STANDARDIZE YOUR WORKFLOW AND OPTIMIZE ASSAY PERFORMANCE
ATCC® Microbiome Standards allow you to optimize your metagenomics research applications with confidence, and improve the consistency and reproducibility of your data run after run. From sample collection to data analysis, ATCC offers a variety of tools to support your microbiome research, including:

- Mock microbial communities
- Microbiome spike-in controls
- Site-specific microbiome standards
- Environmental and pathogen mixtures
- Individual strains and nucleic acids
- State-of-the-art bioinformatics
- Customized solutions

ATCC® Microbiome Standards are the only reference materials on the market completely manufactured from high-quality ATCC® Genuine Cultures that are characterized by polyphasic testing, fully sequenced, and published in various databases.

HARMONIZE GLOBAL RESEARCH EFFORTS WITH THE RIGHT CONTROLS
ATCC® Microbiome Standards support a broad array of applications ranging from method optimization to data interpretation and serve as superior full process and daily run controls for microbial community testing and assay development on any platform. To best support your research, ATCC® Microbiome Standards are provided in a variety of formats and levels of complexity:

- Whole cell and nucleic acid preparations
- Even or staggered gDNA abundance
- Low, medium, or high levels of mock community complexity
- Quantified mixtures comprising 3 to 20 strains per sample

The robust applicability of these controls, combined with ATCC’s commitment to authentication and characterization, make ATCC® Microbiome Standards the ideal tool for standardizing data from a wide range of sources and generating consensus among microbiome applications and analyses.

WHAT CAN YOU EXPECT FROM ATCC® MICROBIOME STANDARDS?
ATCC® Microbiome Standards are fully sequenced, characterized, and authenticated mock microbial communities that mimic mixed metagenomics samples. Each community is prepared from ATCC® Genuine Cultures that have been selected for relevant phenotypic and genomic attributes such as:

- Gram stain
- GC content
- Genome size
- Spore formation
- DNA/RNA genome
- Envelope
- Genome shape
- ITS variability
- Clinical relevance
- Diagnostic relevance
- Aerobic/anaerobic
- Ability to lyse

These standards enable the optimization of metagenomics workflows and microbiome research applications, providing reliable comparative data while improving assay consistency.

Order online at www.atcc.org/Microbiome
ENHANCE YOUR RESEARCH AND APPLICATIONS WITH CONFIDENCE

The complexities involved in 16S rRNA community profiling and shotgun metagenomics methods pose significant challenges for microbiome research. Significant biases can be introduced during sample preparation, DNA extraction, PCR amplification, library preparation, sequencing, and/or data interpretation. One of the primary obstacles in assay standardization is the limited availability of reference materials. To address these biases and provide a measure of standardization within microbiome research and applications, ATCC has developed a set of mock microbial communities comprising fully sequenced, characterized strains that can be used as daily run controls and as universal controls for assay development and optimization.

Sample Collection
- Storage
- Handling
- Processing

DNA extraction
- Cell lysis
- Quality
- Quantity

Library Preparation
- Primers
- Amplification
- Library prep

Sequencing
- Platform
- Chemistry
- Depth

Data Analysis
- Algorithm
- Read quality
- Database

Whole cell standards – Full process controls, including DNA extraction

Genomic DNA standards – Library preparation, sequencing

One Codex analysis

CHOOSE YOUR FORMAT AND LEVEL OF COMPLEXITY

ATCC® Microbiome Standards are available as either whole cell or nucleic acid preparations with even or staggered genomic DNA abundance and varying levels of community complexity. Choose the samples that best suit your research!

Even Distribution
- Acinetobacter baumannii
- Bacillus cereus
- Bifidobacterium adolescentis
- Deinococcus radiodurans
- Escherichia coli
- Lactobacillus gasseri
- Porphyromonas gingivalis
- Pseudomonas aeruginosa
- Staphylococcus aureus
- Streptococcus agalactiae

Staggered Distribution
- Actinomyces odontolyticus
- Bacteroides vulgatus
- Clostridium beijerinckii
- Enterococcus faecalis
- Helicobacter pylori
- Neisseria meningitidis
- Propionibacterium acnes
- Rhodobacter sphaeroides
- Staphylococcus epidermidis
- Streptococcus mutans

2 Order online at www.atcc.org, call 800.638.6597, 703.365.2700, or contact your local distributor.
**IMPROVE ASSAY CONSISTENCY**

When performing your microbiome research, the tools and protocols you choose can significantly affect your results. By using ATCC® Microbiome Standards combined with the One Codex data analysis module in your research, you can compare the performance and overall accuracy of your methods and ensure the validity of your results.

