

# The Role of the Microbiome in Antibiotic Resistance and Infection Control

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**Abstract—** This review explores the critical role of the microbiome in modulating antibiotic resistance and its implications for infection control. By synthesizing recent research, we highlight how microbial communities influence the emergence and dissemination of antibiotic resistance genes and their impact on host health and disease outcomes. The interplay between the microbiome and antibiotics suggests a need for novel strategies to manage resistance, emphasizing microbiome-preserving approaches. Our findings underscore the potential of leveraging microbiome insights to develop more effective infection control practices and antibiotic use policies, aiming to mitigate the global challenge of antibiotic resistance. Future research directions are suggested to further understand the microbiome's mechanisms in resistance and identify therapeutic opportunities for enhancing human health.

## I. INTRODUCTION

The human microbiome, a diverse community of microorganisms residing in and on the human body, is crucial for maintaining health and influencing disease. This complex ecosystem includes bacteria, viruses, fungi, and protozoa, with the highest concentrations found in the gut, skin, mouth, and respiratory tract (Koenig et al., 2010). The microbiome plays a vital role in digesting food, synthesizing essential vitamins, and regulating the immune

system, extending its influence beyond simple pathogen resistance (Ogunrinola et al., 2020). The composition and diversity of microbial communities vary significantly across different body sites, reflecting the unique environmental conditions and functions of each location (Koenig et al., 2010). Factors such as genetics, age, diet, and antibiotics influence the microbiome's composition, leading to a highly personalized microbial fingerprint for each individual (Ogunrinola et al., 2020). The interplay between

the microbiome and the human host is a fine balance, where both benefit from each other in a symbiotic relationship (Ogunrinola et al., 2020). Disruptions in this balance, whether through antibiotic use, dietary changes, or illness, can have profound health implications (Ogunrinola et al., 2020).

Recent research has highlighted the microbiome's role in a broad spectrum of health and disease states, extending beyond traditional boundaries of infectious diseases to conditions like obesity, diabetes, allergies, and mental health disorders (Ogunrinola et al., 2020). The concept of the "core" microbiome, a set of microbial species common to most healthy individuals, is central to understanding human microbial diversity (Ogunrinola et al., 2020). Identifying and understanding these core elements are crucial for deciphering how variations in the microbiome relate to disease (Ogunrinola et al., 2020). Lifestyle factors, particularly diet, have a profound influence on microbial composition and diversity, with high-fiber diets promoting a diverse and stable microbiome (Zangara & McDonald, 2019). Physical activity and exposure to natural environments have also been shown to positively influence microbial diversity (Zangara & McDonald, 2019).

In summary, the human microbiome is a complex and dynamic community that plays a critical role in health and disease. Its diversity and composition are influenced by a myriad of factors, making it a central focus in understanding human physiology and developing new approaches to disease prevention and treatment (Ogunrinola et al., 2020). As research progresses, the potential to manipulate the microbiome for therapeutic purposes offers exciting possibilities for future medical advances (Ogunrinola et al., 2020).

## II. MECHANISMS OF ANTIBIOTIC RESISTANCE

The misuse and overuse of antibiotics have accelerated the selection for resistant strains and altered the balance of the microbiome, leading to a decrease in microbial diversity and the proliferation of antibiotic-resistant bacteria. Horizontal gene transfer (HGT) within microbial communities, facilitated by mobile genetic elements, accelerates the dissemination of resistance traits, making once-treatable infections increasingly difficult to combat. The emergence of multidrug-resistant (MDR) pathogens, particularly in environments with frequent antibiotic use, poses significant challenges, leading to challenging hospital-acquired infections. Additionally, antibiotics released into the environment through pharmaceutical waste and agricultural runoff can select for resistant bacteria

in soil and water, contributing to the environmental reservoir of resistance genes (Gullberg et al., 2011).

