ZYMO RESEARCH

Microbiomics
*Made Simple™*

# ZymoBIOMICS® Microbial Community Standard II (Log Distribution)

Microbial standard with a log distribution used to assess the performance of microbiome workflows

## Highlights

- **Log abundance distribution:** assess detection limit over a broad range ($10^2$ to $10^8$ cells).
- **Accurate composition:** allows for benchmarking and validation of NGS microbiome workflows.
- **Quality control:** ideal control for microbiome profiling quality.

Catalog Number:
D6310

Scan with your smart-phone camera to view the online protocol/video.

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# Product Contents

| ZymoBIOMICS® Microbial Community Standard II (Log Distribution) | D6310 (10 preps.) | Storage Temperature[1] |
|---|---|---|
| ZymoBIOMICS® Microbial Community Standard II (Log Distribution) | 0.75 ml | -80°C |

# Specifications

- **Source –** eight bacteria (three Gram-negative and five Gram-positive) and two yeasts.
- **Biosafety –** this product is not biohazardous as microbes have been fully inactivated.
- **Reference Genomes and 16S & 18S rRNA Genes[2] –** https://s3.amazonaws.com/zymo-files/BioPool/ZymoBIOMICS.STD.refseq.v2.zip
- **Storage Solution –** DNA/RNA Shield™ (R1100-50)
- **Total Cell Concentration –** ~1.5 x $10^9$ cells/ml
- **Impurity Level –** <0.01% foreign microbial DNA
- **Relative Abundance Deviation in Average –** <30%
- **Microbial Composition –** Table 1 shows the theoretical microbial composition of the standard.

The microbial composition of each lot was measured by shotgun metagenomic sequencing post mixing. The results (including the composition, impurities and abundance deviation) can be accessed through the Certificate of Analysis based on the lot number (printed on tube level) by the following link: https://www.zymoresearch.com/pages/certificate-of-analysis.

1 For short-term storage or regular use, -20°C may be used.
2 Several strains within the standard were replaced with similar strains beginning from Lot ZRC190633. This update will not affect the species composition of the standard. Refer to Appendix C to check if your product is from an older lot and find the correct reference database to use accordingly if needed.

## Table 1. Microbial Composition

| Species | Theoretical Composition (%) | | | | |
|---|---|---|---|---|---|
| | Genomic DNA | 16S Only[1] | 16S & 18S[1] | Genome Copy[2] | Cell Number[3] |
| *Listeria monocytogenes* | 89.1 | 95.9 | 91.9 | 94.8 | 94.9 |
| *Pseudomonas aeruginosa* | 8.9 | 2.8 | 2.7 | 4.2 | 4.2 |
| *Bacillus subtilis* | 0.89 | 1.2 | 1.1 | 0.7 | 0.7 |
| *Saccharomyces cerevisiae* | 0.89 | NA | 4.1 | 0.23 | 0.12 |
| *Escherichia coli* | 0.089 | 0.069 | 0.066 | 0.058 | 0.058 |
| *Salmonella enterica* | 0.089 | 0.07 | 0.067 | 0.059 | 0.059 |
| *Lactobacillus fermentum* | 0.0089 | 0.012 | 0.012 | 0.015 | 0.015 |
| *Enterococcus faecalis* | 0.00089 | 0.00067 | 0.00064 | 0.001 | 0.001 |
| *Cryptococcus neoformans* | 0.00089 | NA | 0.0014 | 0.00015 | 0.00007 |
| *Staphylococcus aureus* | 0.000089 | 0.0001 | 0.0001 | 0.0001 | 0.0001 |

[1] The theoretical composition in terms of 16S (or 16S & 18S) rRNA gene abundance was calculated from theoretical genomic DNA composition with the following formula: 16S/18S copy number = total genomic DNA (g) × unit conversion constant (bp/g) / genome size (bp) × 16S/18S copy number per genome. Use this as reference when performing 16S targeted sequencing.

[2] The theoretical composition in terms of genome copy number was calculated from theoretical genomic DNA composition with the following formula: genome copy number = total genomic DNA (g) × unit conversion constant (bp/g) / genome size (bp). Use this as reference when inferring microbial abundance from shotgun sequencing data based on read depth/coverage.