![Relative Abundance (%)](image1)

**Figure 1.** The whole cell mock microbial communities can be used to compare different DNA extraction kits. Here, we show a proof-of-concept study. Total DNA from two aliquots of the whole cell microbiome standards was extracted using two commercial extraction kits. Following extraction, the genomic DNA was analyzed using 16S rRNA and shotgun genomic sequencing analysis on the Illumina® MiSeq® platform, and the resulting data were analyzed using the ATCC bioinformatics tool in One Codex.

![Relative Abundance (%)](image2)

**Figure 2.** The genomic DNA mock microbial communities can be used to compare 16S rRNA and shotgun metagenomics assays. Here, we show a proof-of-concept study. The performance and overall accuracy of the quantitative genomic DNA mock microbial communities were tested using the Illumina® MiSeq® platform, and the resulting data were analyzed using the ATCC bioinformatics tool in One Codex.

Streptococcus mutans
Streptococcus agalactiae
Staphylococcus epidermidis
Staphylococcus aureus
Rhodobacter sphaeroides
Pseudomonas aeruginosa
Propionibacterium acnes
Porphyromonas gingivalis
Neisseria meningitidis
Lactobacillus gasseri
Helicobacter pylori
Escherichia coli
Enterococcus faecalis
Deinococcus radiodurans
Clostridium beijerinckii
Bifidobacterium adolescentis
Bacteroides vulgatus
Bacillus cereus
Actinomyces odontolyticus
Acinetobacter baumannii
SOURCE STANDARDS BASED ON SPECIFIC APPLICATIONS

Pathogen Detection

ATCC has developed a mock microbial community for clinically relevant pathogen detection in partnership with the LGC Group, an international leader in genomics, measurement standards, and reference materials. With the ATCC Metagenomic Control Material for Pathogen Detection (ATCC® MSA-4000™), you can expect:

- Genomic DNA prepared from fully sequenced ATCC® Genuine Cultures
- A combination of strains observed in clinical infections, including antimicrobial-resistant organisms
- Absolute quantification of genomic DNA and assignment of genome copy number using Droplet Digital™ PCR to improve analytical precision

![ATCC Metagenomic Control Material for Pathogen Detection](image)

**Figure 3.** The ATCC Metagenomic Control Material for Pathogen Detection (ATCC® MSA-4000™) can be used to compare various molecular diagnostic methods. Here, we used the (A) control material to evaluate (B) digital PCR and compare (C) 16S rRNA and shotgun metagenomics analysis methods. *The percent relative abundance of Staphylococcus aureus includes both MRSA and MSSA.

Environmental Testing

The ABRF-MGRG metagenomics reference standards were developed and packaged in partnership with the Association of Biomolecular Resource Facilities Metagenomics Research Group (ABRF-MGRG) as part of the Extreme Microbiome Project (XMP). With the ABRF-MGRG metagenomics reference standards (ATCC® MSA-3000™, MSA-3001™, MSA-3002™), you can expect:

- Genomic DNA prepared from fully sequenced ATCC® Genuine Cultures representing bacterial and archaeal species found in extreme environments
- Mock communities that are human DNA-free, RNA-free, and tested to ensure purity via sequencing
- Access to One Codex, the leading bioinformatics platform for microbial genomics

![ABRF-MGRG metagenomics reference standards](image)

**Figure 4.** The ABRF-MGRG metagenomics reference standards can be used to compare different sequencing platforms. As a proof-of-concept, ATCC® MSA-3001™ was used as a control material to compare the performance of the Illumina® MiniSeq™, MiSeq®, NextSeq®, and HiSeq® platforms. Data were analyzed using the ATCC bioinformatics tool in One Codex. ABRF-MGRG metagenomics reference standards can also be used to evaluate run-to-run reproducibility (data not shown).
CALIBRATE YOUR EXPERIMENTS WITH SPIKE-IN CONTROLS

Microbiome spike-in controls from ATCC comprise exogenous bacteria and archaea that do not exist in the human microbiome under physiological conditions, making them easy to distinguish from human bacteria via standard sequencing methods. These microbiome standards offer a valuable way to evaluate the accuracy and reproducibility of library preparation, sequencing, and data analysis in both 16S rRNA community profiling and shotgun metagenomics. Further, they enable inter-sample comparison, thereby providing a way to standardize microbiome research across different laboratories.

