



ZYMO RESEARCH

The Beauty of Science is to Make Things Simple

Microbiome Services

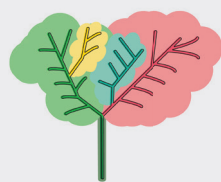
Your Next-Gen Sequencing Partner



Exploring the Microbial World

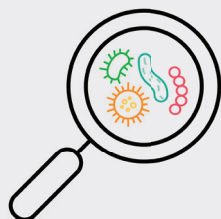
Over the past several years, Zymo Research has devoted tremendous efforts to improving the accuracy of microbiome measurements. We created the first commercial microbiome standard for quality control and profiling accuracy measurement. We released the first DNA extraction kit validated to be unbiased for microbiome profiling. Our sample preservation reagent, DNA/ RNA Shield™, can preserve microbiome profiles at ambient temperature, making it perfect for the cold-free collection and transportation of microbial samples. With all these innovations, we have established the most accurate microbiome sequencing services for both academic research and industry partners.

Whether you need 16S/ITS Sequencing, Metagenomic Shotgun Sequencing, Metatranscriptomic Sequencing, or a custom sequencing solution, our microbiome analysis service team can take you from any stage of your project to a comprehensive microbiome report featuring publication-ready data.



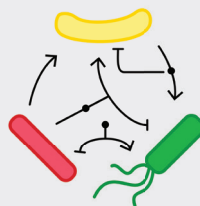
Amplicon Sequencing

Species-level resolution for bacteria and fungi, targeting regions of 16S, 18S & ITS.



Shotgun Metagenomic Sequencing

Multiple kingdom identification & functional profiling with industry-leading sensitivity & precision.



Metatranscriptomic Sequencing

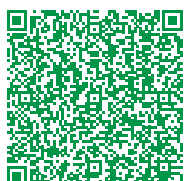
Microbiome gene expression analysis.



Custom Solutions for Industry Partners

Our microbiome analysis services can be customized to meet the individual needs of your application.

Microbiomics
Made Simple™



Visit www.zymoresearch.com/pages/microbiome-analysis-services
for a custom microbiome service quote

Microbiome Sequencing Services

Complete Solutions for Accurate Microbiome Profiling

Sequencing Workflows



16S/ITS Amplicon Sequencing

2

Species-level resolution for bacterial and fungal profiling



Shotgun Metagenomics Sequencing

3

Across kingdom identification and metabolic functional profiling

Custom Solutions for Commercial Applications



Sample Collection & Kit Design

4

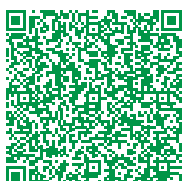
A variety of sample collection devices & branding options available



Custom Data Reporting

5

Bioinformatic reports to fit your application needs



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16S/ITS Amplicon Sequencing

Simple, Fast, & Cost-Effective

16S/ITS sequencing uses PCR to selectively amplify certain regions/genes from different bacteria or fungi and then sequences the amplicons. The taxonomy identification is achieved by comparing the amplicon sequences to reference 16S/ITS sequence databases. 16S/ITS sequencing is generally considered simpler and more cost-effective than metagenomic sequencing, and is the better choice for certain samples that contain microbes with unknown genomes (e.g. soil and water samples).

With recent innovations in bioinformatics analysis (e.g. DADA2), 16S/ITS sequencing can achieve close to zero false positives in taxonomy identification and can differentiate even single-nucleotide variation in amplicon sequences.

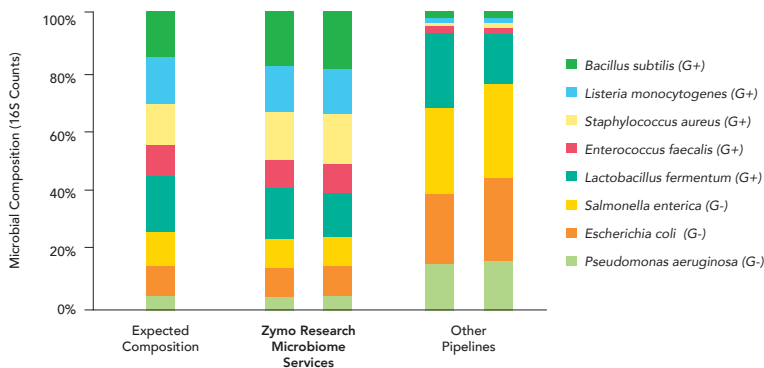
What makes Zymo Research different from other service providers?

