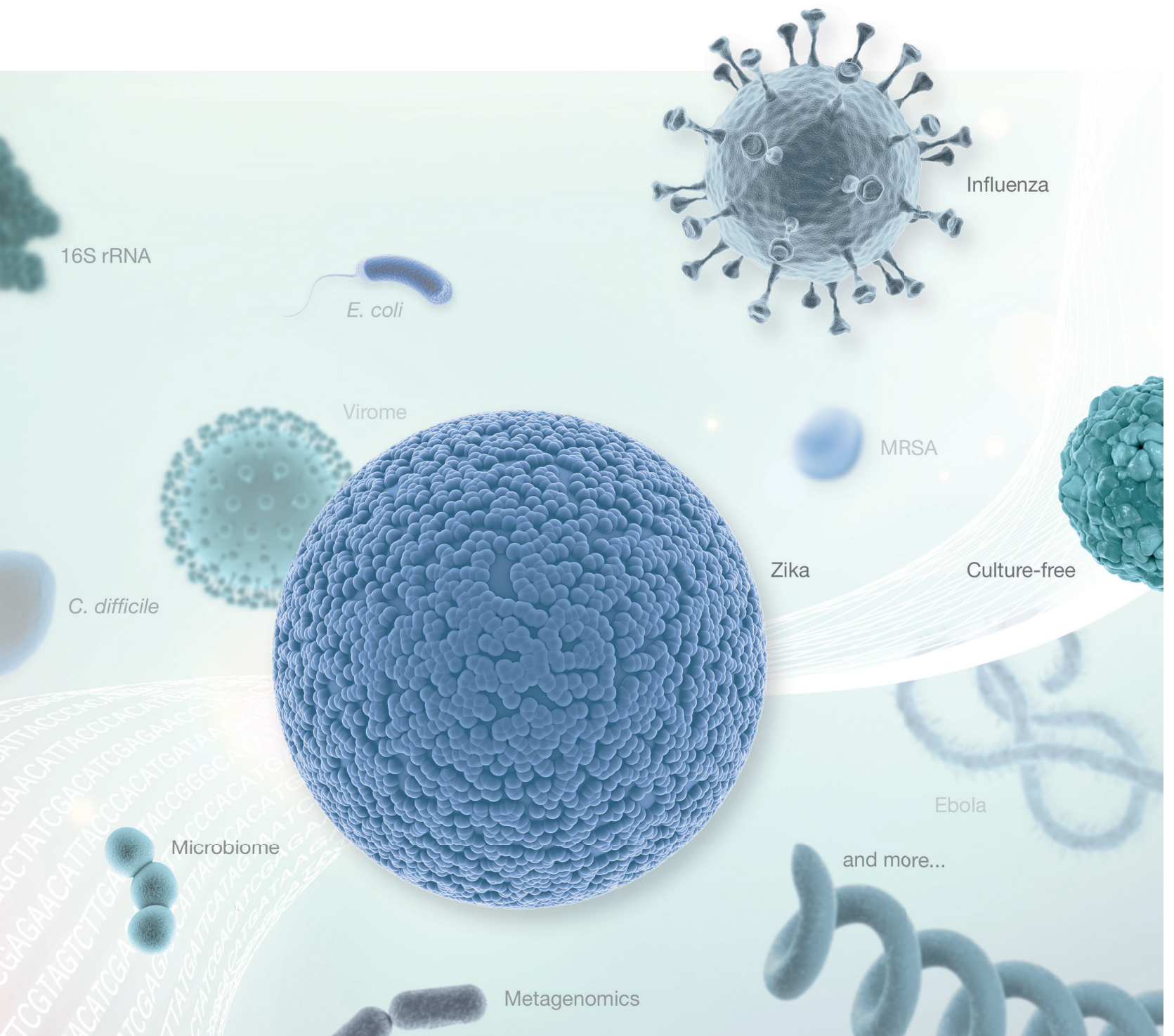
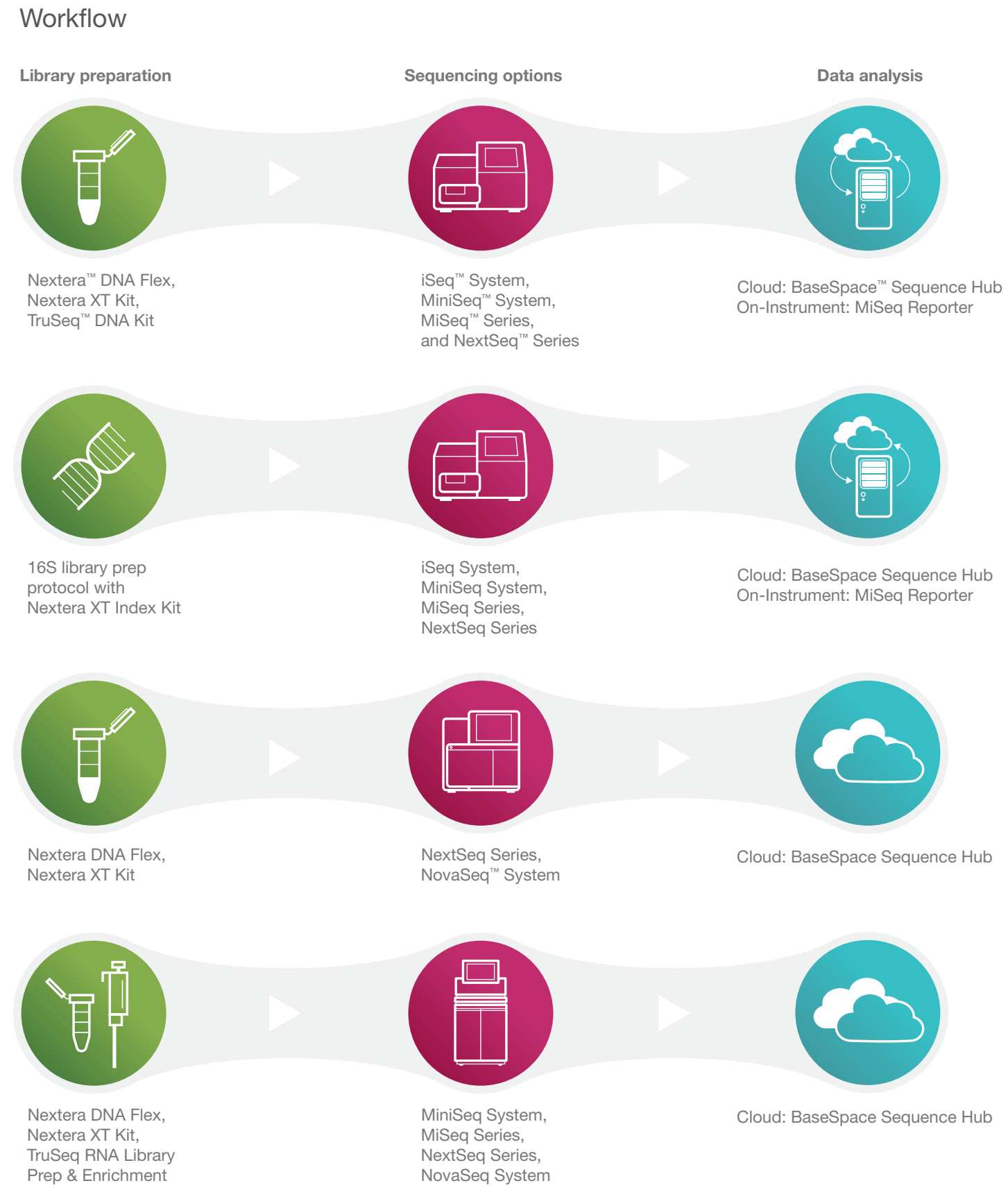


