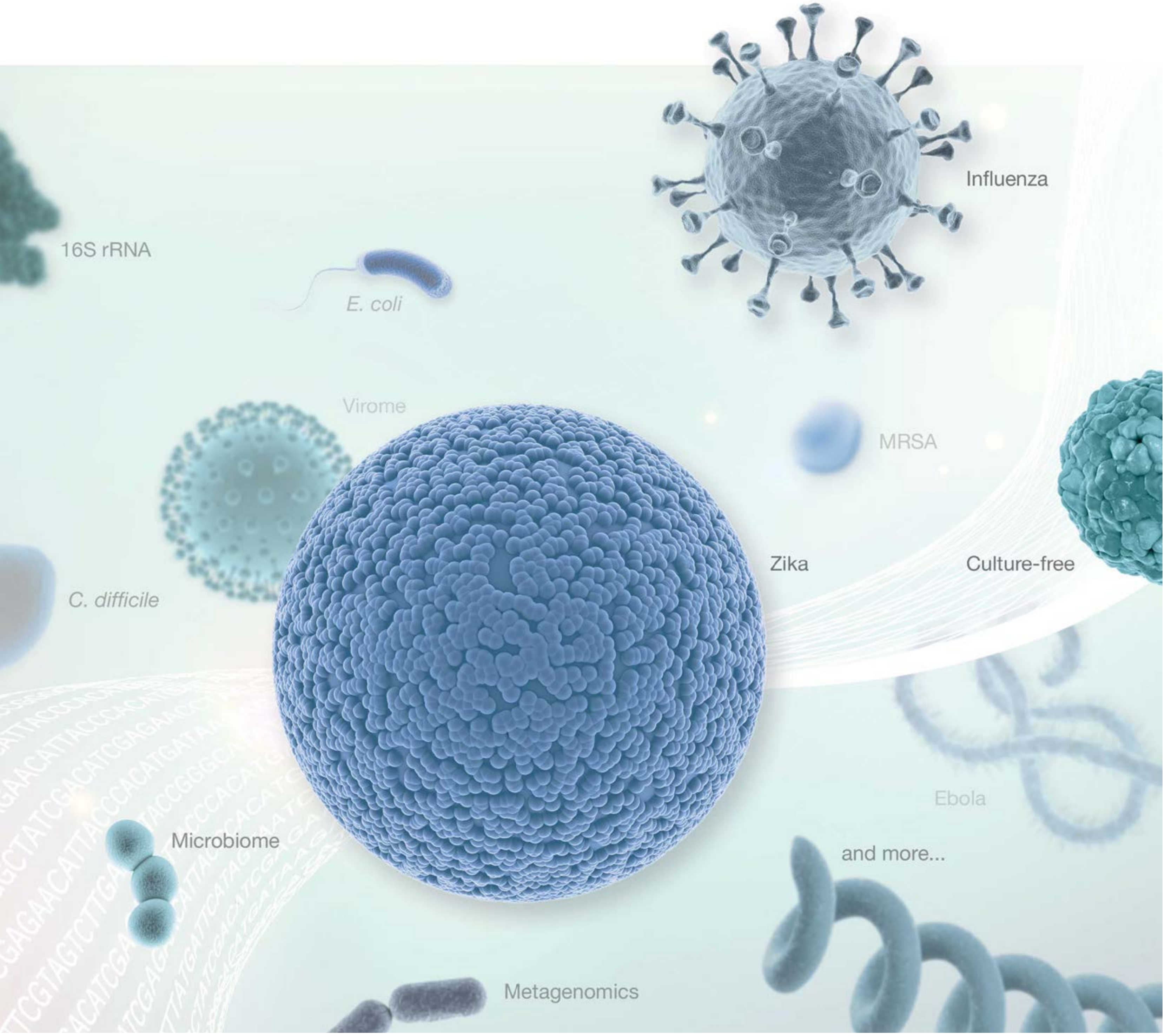
illumina®

Comprehensive microbiology solutions



Illumina next-generation sequencing (NGS) offerings for microbiology

Area of Interest	Method	Workflow			
		DNA preparation	**Library preparation**	**Sequencing**	**Data analysis**
MRSA *C. difficile* *E. coli* and more…	**Whole-genome sequencing** Generate accurate reference genomes for microbial identification and other comparative genomic studies.		Nextera® XT Kit	MiniSeq™ System, MiSeq® Series	Cloud: BaseSpace® Sequence Hub, assemble bacteria *de novo*, SPAdes Genome Assembler, Velvet *de novo* assembly
16S rRNA	**16S rRNA sequencing** Identify and compare bacteria present within a given sample.	16S library prep protocol	Nextera XT Kit	MiSeq Series	Cloud: BaseSpace Sequence Hub Local: MiSeq Reporter, 16S metagenomics
Metagenomics Microbiome Virome Culture-free	**Shotgun metagenomics** Detect low abundance members of the microbial community.		Nextera XT Kit	NextSeq® Series, HiSeq® Series	Cloud: BaseSpace Sequence Hub, Kraken Metagenomics, MetaPhlan
Ebola Zika Influenza and more…	**Virology** Determine the source of infection, route of transmission, and molecular pathway.		Nextera XT Kit	MiniSeq, MiSeq, NextSeq, and HiSeq Series	PathSeq Virome, DeepChek-HBV, DeepChek-HIV

Bioinformatics solutions

BaseSpace® Sequencing Hub is the Illumina cloud-based genomics computing environment for NGS data management and analysis. Store and share sequencing data. Access BaseSpace Hub via an intuitive web-based interface or linux-based command line tool.

Whole-genome sequencing
SPAdes Genome Assembler is an open source tool for *de novo* sequencing. This application is designed to assemble small genomes from MDA single-cell and standard bacterial data sets.

Create a *de novo* assembly pipeline for bacterial samples using the Velvet assemble

16S rRNA Sequencing
The 16S metagenomics app performs taxonomic classification of 16S rRNA targeted amplicon reads using an Illumina-curated version of the GreenGenes taxonomic database.

QIIME is designed to take users from raw sequencing data generated through publication quality graphics and statistics. This includes demultiplexing and quality filtering, OTU picking, taxonomic assignment, phylogenetic reconstruction, and diversity analyses and visualizations.

Shotgun Metagenomics
MetaPhlAn (metagenomic phylogenetic analysis) is a computational tool for profiling the composition of microbial communities from metagenomic shotgun sequencing data.

The Kraken Metagenomics app assigns taxonomic labels to short DNA sequences with high sensitivity and speed using exact alignments of k-mers and a novel classification algorithm.

Getting started is easy

When you partner with Illumina, you become part of a community with more than 9185* publications in microbiology and virology. Our 'starter bundle' packages provide training, library prep, sequencing instrument, and reagent kits that support a wide range of sample volumes. We also offer a program that allows you to trade in your sequencer for an Illumina system.

Explore the exciting discoveries our NGS solutions are enabling. Visit **www.illumina.com/MicroStories** and **www.illumina.com/MicroWebinars**.

*Illumina maintains an up-to-date database of all published scientific articles that use Illumina technology.

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