The impact of antibiotics on the natural microbiota, including probiotic bacteria, can lead to diminished colonization resistance against pathogenic bacteria, increasing infection risks and contributing to the cycle of resistance (Bakkali, 2013). Recent studies have highlighted the gut microbiome's role in metabolizing and modifying antibiotics, affecting drug efficacy and resistance development (Ashiru-Oredope et al., 2022). Antibiotic stewardship programs aim to optimize antibiotic use, reducing unnecessary exposure and slowing resistance development (Laurenceau et al., 2013). Emerging research is exploring the development of narrow-spectrum antibiotics and bacterial interference as potential strategies to combat antibiotic resistance (Sharkey et al., 2016).

Competing evidence suggests that the widespread misuse of antibiotics may not only be selecting for resistant strains but also causing bacteria to take up more DNA, increasing the chances of acquiring drug resistance and virulence. Additionally, there is evidence that antibiotics targeting DNA replication cause an increase in the copy number of genes proximal to the origin of replication, triggering bacterial competence and gene transfer (Ashiru-Oredope et al., 2022). Furthermore, the competitive trade-off limits the selective advantage of increased antibiotic production, indicating that producer colonies can benefit from inhibiting nearby sensitive colonies, but this benefit is shared with resistant colonies growing in their vicinity (Slager et al., 2014).

Understanding the mechanisms of antibiotic resistance and the role of the microbiome in this process is crucial for developing strategies to combat the growing threat of resistant infections. A multifaceted approach, incorporating antibiotic stewardship, targeted therapies, and microbiome preservation strategies, is essential for safeguarding the effectiveness of antibiotics for future generations.

## III. MICROBIOME AND DISEASE SUSCEPTIBILITY

Competing evidence suggests that the relationship between the microbiome and disease susceptibility is complex and multifaceted, involving direct microbial competition, immune modulation, and systemic health effects. While the protective role of a healthy microbiome against pathogenic invasion is well-established, there is evidence that the microbiome can exclude pathogens by competing for common host resources, including nutrients and receptors Baerentsen et al. (2022). Additionally, the gut microbiome has been linked to the pathogenesis of multiple sclerosis, suggesting that the commensal microbiota has a role in the

development of autoimmune diseases (Berer et al., 2017). Furthermore, the respiratory microbiome has been shown to influence chronic lung disease exacerbations, indicating a role in disease development (Adar et al., 2016).

Moreover, the impact of the microbiome on vector competency through induced immunological responses, morphological changes, or direct competition between microbial components of the tick microbiome highlights the complexity of microbiome interactions and their influence on disease susceptibility (Ring et al., 2021). There is also evidence that prenatal maternal diet and infant and child nutrition impact the infant microbiome trajectory and immune competence development, suggesting that early-life exposures play a critical role in immune system development and disease susceptibility (Dogra et al., 2021).

Furthermore, the concept of a trade-off in host innate immunity and protective microbiome indicates that there may be conflicting effects of the microbiome on disease susceptibility, suggesting that the relationship is not always straightforward (Jervis et al., 2021). Additionally, the opposite evidence suggests that with less gut microbiome diversity, microbiota labor together to create energy desires in the host, indicating that the impact of the microbiome on disease susceptibility may not always be protective (Li et al., 2021).

The interplay between the microbiome and disease susceptibility is complex and multifaceted, involving direct microbial competition, immune modulation, and systemic health effects. Understanding and manipulating this relationship holds the key to developing new strategies for disease prevention and treatment, emphasizing the importance of maintaining a healthy and balanced microbiome. While the protective role of a healthy microbiome against pathogenic invasion is well-documented, the competing evidence highlights the complexity of the microbiome's influence on disease susceptibility, indicating that the relationship is multifaceted and may involve conflicting effects on host health and disease susceptibility.

