

## Special Issue

# Molecular Research in Bacterial Vaginosis

### Message from the Guest Editor

Bacterial vaginosis (BV) is a common and often recurrent disease. It is a polymicrobial disease, but the main causative agent is *Gardnerella vaginalis*. Molecular studies have shown genetic heterogeneity and taxonomic diversity within the genus *Gardnerella*. At least 13 distinct groups were found, and they were classified as separate species within the taxon formerly known as *G. vaginalis*. These *Gardnerella* species are closely related genetically; only some of them (pathogenic) can be associated with BV, and non-pathogenic species are found in healthy women. Thanks to the methods of PCR, hybridization and sequencing, it has become possible to quantitatively detect and accurately identify bacteria, including those associated with BV. Combining the efforts of the scientific community in the search for genetic markers of recurrent forms of BV using molecular research methods will allow us to understand the frequent recurrence of BV as well as determine the composition of biofilms formed by *G. vaginalis* and BV-associated microorganisms. In this Special Issue, we want to demonstrate the huge potential of research in the field of molecular studies of BV.

### Guest Editor

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### Deadline for manuscript submissions

closed (20 January 2025)



## International Journal of Molecular Sciences

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Impact Factor 4.9  
CiteScore 9.0  
Indexed in PubMed



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*International Journal of  
Molecular Sciences*  
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The International Journal of Molecular Sciences (*IJMS*, ISSN 1422-0067) is an open access journal, which was established in 2000. The journal aims to provide a forum for scholarly research on a range of topics, including biochemistry, molecular and cell biology, molecular biophysics, molecular medicine, and all aspects of molecular research in chemistry. *IJMS* publishes both original research and review articles, and regularly publishes special issues to highlight advances at the cutting edge of research. We invite you to read recent articles published in *IJMS* and consider publishing your next paper with us.

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### Editor-in-Chief

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