[3] The theoretical composition in terms of cell number was calculated from theoretical genomic DNA composition with the following formula: cell number = total genomic DNA (g) × unit conversion constant (bp/g) / genome size (bp)/ploidy.

# Product Description

**ZymoBIOMICS® Microbial Community Standard II (Log Distribution)** is a mock microbial community consisting of eight bacterial and two fungal strains. This microbial standard can be used to assess the performance of microbiomics workflows and can also be used as a positive control for routine sequencing. Cells of the ten microbes were mixed to create log-distributed abundance (Table 1), which allows one to easily assess the detection limit of a microbiomics workflow. 75 µl of the standard contains about ~100 cells of the *Staphylococcus aureus*, the organism of lowest abundance. If needed, the standard can be spiked into a sample matrix (*e.g.* soil and blood) to mimic real samples of interest.

The microbial standard is accurately characterized and contains negligible impurity (< 0.01%). It was constructed by pooling cells from pure cultures of ten microbial strains. The cells from each pure culture were quantified before pooling. After mixing, the microbial composition was confirmed using NGS-based sequencing (Figure 1).

Details regarding the ten microbial strains (including species name, genome size, ploidy, average GC content, 16S/18S copy number, phylogeny) can be found in Table 2. The 16S/18S rRNA sequences (FASTA format) and genomes (FASTA format) of these strains[1] are available from the link below. Feel free to contact us if we can help to analyze sequencing data generated from this standard.

**Reference Genome Download:**
https://s3.amazonaws.com/zymo-files/BioPool/ZymoBIOMICS.STD.refseq.v2.zip.

1 Several strains within the standard were replaced with similar strains beginning from Lot ZRC190633. This update will not affect the species composition of the standard. Refer to Appendix C to check if your product is from an older lot and find the correct reference database to use accordingly if needed.

## Background on the Need for Microbiome Standards

Microbial composition profiling techniques powered by next-generation sequencing are becoming routine in microbiomics and metagenomics studies. It is well known that these analytical techniques can suffer from bias and errors in every step of the workflow, including DNA extraction, library preparation, sequencing and bioinformatics analysis. To assess the performance of different microbiomics workflows, there is an urgent need in the field for reliable reference materials, *e.g.* a mock microbial community with defined composition.

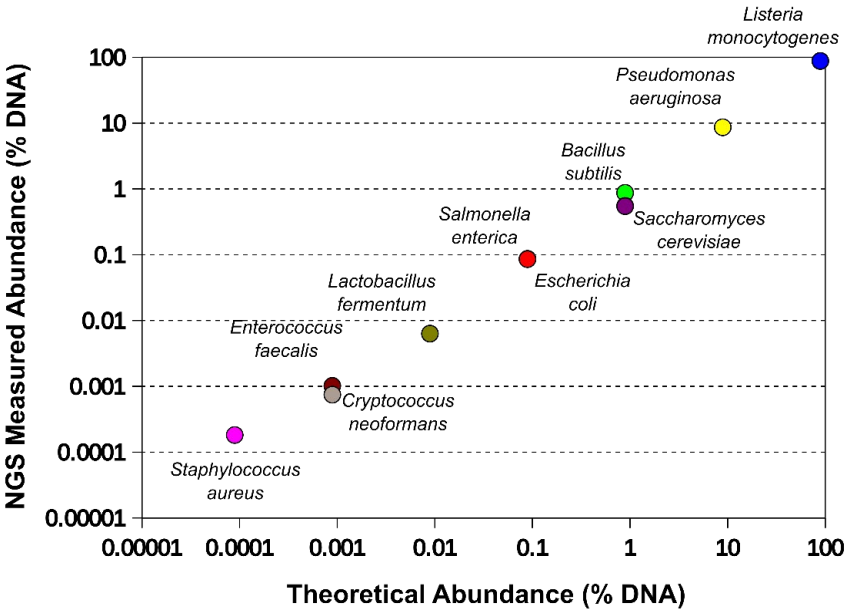


**Figure 1. The microbial composition of the standard measured by NGS shotgun sequencing as compared to the defined composition.** After mixing, the microbial composition of the standard was confirmed using deep Illumina® shotgun sequencing. Briefly, the genomic DNA was extracted using the ZymoBIOMICS® DNA Miniprep. Library preparation was performed using an in-house protocol. Shotgun sequencing was performed using Illumina HiSeq™ or MiSeq™. Microbial abundance was estimated based on the number of reads that were mapped to references genomes of the organisms.