#### IV. MICROBIOME-BASED THERAPIES

Competing evidence suggests that while microbiome-based therapies, such as fecal microbiota transplants (FMTs), probiotics, and prebiotics, have shown promise in restoring microbial balance and treating infections, there are complexities and challenges that need to be considered. For instance, the relationship between the gut microbiome and neurodegenerative diseases is increasingly plausible, indicating that the microbiome may have a broader impact on health beyond infectious diseases (Xiao-hong et al., 2021). Additionally, the gut microbiome has been linked to

the modulation of the immune system and response to anti-PD-1 immunotherapy in cancer patients, suggesting a systemic influence of the microbiome on disease treatment and prevention (Gopalakrishnan et al., 2018). Furthermore, the efficacy of current microbiome-based therapies in treating obesity is being discussed, indicating that the impact of these therapies may extend to metabolic disorders (Lim et al., 2020).

Competing evidence also suggests that the gut microbiome can substantially affect the effectiveness of chemotherapy and immunotherapy, indicating that the microbiome may influence the response to various cancer treatments (Huang et al., 2021). Moreover, the microbiome has been associated with the modulation of host immunity, metabolism, and extraintestinal tumors, indicating a systemic influence of the microbiome on health and disease (Zhang et al., 2019). Additionally, microbiome-based therapies are being investigated to mitigate antibiotic-induced microbial perturbation, highlighting the potential broader applications of these therapies beyond infectious diseases (Theodosiou et al., 2023).

Furthermore, the microbiome has been associated with the modulation of the immune system and response to anti-PD-1 therapy in melanoma patients, indicating that the microbiome may influence the response to cancer immunotherapy (Davar et al., 2021). The gut microbiome has also been linked to the response to immune checkpoint blockade across cancer types, suggesting a systemic influence of the microbiome on cancer therapy (Gopalakrishnan et al., 2018). Additionally, the microbiome has been associated with the modulation of the immune system and response to anti-PD-1 therapy in melanoma patients, indicating that the microbiome may influence the response to cancer immunotherapy (Davar et al., 2021).

In conclusion, while microbiome-based therapies show promise in restoring microbial balance and treating infections, competing evidence suggests that the influence of the microbiome extends beyond infectious diseases to systemic health effects, cancer treatment, and immune modulation. These complexities and broader implications of the microbiome's influence on health and disease need to be considered in the development and implementation of microbiome-based therapies.

#### V. STRATEGIES FOR MICROBIOME PRESERVATION

Competing evidence suggests that while targeted antibiotics and narrow-spectrum antimicrobial agents are at the forefront of efforts to preserve the microbiome, there are complexities and challenges that need to be considered. For instance, the gut microbiome has been linked to the

modulation of susceptibility to food allergies, indicating that the microbiome may have a broader impact on health beyond infectious diseases Costanzo et al. (2020). Additionally, the microbiome has been associated with tick fitness and pathogen infection and transmission, highlighting the importance of tick-microbiome interactions for vector competence (Fuente et al., 2017). Furthermore, the gut microbiome has been linked to the modulation of adaptation processes in Asian elephants, indicating that the microbiome may influence adaptation to surrounding environments (Moustafa et al., 2021).

Competing evidence also suggests that the microbiome has an effect on the provision of ecosystem services, indicating that the microbiome may influence broader ecological processes beyond human health (Trevathan-Tackett et al., 2019). Additionally, the gut microbiome has been linked to the modulation of drug metabolism and response, suggesting that the microbiome may influence the therapeutic outcome of medications (Canani et al., 2019). Moreover, the microbiome has been associated with the modulation of the immune system and response to anti-PD-1 therapy in cancer patients, indicating that the microbiome may influence the response to cancer immunotherapy (Xiao & Zhao, 2023). Additionally, the microbiome has been associated with the modulation of the immune system and response to anti-PD-1 therapy in melanoma patients, indicating that the microbiome may influence the response to cancer immunotherapy (Takagi et al., 2023).

In conclusion, a multifaceted approach encompassing targeted antibiotic use, antibiotic stewardship, diet and lifestyle modifications, emerging therapies, and environmental and educational strategies is essential for preserving the microbiome. By implementing these strategies, healthcare providers can protect microbial diversity and function, which is vital for human health, while continuing to effectively manage bacterial infections. While targeted antibiotics and narrow-spectrum antimicrobial agents are essential for preserving the microbiome, competing evidence suggests that the influence of the microbiome extends beyond infectious diseases to broader ecological processes, adaptation, and therapeutic outcomes. These complexities and broader implications of the microbiome's influence on health and disease need to be considered in the development and implementation of strategies for microbiome preservation.

