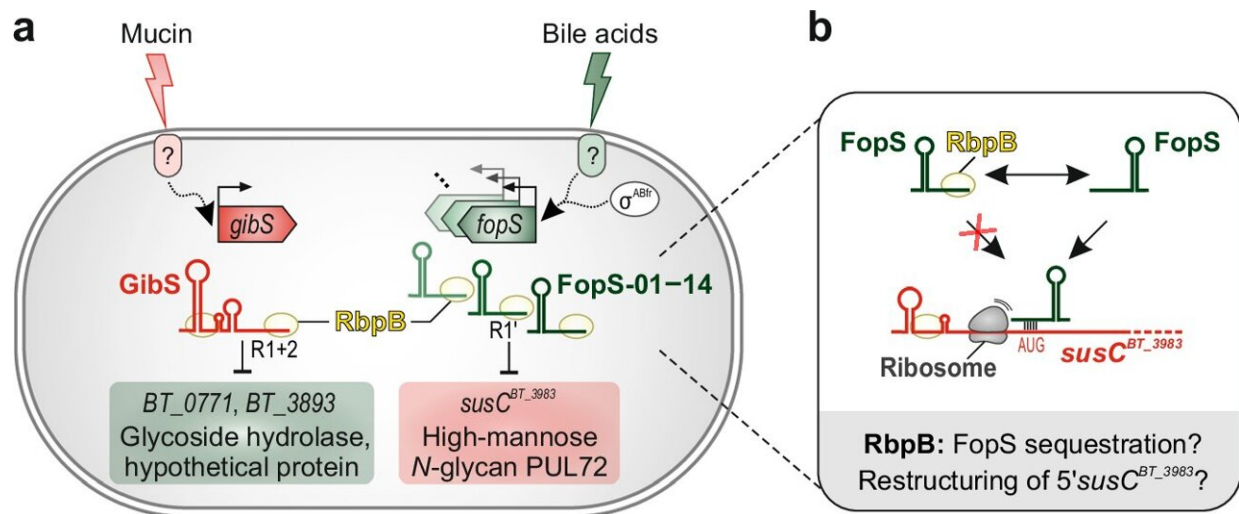


# RNA's influence on sugar metabolism could transform gut health strategies

January 9 2025, by Charlotte Schwenner



Working model for the functional diversification between RbpB-associated sRNAs—GibS and the FopS sRNA cluster—in *B. thetaioaomicron* metabolism control. Credit: *Nature Communications* (2025). DOI: 10.1038/s41467-024-55383-8

Researchers at the Helmholtz Institute for RNA-based Infection Research (HIRI) and the Julius-Maximilians-Universität (JMU) in Würzburg have identified a protein and a group of small ribonucleic acids (sRNAs) in *Bacteroides thetaioaomicron*, which regulate sugar metabolism. These discoveries shed light on how this gut microbe adapts to varying nutritional conditions.

The findings deepen our understanding of this bacterium's role in the [human gut](#) and may pave the way for new therapeutic strategies to promote health through the microbiota. The study was [published](#) in the journal *Nature Communications*.

The gut plays a vital role in human health. The composition of the microbiota and its functions for human well-being are heavily influenced by how well bacteria adjust to the constantly shifting intestinal environment. The question of how intestinal commensals adapt their metabolism to daily nutrient fluctuations has therefore become a central topic of microbiota research.

Although the gut's microbial ecosystem varies from person to person, several species can be found prevalently. One such species is *Bacteroides thetaiotaomicron*. These microbes possess dozens of different multiprotein complexes encoded at specific sites in the genome called polysaccharide utilization loci (PULs). PUL complexes enable the bacteria to bind, break down, and import specific polysaccharides, thus contributing to their successful gut colonization.

The production of PUL complexes is tightly controlled at the transcriptional level. However, how PULs are regulated post-transcriptionally to adapt to environmental changes remains largely unexplored.

Scientists at the Helmholtz Institute for RNA-based Infection Research (HIRI) in Würzburg, a site of the Braunschweig Helmholtz Center for Infection Research (HZI) in cooperation with the Julius-Maximilians-Universität Würzburg (JMU), and of the Chair of Microbiology at JMU have taken up this challenge. In collaboration with Vanderbilt University in Nashville, Tennessee (U.S.), and the University of Toronto in Canada, they have made significant progress through a series of in vitro and in vivo experiments.

"Our investigations revealed a remarkably complex RNA-based regulatory circuit governing PUL expression in *B. thetaiotaomicron*," says corresponding author Alexander Westermann. "This complements previous work focusing on transcriptional control mechanisms."

## **A complex network**

At the heart of this network is the RNA-binding protein RbpB. "We found that the absence of RbpB significantly impairs intestinal colonization," says Ann-Sophie Rüttiger, first author of the study and Ph.D. student in Alexander Westermann's laboratory.

The functional analysis revealed that RbpB interacts with hundreds of cellular transcripts. These include a group of paralogous non-coding RNA molecules (family of paralogous sRNAs, FopS for short) with 14 members. Together, RbpB and FopS control catabolic processes and ensure that the microbes can optimally adapt to changing nutrient conditions.

"This study contributed to our understanding of RNA-coordinated metabolic control, which is crucial for the fitness of dominant microbiota species," adds Rüttiger.

Future studies will investigate the structure of RbpB in more detail and identify the key mechanisms for RNA binding. The team also plans to examine the functional similarities between RbpB and other RNA-binding proteins to uncover central post-transcriptional hubs in other gut microbiota species.

In-depth knowledge of bacterial gene and protein functions could significantly contribute to the development of new therapeutic approaches to combat infectious and intestinal diseases as well as to promote health through the manipulation of the bioactivities of the gut

microbiota. "Our results offer a promising approach to better understand this microbial consortium and to exploit it for new treatment strategies," concludes Westermann.

**More information:** Ann-Sophie Rüttiger et al, The global RNA-binding protein RbpB is a regulator of polysaccharide utilization in *Bacteroides thetaiotaomicron*, *Nature Communications* (2025). [DOI: 10.1038/s41467-024-55383-8](https://doi.org/10.1038/s41467-024-55383-8)

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