## Table 2. Strain Information

| Species | NRRL Accession NO. | Genome Size (Mb) | Ploidy | GC Content (%) | 16/18S Copy Number | Gram Stain |
|---|---|---|---|---|---|---|
| *Pseudomonas aeruginosa* | B-3509 | 6.792 | 1 | 66.2 | 4 | - |
| *Escherichia coli* | B-1109 | 4.875 | 1 | 46.7 | 7 | - |
| *Salmonella enterica* | B-4212 | 4.760 | 1 | 52.2 | 7 | - |
| *Lactobacillus fermentum* | B-1840 | 1.905 | 1 | 52.4 | 5 | + |
| *Enterococcus faecalis* | B-537 | 2.845 | 1 | 37.5 | 4 | + |
| *Staphylococcus aureus* | B-41012 | 2.730 | 1 | 32.9 | 6 | + |
| *Listeria monocytogenes* | B-33116 | 2.992 | 1 | 38.0 | 6 | + |
| *Bacillus subtilis* | B-354 | 4.045 | 1 | 43.9 | 10 | + |
| *Saccharomyces cerevisiae* | Y-567 | 12.1 | 2 | 38.3 | 109[2] | Yeast |
| *Cryptococcus neoformans* | Y-2534 | 18.9 | 2 | 48.3 | 60[2] | Yeast |

## Table 2, *continued*

| Species | NCBI Phylogeny Database |
|---|---|
| *Pseudomonas aeruginosa* | *Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas aeruginosa* group |
| *Escherichia coli* | *Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia* |
| *Salmonella enterica* | *Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella* |
| *Lactobacillus fermentum* | *Bacteria; Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae; Lactobacillus* |
| *Enterococcus faecalis* | *Bacteria; Firmicutes; Bacilli; Lactobacillales; Enterococcaceae; Enterococcus* |
| *Staphylococcus aureus* | *Bacteria; Firmicutes; Bacilli; Bacillales; Staphylococcaceae; Staphylococcus* |
| *Listeria monocytogenes* | *Bacteria; Firmicutes; Bacilli; Bacillales; Listeriaceae; Listeria* |
| *Bacillus subtilis* | *Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus; Bacillus subtilis* group |
| *Saccharomyces cerevisiae* | *Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces* |
| *Cryptococcus neoformans* | *Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; Agaricomycotina; Tremellomycetes; Tremellales; Tremellaceae; Filobasidiella; Filobasidiella/Cryptococcus neoformans* species complex |

2 18S rRNA gene copy numbers in a haploid genome of the two strains of *Saccharomyces cerevisiae* and *Cryptococcus neoformans* were estimated based on read depth information from mapping shotgun sequencing data.

# Protocol

1. Thaw the standard on ice. Once thawed, vortex the standard for at least 30 seconds, then spin down briefly.

***Note**: Cells might aggregate due to freeze-thaw cycling; therefore, it is critical to mix the cellular standard thoroughly before use.*

2. For DNA extraction of the standard, use 75 µl per prep[1]. We recommend using mechanical lysis featured in Zymo Research's microbial DNA isolation kits[2] for unbiased and efficient isolation. Expected yield is approximately 220 ng DNA per prep[3] when using **ZymoBIOMICS® DNA Miniprep Kit** (D4300).