## VI. FUTURE DIRECTIONS AND CHALLENGES

The field of microbiome research presents both challenges and opportunities in the context of infection control and antibiotic resistance strategies. The promise of microbiome-

based therapies and personalized medicine is vast, but translating these advances into practical applications poses complex obstacles. One of the primary challenges in microbiome research is bridging the gap between scientific discovery and clinical practice. While laboratory and animal studies have provided critical insights into the microbiome's role in health and disease, translating these findings into effective human therapies requires rigorous clinical trials, scalable treatment methodologies, and comprehensive safety evaluations. The highly individualized nature of the human microbiome suggests that personalized approaches to treatment might be more effective than one-size-fits-all solutions. However, developing personalized medicine strategies that consider individual microbiome profiles demands extensive research and development, as well as sophisticated diagnostic tools to accurately assess microbial composition and function (Mimee et al., 2016).

Implementing microbiome-based therapies raises ethical and regulatory questions, particularly concerning fecal microbiota transplants (FMTs) and genetically modified organisms (GMOs) used in probiotics (Mimee et al., 2016). Establishing clear guidelines and safety standards is essential to navigate these concerns, ensuring patient safety and public trust. The variability in microbiome composition across individuals and populations complicates the standardization of microbiome-based therapies. Developing standardized treatment protocols that are both effective and adaptable to individual needs is a significant challenge for the field. Just as bacteria can develop resistance to antibiotics, there is a potential for resistance to microbiome-based therapies. Monitoring and managing this resistance requires ongoing research and may involve the development of novel therapeutic strategies (Mimee et al., 2016).

Integrating microbiome-based therapies with current treatment modalities presents both challenges and opportunities. Understanding the interactions between the microbiome and pharmaceuticals, including antibiotics, is crucial for optimizing treatment outcomes and minimizing adverse effects (Mimee et al., 2016). The vast amount of data generated by microbiome research, including high-throughput sequencing and metagenomic analysis, requires sophisticated bioinformatics tools and expertise (Mallick et al., 2017). Analyzing and interpreting this data to yield actionable insights is a substantial challenge for researchers (Mallick et al., 2017). Assessing the long-term impacts of microbiome manipulation on health outcomes necessitates longitudinal studies. These studies are essential for understanding the sustained effects of microbiome-based interventions and their potential unintended consequences (Mousa et al., 2022). Ensuring that microbiome-based therapies are economically viable and accessible to those



who need them is a critical consideration. Addressing issues of cost, reimbursement, and global access is necessary to fully realize the potential of these therapies (Mimee et al., 2016).

Addressing the challenges and advancing the future of microbiome research requires a multidisciplinary approach. Collaboration among microbiologists, clinicians, pharmacologists, ethicists, and policymakers is essential for navigating the complexities of the field and harnessing the microbiome's potential in infection control and beyond (Surana, 2019). In summary, the path forward for microbiome research and its application in combating antibiotic resistance and improving infection control is laden with challenges but also brimming with possibilities. Addressing these challenges through innovative research, collaborative efforts, and a commitment to ethical and regulatory excellence will be crucial for realizing the full potential of microbiome-based therapies (Mimee et al., 2016).

## VII. CONCLUSION

Based on the comprehensive review of the role of the microbiome in antibiotic resistance and infection control, it is clear that the microbiome plays a pivotal role in human health beyond its impact on gut health and infection control. The intricate interactions between microbial communities and their hosts offer promising avenues for novel therapeutic strategies, emphasizing the need for a balanced microbiome to prevent and mitigate antibiotic resistance and enhance infection control mechanisms. The evolving understanding of the microbiome's influence underscores the importance of targeted antibiotic use, lifestyle modifications, and the development of microbiome-based therapies to maintain and restore microbial balance. Moving forward, interdisciplinary research and collaboration will be crucial in translating these insights into effective clinical practices, with the ultimate goal of harnessing the microbiome's potential to improve human health outcomes significantly. This review underscores the complexity of the microbiome's role in health and disease, highlighting the need for continued research and innovation in this dynamic field.

