



Gain greater **insights** into microbial mysteries

Innovative microbial sequencing solutions

Working together to make an impact in the microbial world

Today more than ever, next-generation sequencing (NGS) is empowering a new level of accuracy and speed in obtaining answers in microbial and infectious disease research. This proven sequencing approach greatly enhances research efforts and offers potential solutions to address One Health issues.*

A broader view, a brighter future

With Illumina technology and support, researchers around the world are rapidly sequencing the genomes of microbes and gaining insights into their behavior, interactions with their hosts and environments, evolution, and circulation within and throughout global populations.

Depending on the microbes of interest, sample type, and the kind of questions you want answered, different NGS workflows and solutions can be used. The optimal workflow should be determined by what goals need to be achieved.

Illumina NGS solutions are up for the challenge

Single genome, multipathogen, and discovery workflows can support the full array of microbiology and infectious disease research applications.

Illumina offers powerful library preparation kits, sequencing systems, and corresponding analysis and reporting solutions that enable discoveries and provide insights to better understand the microbes most relevant to your research.



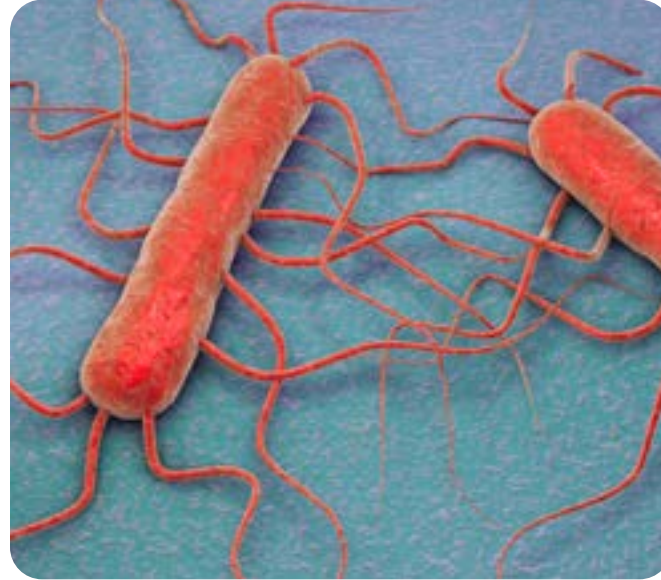
ADVANCE YOUR RESEARCH: With the right suite of NGS tools, you can gain a more complete picture of microbial genomes for research, clinical, and surveillance applications.

*One Health: [cdc.gov/onehealth](https://www.cdc.gov/onehealth)

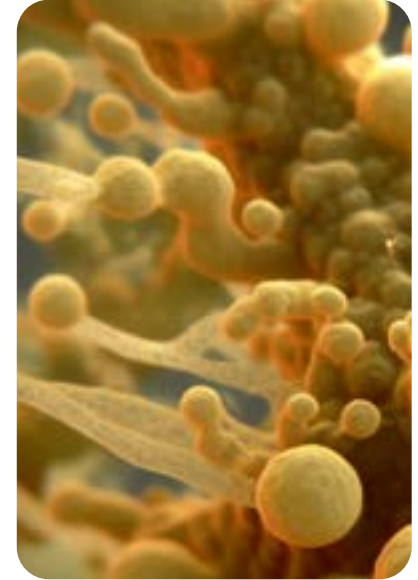
For research use only. Not for use in diagnostic procedures.



Escherichia coli bacteria



Listeria monocytogenes bacteria



Candida auris fungus



WORKFLOW APPLICATION

Single-genome sequencing

Sequencing of a single pathogen is best used in situations when a single, known microbe is being analyzed.* These solutions will help you gain valuable insights in your research as you work to develop effective diagnostic tools, vaccines, and targeted therapies.

Small whole-genome sequencing

Illumina DNA Prep

Fast, flexible library preparation kit for characterization of cultured isolates. Ideal for investigating foodborne outbreaks and health care-associated infections:

- Run multiple sample types, DNA or cDNA input amounts, and methods
- Access fast library prep with total turnaround time ~3.5 hours



MONITOR MORE: Single-genome sequencing also helps in tracking and monitoring the spread of disease outbreaks.