- ✓ **Quick Turnaround:** From sample collection to report in as little as 2 weeks.
- ✓ **Species-Level Resolution:** We provide species level resolution in 16S sequencing while others normally restrict to genus.
- ✓ **Unbiased Microbial Lysis:** Our DNA extraction methods are validated unbiased for microbiome profiling.
- ✓ **Absolute Quantification:** 16S/ITS copy number measurement for each species along with standard percentage measurement.

Species-Level Resolution

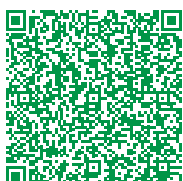
By combining sequence-analysis algorithm, DADA2, and a well-curated 16S reference database, we can provide species-level resolution with regular Illumina® sequencing of different 16S regions, e.g. V3-V4, V1-V2 and V1-V3.

Species	16S Pipeline (Zymo Research)	Competitors
<i>Listeria monocytogenes</i>	✓	✗
<i>Staphylococcus aureus</i>	✓	✓
<i>Enterococcus faecalis</i>	✓	✗
<i>Lactobacillus fermentum</i>	✓	✗
<i>Escherichia coli</i>	✓	✗
<i>Salmonella enterica</i>	✓	✗
<i>Pseudomonas aeruginosa</i>	✓	✗
<i>Bacillus subtilis</i>	✗	✗
Species-level resolution	Yes	No



Unbiased Microbial Lysis

Many service providers use DNA extraction kits that are not validated for microbiome profiling, which can result in massive skew in the final profile. Our DNA extraction step is validated unbiased using the ZymoBIOMICS™ Microbial Community Standard. The standard is used as a positive control in every run.



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Shotgun Metagenomic Sequencing

Accurate, Robust, & Comprehensive

Shotgun Metagenomic Sequencing, in comparison to amplicon sequencing (e.g. 16S sequencing), is a more comprehensive way to characterize a microbiome sample. Shotgun sequencing provides across-kingdom identification and in theory, can detect all microbes except RNA viruses.

Metagenomic approaches provide strain-level taxonomy resolution with sufficient sequencing depth. Unlike amplicon sequencing, identification of functional genes and pathways is also possible.

Shotgun Metagenomic Sequencing is now more affordable with advanced sequencing technology.

What makes Zymo Research different from other service providers?

- ✓ **Quick Turnaround:** Results from sample to report in as little as 3 weeks
- ✓ **Strain-Level Resolution:** High confidence strain identification through our curated reference database
- ✓ **Comprehensive Bioinformatic Analysis:** Includes bar plots, heatmaps, diversity analysis, gene family & metabolic pathway profiling, identification of virulence genes & antibiotic resistance genes, and statistical group analysis.
- ✓ **Minimize False Positives:** innovative algorithms that minimize the number of false positives

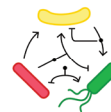
Species	Zymo Research (%)	Service Provider D (%)
<i>Lactobacillus iners</i>	48.9	20.3
<i>Klebsiella michiganensis</i>	46.7	0.5
<i>Candida albicans</i>	1.9	0.1
<i>Enterococcus faecalis</i>	1.7	0.2
<i>Klebsiella oxytoca</i>	0.7	4.1
<i>Coprobacillus sp.</i>	-	48.2
<i>Klebsiella sp.</i>	-	6.7
<i>Beggiatoa sp.</i>	-	7.5
<i>Candidatus Pelagibacter</i>	-	4.5
(k) <i>Bacteria sp.</i>	-	2.6
(f) <i>Enterobacteriaceae</i>	-	1.1
(o) <i>Enterobacterales</i>	-	0.3
<i>Vibrio campbellii</i>	-	0.3
<i>Psychrobacillus sp. FJAT-21963</i>	-	0.3
<i>Vibrio agarivorans</i>	-	0.2
<i>Mycobacterium kansasii</i>	-	0.1
<i>Paeniglutamicibacter antarcticus</i>	-	0.1
<i>Salmonella enterica</i>	-	0.1
181 more taxa	-	2.7