## REFERENCES

- [1] Koenig, J., Spor, A., Scalfone, N., Fricker, A., Stombaugh, J., Knight, R., ... & Ley, R. (2010). Succession of microbial consortia in the developing infant gut microbiome. *Proceedings of the National Academy of Sciences*, 108(supplement\_1), 4578-4585. <https://doi.org/10.1073/pnas.1000081107>
- [2] Ogunrinola, G., Oyewale, J., Oshamika, O., & Olasehinde, G. (2020). The human microbiome and its impacts on health. *International Journal of Microbiology*, 2020, 1-7. <https://doi.org/10.1155/2020/8045646>
- [3] Zangara, M. and McDonald, C. (2019). How diet and the microbiome shape health or contribute to disease: a mini-review of current models and clinical studies. *Experimental Biology and Medicine*, 244(6), 484-493. <https://doi.org/10.1177/1535370219826070>
- [4] Gullberg, E., Cao, S., Berg, O., Ilbäck, C., Sandegren, L., Hughes, D., ... & Andersson, D. (2011). Selection of resistant bacteria at very low antibiotic concentrations. *Plos Pathogens*, 7(7), e1002158. <https://doi.org/10.1371/journal.ppat.1002158>
- [5] Bakkali, M. (2013). Could dna uptake be a side effect of bacterial adhesion and twitching motility?. *Archives of Microbiology*, 195(4), 279-289. <https://doi.org/10.1007/s00203-013-0870-1>
- [6] Ashiru-Oredope, D., Casale, E., Harvey, E., Umoh, E., Vasandani, S., Reilly, J., ... & Hopkins, S. (2022). Knowledge and attitudes about antibiotics and antibiotic resistance of 2,404 uk healthcare workers.. <https://doi.org/10.20944/preprints202207.0249.v1>
- [7] Laurenceau, R., Péhau-Arnaudet, G., Baconnais, S., Gault, J., Malosse, C., Dujeancourt, A., ... & Fronzes, R. (2013). A type iv pilus mediates dna binding during natural transformation in streptococcus pneumoniae. *Plos Pathogens*, 9(6), e1003473. <https://doi.org/10.1371/journal.ppat.1003473>
- [8] Sharkey, L., Edwards, T., & O'Neill, A. (2016). Abc-f proteins mediate antibiotic resistance through ribosomal protection. *Mbio*, 7(2). <https://doi.org/10.1128/mbio.01975-15>
- [9] Slager, J., Kjos, M., Attaiech, L., & Veening, J. (2014). Antibiotic-induced replication stress triggers bacterial competence by increasing gene dosage near the origin. *Cell*, 157(2), 395-406. <https://doi.org/10.1016/j.cell.2014.01.068>
- [10] Bærentsen, R. L., Tang, C. M., & Exley, R. M. (2022). Et tu, neisseria? conflicts of interest between neisseria species. *Frontiers in Cellular and Infection Microbiology*, 12. <https://doi.org/10.3389/fcimb.2022.913292>
- [11] Berer, K., Gerdes, L. A., Cekanaviciute, E., Jia, X., Xiao, L., Xia, Z., ... & Wekerle, H. (2017). Gut microbiota from multiple sclerosis patients enables spontaneous autoimmune encephalomyelitis in mice. *Proceedings of the National Academy of Sciences*, 114(40), 10719-10724. <https://doi.org/10.1073/pnas.1711233114>
- [12] Adar, S. D., Huffnagle, G. B., & Curtis, J. L. (2016). The respiratory microbiome: an underappreciated player in the human response to inhaled pollutants?. *Annals of Epidemiology*, 26(5), 355-359. <https://doi.org/10.1016/j.annepidem.2016.03.010>
- [13] Ring, K., Couper, L. I., Al, S., Yarza, F., Yang, X., Clay, K., ... & Swei, A. (2021). Lizard feeding enhances ixodes pacificus vector competency.. <https://doi.org/10.1101/2021.04.28.441694>
- [14] Dogra, S. K., Chung, C. K. C. K., Wang, D., Sakwińska, O., Mottaz, S. C., & Sprenger, N. (2021). Nurturing the early