***Note**: The duration of homogenization (bead beating) will vary depending on the homogenization device, and may require optimized by the end-user. Zymo Research has validated optimized lysis parameters for many common homogenization devices, which can be found here:* https://files.zymoresearch.com/documents/bead_beating_short_protocol_tables.pdf

1. For use with kits that are incompatible with DNA/RNA Shield and other sample preservation reagents, such as Qiagen's PowerFecal and PowerSoil kits, reducing the input volume can improve compatibility. For kits such as these, it is recommended to reduce the input of this standard to ≤ 20 µl.
2 This microbial standard contains several tough-to-lyse microbes; therefore, to extract DNA from this standard, we strongly recommend using ZymoBIOMICS® DNA Miniprep Kit (D4300), Quick-DNA™ Fungal/Bacteria DNA Miniprep Kit (D6005), Quick-DNA™ Fecal/Soil Microbe Miniprep Kit (D6010). These kits feature a unique lysis matrix that contains our ultra-high-density BashingBeads™, which provides unbiased lysis of bacteria and fungi for accurate microbial composition profiling.
3 The expected yield for one prep (75 µl) of the standard is approximately 220 ng. Yields significantly lower than 220 ng may suggest inefficient lysis during DNA extraction.

# Appendices

## Appendix A: Bioinformatics Analysis Recommendations

### Assessing accuracy of taxonomy identification

A fundamental goal in microbiome studies is to identify what microbes are present in a sample. After analyzing this microbiome standard using a workflow that includes wet-lab processing and dry-lab interpretation, the taxa identified can be compared with the taxonomy information of the ten strains included in the standard (Table 2). This allows a performance assessment of a workflow regarding the limit of the taxonomy resolution, false positives, and false negatives. False positives can be caused by contaminations from wet-lab processes, chimeric sequences during library prep, sequencing errors, demultiplexing errors and defects in bioinformatics analysis. We certify that the impurity level of the standard is <0.01% (by DNA abundance). Therefore, it can be concluded that any alien taxa present at >0.01% (by DNA abundance) in the standard is introduced artificially by the user's workflow. The detection limit of a workflow can be easily determined by checking what strains are detected in the microbiome standard as their abundance follows log distribution.

### Assessing bias in composition profiling

To assess composition bias, compare the composition profile determined by the user's workflow to the defined composition shown in Table 1. Both wet-lab and dry-lab processes can introduce bias. To determine the quality of a wet-lab process, an accurate/unbiased dry-lab analysis method is needed to interpret the sequencing data from the standard. A straightforward and accurate method to infer the microbial composition from sequencing data of our microbiome standard is through direct read-mapping against reference genomes (or against reference 16S & 18S sequences in the case of targeted sequencing). The reference sequences of this microbiome standards can be found in the Specifications.

***Note:*** *Bacterial strains that are phylogenetically distant can potentially share highly similar sequences in their genomes, e.g. ribosomal RNA sequences and conserved single-copy genes. In the process of direct read mapping, the presence of these highly homologous regions can cause reads that are derived from high-abundance microbes to be assigned to low-abundance microbes, resulting in the overestimation of low-abundance microbes in the standard. One way to overcome this issue is to use a mapping tool that can choose to ignore reads that map to more than one genome. Another way to address this problem is to filter these highly conserved sequences from the reference genomes. Please contact us if you need assistance.*

## Appendix B: Additional Strain Information

| Species | NRRL Accession NO. | Strain Name[1] |
|---|---|---|
| *Bacillus subtilis* | B-354 | *Bacillus subtilis* (Ehrenberg 1835) Cohn 1872 ATCC 6633=NRRL B-209=NRS-231=PCI 219 |
| *Cryptococcus neoformans* | Y-2534 | *Cryptococcus deneoformans* T. Boekout & F. Hagen (2014) 32045=ATCC 32719=CBS 132=CCRC 20528=CCY 17-1-2=DBVPG 6010=IFO 0608=IGC 3957=NRRL Y-8347=PYCC 3957 |
| *Enterococcus faecalis* | B-537 | *Enterococcus faecalis* (Andrewes and Horder 1906) Schleifer and Kilpper-Bälz 1984 ATCC 7080 |
| *Escherichia coli* | B-1109 | Castellani and Chalmers 1919, 01485cm |
| *Lactobacillus fermentum* | B-1840 | *Lactobacillus fermentum* Beijerinck 1901 19lc3=ATCC 14931=BCRC 12190=CCUG 30138=CECT 4007=CIP 102980=DSM 20052=IFO 15885=JCM 1173=KCTC 3112=LMG 6902=NBRC 15885=NCDO 1750=NCIMB 11840=NRIC 1752=NRRL B-4524. |
| *Listeria monocytogenes* | B-33116 | *Listeria monocytogenes* (Murray et al. 1926) Pirie 1940 2847=ATCC 19117 |
| *Pseudomonas aeruginosa* | B-3509 | *Pseudomonas aeruginosa* (Schroeter 1872) Migula 1900 ATCC 15442=NCIB 10421=Pdd-10 |
| *Saccharomyces cerevisiae* | Y-567 | *Saccharomyces cerevisiae* Meyen ex E. C. Hansen (1883) ATCC 9763=CBS 2978=CBS 5900=CCY 21-4-48=CCY 21-4-54=NCTC 10716=NCTC 7239=NCYC 87=Pattee 6=PCI M-50 |
| *Salmonella enterica* | B-4212 | *Salmonella enterica* subspecies *enterica*, Castellani and Chalmers 1919, TA1536 |
| *Staphylococcus aureus* | B-41012 | *Staphylococcus aureus* Rosenbach 1884 |