Comprehensive microbiology solutions



Illumina next-generation sequencing (NGS) offerings for microbiology

Area of Interest	Technology & Applications
<ul style="list-style-type: none"> Antimicrobial resistance Basic research Epidemiology Infectious disease 	Whole-genome sequencing Generate accurate reference genomes for microbial identification and/or other comparative genomic studies starting from culture.
<ul style="list-style-type: none"> Culture-free Microbiome Bacteria and archaea Phylogenetic classifications 	16S rRNA sequencing Identify and compare bacteria and archaea present within a given sample.
<ul style="list-style-type: none"> Community profiling Culture-free Environmental Microbiome Resistome Virome 	Shotgun metagenomics Identify, characterize, and detect low-abundance members of the microbial community.
Virology <ul style="list-style-type: none"> Pan-viral Ebola Zika Influenza and more... 	Shotgun metagenomics RNA sequencing Gene expression, functional profiling, and viral sequencing.



Data analysis & Bioinformatics solutions

BaseSpace™ Sequence Hub is a powerful cloud-based computing environment where NGS data can be easily stored, analyzed, and shared. Sequencing data from Illumina instruments are streamed in real-time over the internet to BaseSpace. The data is automatically converted to standard file formats (FASTQ) for analysis by applications (apps). Users launch apps in BaseSpace with just a few mouse clicks to analyze and visualize their data.

Whole-genome sequencing

- Bacterial Analysis Pipeline:** Identifies species, multilocus sequence type, plasmids, virulence, and antimicrobial resistance genes in bacteria.
- SPAdes Genome Assembler:** An open source tool for *de novo* sequencing. This app is designed to assemble small genomes.
- SRST2:** Reports sequence types from a MLST database and/or reference genes from a database of sequences for virulence genes, resistance genes, and plasmid replicons.
- Velvet *de novo* Assembly:** Use the Velvet assembler for *de novo* assembly of bacterial genomes.

16S rRNA sequencing

- 16S Metagenomics:** Performs taxonomic classification of 16S rRNA targeted amplicon reads using an Illumina-curated version of the GreenGenes taxonomic database.
- Kraken Metagenomics:** Assigns taxonomic labels to short DNA sequences with high sensitivity and speed using exact alignments of k-mers and a novel classification algorithm.
- QIIME:** An open-source bioinformatics pipeline for performing microbiome analysis from raw DNA sequencing data.

Shotgun metagenomics

- GENIUS Metagenomics:** Know Now: CosmosID's curated genome database provides rapid, accurate, and actionable bacterial identification at the species, subspecies, and/or strain level.
- Kraken Metagenomics:** Assigns taxonomic labels to short DNA sequences with high sensitivity and speed using exact alignments of k-mers and a novel classification algorithm.
- MetaPhlAn (metagenomic phylogenetic analysis):** A computational tool for profiling the composition of microbial communities from metagenomic shotgun sequencing data.

Virology

- DeepChek® (HBV, HCV, HIV):** Performs deep sequencing analyses and reports on subtyping, genotyping, and inferred levels of resistance.
- Kraken Metagenomics:** 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 10,000* 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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