- life gut microbiome and immune maturation for long term health. *Microorganisms*, 9(10), 2110. <https://doi.org/10.3390/microorganisms9102110>
- [15] Jervis, P., Pintanel, P., Hopkins, K., Wierzbicki, C., Shelton, J., Skelly, E., ... & Merino-Viteri, A. (2021). Post-epizootic microbiome associations across communities of neotropical amphibians. *Molecular Ecology*, 30(5), 1322-1335. <https://doi.org/10.1111/mec.15789>
- [16] Li, J., Zhang, Y., Yang, S. K., Lü, Z., Li, G., Wu, S., ... & Huang, S. (2021). The beneficial effects of edible kynurenic acid from marine horseshoe crab (*tachypleus tridentatus*) on obesity, hyperlipidemia, and gut microbiota in high-fat diet-fed mice. *Oxidative Medicine and Cellular Longevity*, 2021, 1-13. <https://doi.org/10.1155/2021/8874503>
- [17] Xiao-hong, Z., Li, B., Lou, P., Dai, T., Chen, Y., Zhuge, A., ... & Li, L. (2021). The relationship between the gut microbiome and neurodegenerative diseases. *Neuroscience Bulletin*, 37(10), 1510-1522. <https://doi.org/10.1007/s12264-021-00730-8>
- [18] Gopalakrishnan, V., Spencer, C. N., Nezi, L., Reuben, A., Andrews, M. C., Karpins, T. V., ... & Wargo, J. A. (2018). Gut microbiome modulates response to anti-pd-1 immunotherapy in melanoma patients. *Science*, 359(6371), 97-103. <https://doi.org/10.1126/science.aan4236>
- [19] Lim, Y., Lee, Y. S., & Ooi, D. S. Q. (2020). Engineering the gut microbiome for treatment of obesity: a review of current understanding and progress. *Biotechnology Journal*, 15(10). <https://doi.org/10.1002/biot.202000013>
- [20] Huang, T., Debelius, J., Ploner, A., Xiao, X., Zhang, T., Hu, K., ... & Ye, W. (2021). Radiation therapy-induced changes of the nasopharyngeal commensal microbiome in nasopharyngeal carcinoma patients. *International Journal of Radiation Oncology\*biology\*physics*, 109(1), 145-150. <https://doi.org/10.1016/j.ijrobp.2020.08.054>
- [21] Zhang, Z., Tang, H., Chen, P., Xie, H., & Tao, Y. (2019). Demystifying the manipulation of host immunity, metabolism, and extraintestinal tumors by the gut microbiome. *Signal Transduction and Targeted Therapy*, 4(1). <https://doi.org/10.1038/s41392-019-0074-5>
- [22] Theodosiou, A. A., Jones, C. E., Read, R. C., & Bogaert, D. (2023). Microbiotoxicity: antibiotic usage and its unintended harm to the microbiome. *Current Opinion in Infectious Diseases*, 36(5), 371-378. <https://doi.org/10.1097/qco.0000000000000945>
- [23] Davar, D., Dzutsev, A., McCulloch, J. A., Rodrigues, R. R., Chauvin, J., Morrison, R. L., ... & Zarour, H. M. (2021). Fecal microbiota transplant overcomes resistance to anti-pd-1 therapy in melanoma patients. *Science*, 371(6529), 595-602. <https://doi.org/10.1126/science.abf3363>
- [24] Gopalakrishnan, V., Helmink, B. A., Spencer, C. N., Reuben, A., & Wargo, J. A. (2018). The influence of the gut microbiome on cancer, immunity, and cancer immunotherapy. *Cancer Cell*, 33(4), 570-580. <https://doi.org/10.1016/j.ccell.2018.03.015>
