar A, McSkimming DI. Gut Microbiota and Immune System Interactions. *Microorganisms.* 2020;8(10):1587. doi:10.3390/microorganisms8101587
- Arrieta MC, Stiemsma LT, Dimitriu PA, et al. Early infancy microbial and metabolic alterations affect risk of childhood asthma. *Sci Transl Med.* 2015;7(307):307ra152. doi:10.1126/scitranslmed.aab2271
- Liu C, Makrinioti H, Saglani S, et al. Microbial dysbiosis and childhood asthma development: integrated role of the airway and gut microbiome, environmental exposures, and host metabolic and immune response. *Front Immunol.* 2022;13:1028209. doi:10.3389/fimmu.2022.1028209
- Boulund U, Thorsen J, Trivedi U, et al. The role of the early-life gut microbiome in childhood asthma. *Gut Microbes.* 2025;17(1):2457489. doi:10.1080/19490976.2025.2457489
- Zhang M, Tang H, Chen Y, et al. Impact of environmental characteristics on children's gut microbiota - A pilot study in assessing the role of indoor microbiome and metabolites. *Environ Res.* 2023;234:116114. doi:10.1016/j.envres.2023.116114
- Jacobse J, Li J, Ehm R, Samsom JN, Goettel JA. Intestinal Regulatory T Cells as Specialized Tissue-Restricted Immune Cells in Intestinal Immune Homeostasis and Disease. *Front Immunol.* 2021;12:716499. doi:10.3389/fimmu.2021.716499