SOURCE STANDARDS BASED ON BODY SITE

ATCC has developed several site-specific mock microbial communities for research on the human microbiome. With these standards, you can expect:

- Mock microbial communities representing the oral, skin, gut, and vaginal microbiomes
- Comprising normal and atypical flora
- Genomic DNA or whole cells prepared from fully sequenced ATCC® Genuine Cultures
- Anaerobic and aerobic microbial strains
- A combination of Gram-positive and -negative bacterial cultures

These site-specific microbiome standards are ideal for use as controls in microbial profiling of mixed populations or for research on the effects of dysbiosis on human health.
COMBINE THE POWER OF PHYSICAL STANDARDS WITH STATE-OF-THE-ART BIOINFORMATICS

ATCC has collaborated with One Codex to bring microbiome research to a completely new level, by combining the power of both physical laboratory standards with the leading bioinformatics platform for microbial genomics and metagenomics. The One Codex platform, powered by a database containing roughly 83,000 whole genomes, provides microbial identification with best-in-class accuracy. Moreover, ATCC has worked in conjunction with One Codex to develop an ATCC Microbiome Standards analysis tool, including:

- Pre-loaded metadata from ATCC® Microbiome Standards
- 16S rRNA and shotgun metagenomic sequencing analysis
- Automated quality scores assessing true positives, false positives, and relative abundance
- Data management, storage, and graphing capabilities

ONE CODEX WITH EVERY ATCC® MICROBIOME STANDARDS PURCHASE

ATCC has developed a product that will deliver reliable and consistent results, and packaged that with the One Codex platform to move microbiome research towards standardization. That is why every purchase of an ATCC Microbiome Standard comes with access* to the One Codex platform, allowing you to:

- Upload data files for analysis against pre-loaded metadata
- Ability to compare your data against data sets generated by ATCC or submitted by other researchers
- Create charts and graphs that help you relay your analysis in visual format