■ Accurate Species Identification
 ■ False Positives

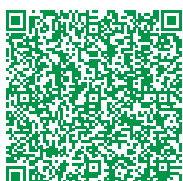
Results of two bioinformatics pipelines analyzing the same raw sequence data derived from a vaginal swab sample.

Controlling False Positives

Many other service providers suffer from false positive species identification due to the presence of host DNA in samples and the use of reference microbial genomes contaminated by human genome sequences. The pipeline of service provider D (built on Kraken) reported 202 total taxa from a vaginal swab sample and 197 of these taxa were determined to be false positives. Zymo Research's bioinformatic pipeline is able to accurately identify 5 taxa in the sample.



Ask us about our Metatranscriptomic pipeline



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Sample Collection & Kit Design

Simple, Safe, & Stable

Zymo Research's comprehensive catalog offers a way to partner with a single company for all your service and product needs. With Zymo Research, a variety of sample collection devices can be seamlessly paired with customizable Direct-to-Consumer kits. With our DNA/RNA Shield™ collection reagent, samples can be safely collected, stored, and shipped at ambient temperature without worrying about their stability.

Our experienced scientists will work directly with you to implement a personalized workflow for your business needs. Working with an industry-trusted partner ensures that your customers are getting the best results and de-risks your investment.

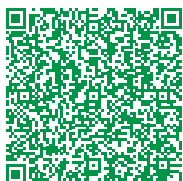


Swabs, Tubes, & Buffers for All Your Collection Needs

Collect the Following Sample Types:

- ✓ Saliva
- ✓ Blood
- ✓ Stool
- ✓ Urine
- ✓ Vaginal
- ✓ Environmental

Ask us how we can implement your custom branding into your kits and reports!



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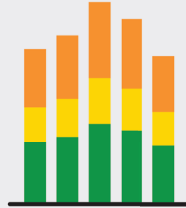


Custom Data Reporting

Your Results, Your Way



Customizable Data Reports



Automatically Generated Plots

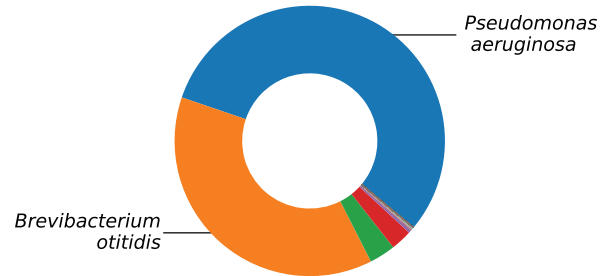


Detect Pathogens, Antibiotic Resistance, etc.

Simplify NGS Data Interpretation for Your Clients

Patient: John Doe DOB: 6/7/89
Test: Metagenomic Pathogen Detection Ordered by: Dr. Smith

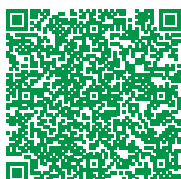
Comprehensive Microbial Analysis



Detected Pathogens

Bacteria

Species Name	Relative Abundance (%)	Absolute Abundance (# of cells)	Associated Disorder (if any)
Pseudomonas aeruginosa	55.9	1.7×10^7	
Brevibacterium otitidis	37.7	1.6×10^7	Bacteremia, Endocarditis, Ear Infections [1] [7]
Staphylococcus aureus	3.13	6.7×10^5	Otitis Media, Upper Respiratory Infection, Throat infections [2] [3] [4]



Learn more and inquire about custom microbiome solutions at www.zymoresearch.com/pages/custom-manufacturing-solutions



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