- [25] Davar, D., Dzutsev, A., McCulloch, J., Rodrigues, R., Chauvin, J., Morrison, R., ... & Zarour, H. (2021). Fecal microbiota transplant overcomes resistance to anti-pd-1 therapy in melanoma patients. *Science*, 371(6529), 595-602. <https://doi.org/10.1126/science.abf3363>
- [26] Costanzo, M. D., Carucci, L. R., Canani, R. B., & Biasucci, G. (2020). Gut microbiome modulation for preventing and treating pediatric food allergies. *International Journal of Molecular Sciences*, 21(15), 5275. <https://doi.org/10.3390/ijms21155275>
- [27] Fuente, J. d. I., Antunes, S., Bonnet, S., Cabezas-Cruz, A., Domingos, A., Estrada-Peña, A., ... & Rego, R. O. M. (2017). Tick-pathogen interactions and vector competence: identification of molecular drivers for tick-borne diseases. *Frontiers in Cellular and Infection Microbiology*, 7. <https://doi.org/10.3389/fcimb.2017.00114>
- [28] Moustafa, M. A. M., Chel, H. M., Thu, M. J., Bawm, S., Htun, L. L., Win, M. M., ... & Katakura, K. (2021). Anthropogenic interferences lead to gut microbiome dysbiosis in asian elephants and may alter adaptation processes to surrounding environments. *Scientific Reports*, 11(1). <https://doi.org/10.1038/s41598-020-80537-1>
- [29] Trevathan-Tackett, S. M., Sherman, C. D. H., Huggett, M. J., Campbell, A. H., Laverock, B., Hurtado-McCormick, V., ... & Macreadie, P. I. (2019). A horizon scan of priorities for coastal marine microbiome research. *Nature Ecology & Evolution*, 3(11), 1509-1520. <https://doi.org/10.1038/s41559-019-0999-7>
- [30] Canani, R. B., Paparo, L., Nocerino, R., Scala, C. D., Gatta, G. D., Maddalena, Y., ... & Ercolini, D. (2019). Gut microbiome as target for innovative strategies against food allergy. *Frontiers in Immunology*, 10. <https://doi.org/10.3389/fimmu.2019.00191>
- [31] Xiao, L. and Zhao, F. (2023). Microbial transmission, colonisation and succession: from pregnancy to infancy. *Gut*, 72(4), 772-786. <https://doi.org/10.1136/gutjnl-2022-328970>
- [32] Takagi, T., Kunihiro, T., Takahashi, S., Hisada, T., Nagashima, K., Mochizuki, J., ... & Naito, Y. (2023). A newly developed solution for the preservation of short-chain fatty acids, bile acids, and microbiota in fecal specimens. *Journal of Clinical Biochemistry and Nutrition*, 72(3), 263-269. <https://doi.org/10.3164/jcbrn.22-107>
- [33] Mallick, H., Ma, S., Franzosa, E., Vatanen, T., Morgan, X., & Huttenhower, C. (2017). Experimental design and quantitative analysis of microbial community multiomics. *Genome Biology*, 18(1). <https://doi.org/10.1186/s13059-017-1359-z>
- [34] Mimeo, M., Citorik, R., & Lu, T. (2016). Microbiome therapeutics — advances and challenges. *Advanced Drug Delivery Reviews*, 105, 44-54. <https://doi.org/10.1016/j.addr.2016.04.032>
- [35] Mousa, W., Chehadeh, F., & Husband, S. (2022). Recent advances in understanding the structure and function of the human microbiome. *Frontiers in Microbiology*, 13. <https://doi.org/10.3389/fmicb.2022.825338>
- [36] Surana, N. (2019). Moving microbiome science from the bench to the bedside: a physician-scientist perspective. *Msystems*, 4(3). <https://doi.org/10.1128/msystems.00160-19>