15. Samuelson DR, Welsh DA, Shellito JE. Regulation of lung immunity and host defense by the intestinal microbiota. *Front Microbiol.* 2015;6:1085. doi:10.3389/fmicb.2015.01085
16. Abdel-Aziz MI, Vijverberg SJH, Neerinx AH, Kraneveld AD, Maitland-van der Zee AH. The crosstalk between microbiome and asthma: exploring associations and challenges. *Clin Exp Allergy.* 2019;49(8):1067–1086. doi:10.1111/cea.13444
17. Lejeune S, Deschildre A, Le Rouzic O, et al. Childhood asthma heterogeneity at the era of precision medicine: modulating the immune response or the microbiota for the management of asthma attack. *Biochem Pharmacol.* 2020;179:114046. doi:10.1016/j.bcp.2020.114046
18. Sam QH, Ling H, Yew WS, et al. The Divergent Immunomodulatory Effects of Short Chain Fatty Acids and Medium Chain Fatty Acids. *Int J Mol Sci.* 2021;22(12):6453. doi:10.3390/ijms22126453
19. Melgaard ME, Jensen SK, Eliassen A, et al. Asthma development is associated with low mucosal IL-10 during viral infections in early life. *Allergy.* 2024;79(11):2981–2992. doi:10.1111/all.16276
20. Indrio F, Gutierrez Castellon P, Vandenplas Y, et al. Health Effects of Infant Formula Supplemented with Probiotics or Synbiotics in Infants and Toddlers: systematic Review with Network Meta-Analysis. *Nutrients.* 2022;14(23):5175. doi:10.3390/nu14235175
21. Alcazar CG, Paes VM, Shao Y, et al. The association between early-life gut microbiota and childhood respiratory diseases: a systematic review. *Lancet Microbe.* 2022;3(11):e867–e880. doi:10.1016/S2666-5247(22)00184-7
22. Chiu CJ, Huang MT. Asthma in the Precision Medicine Era: biologics and Probiotics. *Int J Mol Sci.* 2021;22(9):4528. doi:10.3390/ijms22094528
23. Martins J, Gonçalves R, Branco F. A bibliometric analysis and visualization of e-learning adoption using VOSviewer. *Univers Access Inf Soc.* 2022. doi:10.1007/s10209-022-00953-0
24. Synnæstvedt MB, Chen C, Holmes JH. CiteSpace II: visualization and knowledge discovery in bibliographic databases. *AMIA Annu Symp Proc.* 2005;2005:724–728.
25. Bisgaard H, Phipps CB, Bønnelykke K. Endotyping early childhood asthma by quantitative symptom assessment. *J Allergy Clin Immunol.* 2011;127(5):1155–64.e2. doi:10.1016/j.jaci.2011.02.007
26. Teo SM, Mok D, Pham K, et al. The infant nasopharyngeal microbiome impacts severity of lower respiratory infection and risk of asthma development. *Cell Host Microbe.* 2015;17(5):704–715. doi:10.1016/j.chom.2015.03.008
27. Stokholm J, Blaser MJ, Thorsen J, et al. Maturation of the gut microbiome and risk of asthma in childhood. *Nat Commun.* 2018;9(1):141. doi:10.1038/s41467-017-02573-2
28. Ege MJ, Mayer M, Normand AC, et al. Exposure to environmental microorganisms and childhood asthma. *N Engl J Med.* 2011;364(8):701–709. doi:10.1056/NEJMoa1007302
29. hertz S, Anderson JM, Nielsen HL, et al. Fecal microbiota is associated with extraintestinal manifestations in inflammatory bowel disease. *Ann Med.* 2024;56(1):2338244. doi:10.1080/07853890.2024.2338244
30. Bisgaard H, Hermansen MN, Buchvald F, et al. Childhood asthma after bacterial colonization of the airway in neonates. *N Engl J Med.* 2007;357(15):1487–1495. doi:10.1056/NEJMoa052632
31. Donald K, Finlay BB. Early-life interactions between the microbiota and immune system: impact on immune system development and atopic disease. *Nat Rev Immunol.* 2023;23(11):735–748. doi:10.1038/s41577-023-00874-w
32. Nettle D, Frankenhuis WE. The evolution of life-history theory: a bibliometric analysis of an interdisciplinary research area. *Proc Biol Sci.* 2019;286(1899):20190040. doi:10.1098/rspb.2019.0040
33. Hilty M, Burke C, Pedro H, et al. Disordered microbial communities in asthmatic airways. *PLoS One.* 2010;5(1):e8578. doi:10.1371/journal.pone.0008578
34. Huang YJ, Porsche C, Kozik AJ, Lynch SV. Microbiome-Immune Interactions in Allergy and Asthma. *J Allergy Clin Immunol Pract.* 2022;10(9):2244–2251. doi:10.1016/j.jaip.2022.05.038
35. Cox MJ, Allgaier M, Taylor B, et al. Airway microbiota and pathogen abundance in age-stratified cystic fibrosis patients. *PLoS One.* 2010;5(6):e11044. doi:10.1371/journal.pone.0011044
36. Taylor SL, Leong LEX, Choo JM, et al. Inflammatory phenotypes in patients with severe asthma are associated with distinct airway microbiology. *J Allergy Clin Immunol.* 2018;141(1):94–103.e15. doi:10.1016/j.jaci.2017.03.044
37. Edwards MR, Bartlett NW, Hussell T, Openshaw P, Johnston SL. The microbiology of asthma. *Nat Rev Microbiol.* 2012;10(7):459–471. doi:10.1038/nrmicro2801
38. Ratajczak W, Rył A, Mizerski A, Walczakiewicz K, Sipak O, Laszczyńska M. Immunomodulatory potential of gut microbiome-derived short-chain fatty acids (SCFAs). *Acta Biochim Pol.* 2019;66(1):1–12. doi:10.18388/abp.2018_2648
39. Trompette A, Gollwitzer ES, Yadava K, et al. Gut microbiota metabolism of dietary fiber influences allergic airway disease and hematopoiesis. *Nat Med.* 2014;20(2):159–166. doi:10.1038/nm.3444
40. Li C, Yao J, Yang C, et al. Gut microbiota-derived short chain fatty acids act as mediators of the gut-liver-brain axis. *Metab Brain Dis.* 2025;40(2):122. doi:10.1007/s11011-025-01554-5
41. Sbihi H, Boutin RC, Cutler C, Suen M, Finlay BB, Turvey SE. Thinking bigger: how early-life environmental exposures shape the gut microbiome and influence the development of asthma and allergic disease. *Allergy.* 2019;74(11):2103–2115. doi:10.1111/all.13812
42. Ohno H. Impact of commensal microbiota on the host pathophysiology: focusing on immunity and inflammation. *Semin Immunopathol.* 2015;37(1):1–3. doi:10.1007/s00281-014-0472-2
43. von Mutius E. The “Hygiene Hypothesis” and the Lessons Learnt From Farm Studies. *Front Immunol.* 2021;12:635522. doi:10.3389/fimmu.2021.635522
44. Strachan DP. Hay fever, hygiene, and household size. *BMJ.* 1989;299(6710):1259–1260. doi:10.1136/bmj.299.6710.1259
45. Matricardi PM, Franzinelli F, Franco A, et al. Sibship size, birth order, and atopy in 11,371 Italian young men. *J Allergy Clin Immunol.* 1998;101(4):439–444. doi:10.1016/s0091-6749(98)70350-1
46. Cui P, Lin Q, Ding F, et al. A comparison between ribo-minus RNA-sequencing and polyA-selected RNA-sequencing. *Genomics.* 2010;96(5):259–265. doi:10.1016/j.ygeno.2010.07.010
47. Elie C, Perret M, Hage H, et al. Comparison of DNA extraction methods for 16S rRNA gene sequencing in the analysis of the human gut microbiome. *Sci Rep.* 2023;13(1):10279. doi:10.1038/s41598-023-33959-6
48. Lee JJ, Kim SH, Lee MJ, et al. Different upper airway microbiome and their functional genes associated with asthma in young adults and elderly individuals. *Allergy.* 2019;74(4):709–719. doi:10.1111/all.13608

