Master the Microbiome
Obtain a complete picture of complex microbial communities

The ProxiMeta Metagenome Deconvolution Platform combines cost-effective proximity ligation data with shotgun sequencing data, to assemble high-quality metagenomes and associate mobile genetic elements with their hosts. Capture strain-resolution insights without relying on 16S-based techniques, binning or culturing.

Key features:
- Assemble high-quality genomes directly from the microbiome
- Associate plasmids, phages and antimicrobial resistance genes (ARGs) with their hosts
- No high-molecular weight DNA or culturing required
- Short-read compatible; yields libraries for Illumina® sequencing
- User-friendly, 8-pack ProxiMeta Kit with cloud-based ProxiMeta Analysis included
**Technology**

1. DNA is crosslinked in vivo to fix DNA sequences present inside the same cell. Crosslinking traps sequence interactions across the entire genome and between different chromosomes and plasmids.

2. Crosslinked DNA is fragmented with endonucleases.

3. Fragmented loci are then biotinylated and proximity ligated, creating chimeric junctions between adjacent sequences. Any two sequences that create a junction must have originated within the same cell.

4. Biotinylated junctions are purified and subjected to paired-end sequencing.

5. Sequences of the proximity junctions are used to cluster genome, plasmid, and viral DNA by cellular origin. The computational platform assembles genomes, deconvolutes strains and assigns plasmids/phage to their hosts.

For Research Use Only. Not for use in diagnostic procedures.
**Applications**

**Assemble high-quality genomes without guesswork**

Metagenome assembled genomes (MAGs) generated by binning leaves genomes fragmented and contaminated. Unlike binning, proximity ligation provides direct, physical evidence of sequences co-located in the same cell. The ProxiMeta™ computational platform uses this information to cluster proximity-assembled genomes (PAGs) for both eukaryotic and prokaryotic members of the microbiome population. Each genome is assessed for completeness, contamination and novelty.

Simply upload your sequencing data to our cloud-based ProxiMeta Analysis platform.

![ProxiMeta Results](image)

- More complete
- Less complete
- Binning
- Contamination

**Link mobile genetic elements to their hosts**

In addition to the genome assemblies for members of a metagenomic sample, the ProxiMeta workflow also yields sequence information for mobile genetic elements (MGEs). These may include plasmids, transposons and antibiotic resistance genes (ARGs).

Since proximity ligation is performed on intact cells, MGE-host interactions are also captured. During the ProxiMeta assembly, mobile genetic elements are associated with their hosts with a high degree of confidence. This allows you to gain insight into horizontal gene transfer in complex microbial communities.

![Genomes assembled from wastewater](image)

Genomes assembled from wastewater arranged in an evolutionary tree (center), showing which are hosts to different mobile elements (middle rings). Bacterial families for each genome are displayed in the colored outer ring. From: Stadler, T. et al. The ISME Journal 2019; 13: 2437.

**View more published metagenomics research at:**

[http://phasegenomics.com/publications/#papers](http://phasegenomics.com/publications/#papers)

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Complete Sample-to-Analysis Solution

Accelerate your metagenomics research with our user-friendly sample prep kits and ProxiMeta™ Metagenome Deconvolution Analysis software. The kit yields a dual-indexed proximity ligation library, to be sequenced at 50 – 100 million paired-end reads on an Illumina® sequencer.

Proximity Ligation Sample Prep Workflow

1Hr 1.5Hrs 2Hrs 5Hrs 30M 1Hr 1.5Hrs 1Hr

- Crosslinking
- Cell Lysis
- Ligation & Reverse Crosslinks
- Bond Binding
- Purify DNA
- Library Prep
- Library Cleanup

NEW: 8-pack ProxiMeta Kit

- Everything needed for eight sample preps, starting from intact cells
- Only 3 hours hands-on time
- ProxiMeta analysis included

Take advantage of our expertise

Not an expert in sample preparation? Let us do the hard work with our full ProxiMeta service, which includes proximity library preparation, sequencing and analysis. Preparation and sequencing of shotgun metagenomic libraries are available as a separate service.

Not doing metagenomics research? Contact us for the genome scaffolding services listed below.

Proximo™ Genome Scaffolding

- Chromosome-scale genome scaffolding for virtually any organism, no high-molecular weight DNA required.

Proximo SV

- Identify large-scale structural variation and determine epigenetic changes using Hi-C data.

FALCON-Phase™

- Integrate PacBio long-read assemblies with Hi-C data to generate phased, diploid genome assemblies.

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