Visit us online at www.atcc.org/bioinformatics to learn more!
<table>
<thead>
<tr>
<th>Collaboration</th>
<th>Preparation</th>
<th>ATCC® No.</th>
<th>Number of organisms</th>
<th>Composition</th>
<th>Complexity</th>
<th>Importance</th>
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</thead>
<tbody>
<tr>
<td><strong>Mock Microbial Communities</strong></td>
<td>Genomic DNA</td>
<td>MSA-1000™</td>
<td>10</td>
<td>Even</td>
<td>Medium</td>
<td>Mock microbial communities comprising diverse strains selected on the basis of diversity, genome size, GC content, Gram stain, and other special features</td>
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<tr>
<td></td>
<td></td>
<td>MSA-1001™</td>
<td>10</td>
<td>Staggered</td>
<td>Medium</td>
<td></td>
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<tr>
<td></td>
<td></td>
<td>MSA-1002™</td>
<td>20</td>
<td>Even</td>
<td>High</td>
<td></td>
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<tr>
<td></td>
<td></td>
<td>MSA-1003™</td>
<td>20</td>
<td>Staggered</td>
<td>High</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Whole Cells</td>
<td>MSA-2003™</td>
<td>10</td>
<td>Even</td>
<td>Medium</td>
<td></td>
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<tr>
<td></td>
<td></td>
<td>MSA-2002™</td>
<td>20</td>
<td>Even</td>
<td>High</td>
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<tr>
<td><strong>Mock Viral Communities</strong></td>
<td>Genomic DNA/RNA</td>
<td>MSA-1008™</td>
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<td>Even</td>
<td>Medium</td>
<td>Mock viral communities comprising diverse strains selected on the basis of genomic size, DNA/RNA genome, envelope/non-envelope, and other special features</td>
</tr>
<tr>
<td></td>
<td>Whole Virus</td>
<td>MSA-2008™</td>
<td>6</td>
<td>Even</td>
<td>Medium</td>
<td></td>
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<tr>
<td><strong>Mock Fungal Communities</strong></td>
<td>Genomic DNA</td>
<td>MSA-1010™</td>
<td>10</td>
<td>Even</td>
<td>Medium</td>
<td>Mock fungal communities comprising diverse strains selected on the basis of genome size, ITS variability, and other special features</td>
</tr>
<tr>
<td></td>
<td>Whole Cells</td>
<td>MSA-2010™</td>
<td>10</td>
<td>Even</td>
<td>Medium</td>
<td></td>
</tr>
<tr>
<td><strong>Metagenomic Control Material for Pathogen Detection</strong></td>
<td>Genomic DNA</td>
<td>MSA-4000™</td>
<td>11</td>
<td>Staggered</td>
<td>Medium</td>
<td>Metagenomic control material (MCM) encompassing pathogenic bacterial species commonly observed in clinical infections</td>
</tr>
<tr>
<td><strong>ABRF-MGRG Metagenomics Reference Standard</strong></td>
<td>Genomic DNA</td>
<td>MSA-3000™</td>
<td>6</td>
<td>Even</td>
<td>Low</td>
<td>Genomic DNA microbiome standards comprising strains observed in soil, freshwater, seawater, feces, and high salinity ecosystems</td>
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<tr>
<td></td>
<td></td>
<td>MSA-3001™</td>
<td>10</td>
<td>Even</td>
<td>Medium</td>
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<td></td>
<td>MSA-3002™</td>
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<td>Staggered</td>
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<td><strong>Site-Specific Microbiome Standards</strong></td>
<td>Genomic DNA</td>
<td>MSA-1004™</td>
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<td>Medium</td>
<td>Oral mock community DNA standard</td>
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<td>MSA-1005™</td>
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<td>Even</td>
<td>Medium</td>
<td>Skin mock community DNA standard</td>
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<tr>
<td></td>
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<td>MSA-1006™</td>
<td>12</td>
<td>Even</td>
<td>Medium</td>
<td>Gut mock community DNA standard</td>
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<td></td>
<td>MSA-1007™</td>
<td>6</td>
<td>Even</td>
<td>Medium</td>
<td>Vaginal mock community DNA standard</td>
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<td>Whole Cells</td>
<td>MSA-2004™</td>
<td>6</td>
<td>Even</td>
<td>Medium</td>
<td>Oral mock community whole cell standard - New!</td>
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<td></td>
<td></td>
<td>MSA-2005™</td>
<td>6</td>
<td>Even</td>
<td>Medium</td>
<td>Skin mock community whole cell standard - New!</td>
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<td></td>
<td>MSA-2006™</td>
<td>12</td>
<td>Even</td>
<td>Medium</td>
<td>Gut mock community whole cell standard</td>
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<td></td>
<td></td>
<td>MSA-2007™</td>
<td>6</td>
<td>Even</td>
<td>Medium</td>
<td>Vaginal mock community whole cell standard</td>
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<td><strong>Microbiome Spike-in Controls</strong></td>
<td>Genomic DNA</td>
<td>MSA-1009™</td>
<td>3</td>
<td>Even</td>
<td>Medium</td>
<td>Spike-in controls for optimizing assay development and metagenomics-based profiling</td>
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<tr>
<td></td>
<td>Whole Cells</td>
<td>MSA-2009™</td>
<td>3</td>
<td>Even</td>
<td>Medium</td>
<td></td>
</tr>
</tbody>
</table>

*Products are coming soon.*
A PORTFOLIO OF PRODUCTS TO MEET YOUR NEEDS

ATCC has been at the heart of microbiological research for over 90 years, delivering consistent controls for reliable data. Whether you are testing out the sensitivity or specificity of a new microbiome assay, performing next-generation sequencing, or developing primers for a set of drug resistance genes in a clinical sample, ATCC has the products and services you need to ensure the accuracy and reproducibility of your research, including:

- Individual strains relevant to the diseased microbiome
- Antimicrobial-resistant strains
- Environmental isolates
- Nucleic acid standards

Additionally, ATCC has a long history of experience with in vitro cultivation, applications and research, preservation techniques and master cell banking, as well as packaging a variety of formats and shipping to international locations. Collaborating with ATCC provides you with access to a wide range of services and customized solutions, including:

- Cellular and microbial expansion (MCB, WCB)
- Small- and large-scale production of nucleic acids
- Quantitation and inactivation services
- Viral purification
- Cell line authentication (STR profiling, CO1 testing, Mycoplasma testing)
- Cell derivation (primary, hematopoietic, iPS cells)
- Custom manufacturing
- Biorepository Services™ with global distribution

Visit us online at www.atcc.org/Microbiome to learn more about our products and services for next-generation sequencing and metagenomics analysis.

Register to get notification of new microbiome products from ATCC at www.atcc.org/Microbiome

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