49. Shi N, Li N, Duan X, Niu H. Interaction between the gut microbiome and mucosal immune system. *Mil Med Res.* 2017;4:14. doi:10.1186/s40779-017-0122-9
50. Wang M, Zhang Y, Li C, Chang W, Zhang L. The relationship between gut microbiota and COVID-19 progression: new insights into immunopathogenesis and treatment. *Front Immunol.* 2023;14:1180336. doi:10.3389/fimmu.2023.1180336
51. Young RP, Hopkins RJ, Marsland B. The Gut-Liver-Lung Axis. Modulation of the Innate Immune Response and Its Possible Role in Chronic Obstructive Pulmonary Disease. *Am J Respir Cell Mol Biol.* 2016;54(2):161–169. doi:10.1165/rcmb.2015-0250PS
52. He Y, Wen Q, Yao F, Xu D, Huang Y, Wang J. Gut-lung axis: the microbial contributions and clinical implications. *Crit Rev Microbiol.* 2017;43(1):81–95. doi:10.1080/1040841X.2016.1176988
53. Heinrich VA, Uvalle C, Manni ML, et al. Meta-omics profiling of the gut-lung axis illuminates metabolic networks and host-microbial interactions associated with elevated lung elastance in a murine model of obese allergic asthma. *Front Microbiomes.* 2023;2:1153691. doi:10.3389/fmibi.2023.1153691
54. Stern J, Pier J, Litonjua AA. Asthma epidemiology and risk factors. *Semin Immunopathol.* 2020;42(1):5–15. doi:10.1007/s00281-020-00785-1
55. Huang YJ, Nariya S, Harris JM, et al. The airway microbiome in patients with severe asthma: associations with disease features and severity. *J Allergy Clin Immunol.* 2015;136(4):874–884. doi:10.1016/j.jaci.2015.05.044
56. Huang YJ, Nelson CE, Brodie EL, et al. Airway microbiota and bronchial hyperresponsiveness in patients with suboptimally controlled asthma. *J Allergy Clin Immunol.* 2011;127(2):372–381.e3813. doi:10.1016/j.jaci.2010.10.048
57. Gasaly N, de Vos P, Hermoso MA. Impact of Bacterial Metabolites on Gut Barrier Function and Host Immunity: a Focus on Bacterial Metabolism and Its Relevance for Intestinal Inflammation. *Front Immunol.* 2021;12:658354. doi:10.3389/fimmu.2021.658354
58. Hachim MY, Alqutami F, Hachim IY, et al. The Role of Systems Biology in Deciphering Asthma Heterogeneity. *Life.* 2022;12(10):1562. doi:10.3390/life12101562
59. Akowicz D, Lou S, Barron B, et al. Approaches for integrating heterogeneous RNA-seq data reveal cross-talk between microbes and genes in asthmatic patients. *Genome Biol.* 2020;21(1):150. doi:10.1186/s13059-020-02033-z
60. Li H, Wang H, Sokulsky L, et al. Single-cell transcriptomic analysis reveals key immune cell phenotypes in the lungs of patients with asthma exacerbation. *J Allergy Clin Immunol.* 2021;147(3):941–954. doi:10.1016/j.jaci.2020.09.032. [published correction appears in *J Allergy Clin Immunol.* 2024 Mar;153(3):876. doi: 10.1016/j.jaci.2023.12.016].
61. Chen CY, Wu KH, Guo BC, et al. Personalized Medicine in Severe Asthma: from Biomarkers to Biologics. *Int J Mol Sci.* 2023;25(1):182. doi:10.3390/ijms25010182

Journal of Multidisciplinary Healthcare

Publish your work in this journal

The Journal of Multidisciplinary Healthcare is an international, peer-reviewed open-access journal that aims to represent and publish research in healthcare areas delivered by practitioners of different disciplines. This includes studies and reviews conducted by multidisciplinary teams as well as research which evaluates the results or conduct of such teams or healthcare processes in general. The journal covers a very wide range of areas and welcomes submissions from practitioners at all levels, from all over the world. The manuscript management system is completely online and includes a very quick and fair peer-review system. Visit <http://www.dovepress.com/testimonials.php> to read real quotes from published authors.

Submit your manuscript here: <https://www.dovepress.com/journal-of-multidisciplinary-healthcare-journal>

Dovepress
Taylor & Francis Group