1 The strain information was extracted from the website of the Agricultural Research Service Culture Collection (NRRL, https://nrrl.ncaur.usda.gov/).

# Ordering Information

| Product Description | Catalog No. | Size |
|---|---|---|
| **ZymoBIOMICS® Microbial Community Standard II (Log Distribution)** | D6310 | 10 preps. |

| Related Products | Catalog No. | Amount |
|---|---|---|
| **ZymoBIOMICS® Microbial Community Standard** | D6300 | 10 preps. |
| **ZymoBIOMICS® Microbial Community DNA Standard (200ng)** | D6305 | 200 ng |
| **ZymoBIOMICS® Microbial Community DNA Standard (2000ng)** | D6306 | 2000 ng |
| **ZymoBIOMICS® Microbial Community DNA Standard II (Log Distribution)** | D6311 | 220 ng |
| **ZymoBIOMICS® Spike-in Control I (High Microbial Load)** | D6320<br>D6320-10 | 25 preps.<br>250 preps. |
| **ZymoBIOMICS® Spike-in Control II (Low Microbial Load)** | D6321<br>D6321-10 | 25 preps.<br>250 preps. |
| **ZymoBIOMICS® HMW DNA Standard** | D6322 | 5000 ng |
| **ZymoBIOMICS® Gut Microbiome Standard** | D6331 | 10 preps. |

# Complete Your Workflow

✓ To collect and transport microbiome samples at ambient temperatures:

| DNA/RNA Shield™ and Collection Devices | |
|---|---|
| 1X Reagent (R1100) | For sample lysis and stabilization of DNA/RNA |
| 2X Concentrate (R1200) | Reagent concentrate (2X) for use with liquids at 1:1 ratio |
| Fecal Collection Tube (R1101) | 15 mL container (prefilled with 9 mL DNA/RNA Shield™). Direct collection of up to 1g or 1 mL stool |
| Collection Tube w/ Swab (R1106) | 12 x 80 mm screwcap container filled with 1 mL DNA/RNA Shield™ and sterile swab for specimen collection |

✓ Unbiased and inhibitor-free DNA and RNA extraction (high-throughput and automatable) for microbiome profiling:

| ZymoBIOMICS® DNA and RNA Kits | |
|---|---|
| DNA Miniprep (D4300) | Up to 25 µg DNA |
| DNA Microprep (D4301) | Up to 5 µg DNA |
| MagBead DNA (D4302) | Automatable (Tecan, Hamilton, Kingfisher, etc.) |
| 96-Well DNA (D4309) | Spin-plate |
| DNA/RNA Miniprep Kit (R2002) | Up to 100 µg DNA/RNA |

✓ Streamlined workflows with comprehensive bioinformatics analysis and publication-ready plots and figures:

| ZymoBIOMICS® Services | |
|---|---|
| Targeted Sequencing Service 16S (Q2001) | With DNA Extraction |
| Targeted Sequencing Service 16S (Q2012) | Without DNA Extraction |
| Targeted Sequencing Service ITS (Q2003) | With DNA Extraction |
| Targeted Sequencing Service ITS (Q2003) | Without DNA Extraction |

# Notes

# Notes


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