













The Need for Standardization in Metagenomics

In recent years, accelerated advancements in sequencing technology have facilitated the metagenomic analysis of microbial communities. In turn, these studies have enabled a comprehensive understanding of microbial diversity and abundance within the human

microbiome as well as how these communities contribute to human health and disease. However, though this burgeoning field of research has the potential to become one of the most important tools for personalized health and precision medicine, it is still limited by the challenges associated with the lack of standardization.

In every stage of a metagenomics investigation, bias can be introduced, which may lead to data misinterpretation. To minimize this issue, reference materials can be used to standardize common methods and techniques used in microbiome analyses, including nucleic acid extraction, 16S rRNA sequencing, whole-genome sequencing, next-generation sequencing, library preparation, and establishing limits of detection.

To support the need for standardization, ATCC offers a number of microbial cultures isolated from human clinical samples, including <u>anaerobic bacterial strains</u>. These strains are fully authenticated and characterized, and are provided with historical information, growth media formulations, atmospheric growth conditions, and expert technical advice. Browse these strains and the rest of our human clinical isolates <u>online</u>.

Also, stay tuned for our upcoming microbiome reference standards, which comprise fully sequenced, characterized, and authenticated mock microbial communities representing mixed samples. If you'd like to be a part of the design and development process, tell us about your research needs for metagenomic controls!

Submit your feedback now!



Webinar: The Biology of Anaerobic Bacteria and Predominant **Propagation Practices**

In this webinar, Ms. Faust, Senior Biologist, ATCC and Ms. Krueger, Senior Biologist, ATCC will discuss the various methods used to achieve successful growth conditions for a wide variety of anaerobes. Here, they will expand on common gas mixtures, media selection, and how to obtain anaerobic conditions in the lab.

November 3, 2016 12:00 PM ET

Register for the webinar



Zika Virus Research Solutions

ATCC is supporting Zika virus research efforts, such as vaccine efficacy testing and the development of detection assays, with an expanding collection of Zika virus reference

materials and solutions. Our growing collection includes in vivo and tissue culture-adapted strains, genomic and synthetic nucleic acid preparations, host cell lines and reagents, and custom solutions for expansion, titering, and banking.

Check out our growing list of products



Ouiz the Scientist

I am a Gram-negative obligate anaerobe that inhabits the human colon. I am one of the most common species isolated in Bacteroidaceae infections. Can you guess what I

am?

Click here for more clues.



Test your microbial

expertise with the ATCC puzzle!

Download the puzzle

Publications

- ATCC[®] Culture Guides
- Human Anaerobes for Microbiome Research
- Synthetic Nucleic Acids for the Development and Evaluation of in vitro Diagnostic Devices Designed to Detect

Still puzzled?

View the answers to last month's puzzle

Dengue, Chikungunya, and Zika

Frequently Asked Questions

Q: If I do not have an anaerobe chamber, what is the best way for me to open and rehydrate an anaerobic culture?

A: If all that is available for use is anaerobe jar or gas pack and not an anaerobe chamber, in many cases, you should still be able to open the culture. The day before opening the culture vial, add a little cysteine solution (or other reducing agent) to the broth which will be used for rehydration. The broth and plates should then be left in the jar overnight with a gas pack to pre-reduce (the broth caps should be loose)...read more.

Have more questions?

Quality Control

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Microbiology Resources

View from the Petri Dish

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