Single-genome sequencing

Targeted virus characterization

COVIDSeq™ Assay and COVIDSeq Test

Scalable, simple, and affordable solutions for whole-genome analysis of the SARS-CoV-2 virus to aid in COVID surveillance and viral research efforts:

- 96 and 3072 sample kit versions
- Allows for flexible input for multiple sample types, including nasal swabs and wastewater samples
- Produces highly accurate virus characterization of results enabled by the Illumina DRAGEN™ COVID Lineage App*

Illumina Microbial Amplicon Prep–Influenza A/B

Simple and affordable whole-genome characterization of influenza A and B viruses for surveillance and seasonal vaccine research:

- > 98% coverage for both A and B influenza viruses*
- Streamlines workflows; nine hours from extracted RNA to sequence-ready library
- Simplifies whole-genome analysis and variant interpretation with the DRAGEN Targeted Microbial App

Illumina Microbial Amplicon Prep

Flexible support of user-defined pathogen sequencing with a single, efficient workflow:

- Pairs with lab-designed primers, published primers, or commercially available primer sets
- Enhances flexibility to accommodate different sample types, including nasal swabs, wastewater, and culture
- Analysis powered by DRAGEN Targeted Microbial App

Targeted tuberculosis sequencing

Illumina and GenoScreen Deeplex® Myc-TB Combo Kit

Determine TB strain and drug-resistance profiles faster than traditional culture-based methods for a more timely response to this critical public health threat:

- Produces results in < 48 hours directly from sputum, no culture required
- Predicts resistance to 15 anti-tuberculosis drugs
- Provides secure and automated analysis and easy interpretation of results via the Deeplex Web App



Mycobacterium tuberculosis bacteria



Multipathogen sequencing

Hybrid-capture enrichment sequencing solutions are ideal for when certain pathogens are suspected to be present—or for surveillance of multiple known pathogens. They allow for targeted or whole-genome sequencing of multiple organisms without requiring the high read depth needed for shotgun metagenomic sequencing of unenriched libraries.*

Broad viral, zoonotic, and environmental surveillance

Viral Surveillance Panel

Extensive, whole-genome sequencing panel to reliably characterize the most critical viral public health threats for broad-based surveillance efforts:

- Conduct whole-genome sequencing of **> 60 RNA and DNA viruses** identified as high risk to public health
- Benefit from compatibility with a range of host and environmental sample types
- Detect low-abundance viruses that shotgun sequencing would miss*
- Analyze and interpret data with ease using the DRAGEN Targeted Microbial App

Pan-Coronavirus Panel

Expertly designed panel for research and surveillance of known and closely related novel coronaviruses:

- Characterization of > 200 known coronaviruses
- Analysis and interpretation of data with the easy-to-use DRAGEN Microbial Enrichment App

Respiratory Virus Enrichment Kit

Extensive, streamlined workflow offering highly sensitive detection and characterization of common respiratory viruses:

- Conduct whole-genome sequencing of **> 40 respiratory viruses**, including influenza A and B viruses, SARS-CoV-2, and many more
- Identify targeted viruses and new variants present and track variants from a variety of sample types
- Detect low-abundance viruses that shotgun sequencing would miss*
- Analyze and interpret data with the intuitive DRAGEN Targeted Microbial App

ANALYZE MORE: Compared with amplicon sequencing, multipathogen sequencing supports comprehensive profiling of more pathogens and difficult-to-sequence genomes.



Multipathogen sequencing

Flexible, comprehensive syndromic sequencing and antimicrobial resistance surveillance

Respiratory Pathogen ID/AMR Enrichment Panel Kit

Comprehensive panel designed to provide reliable identification and quantitation of respiratory pathogens and characterization of associated antimicrobial resistances for clinical research and surveillance:

- Identifies > 280 pathogens associated with respiratory tract infections
- Characterizes antimicrobial resistance of > 2000 markers associated to 26 antimicrobial classes
- Accommodates a variety of sample types
- Performs automated analysis powered by Explify RPIP Data Analysis

Urinary Pathogen ID/AMR Enrichment Panel Kit

The broadest sequencing-based panel to detect urinary pathogens and their associated antimicrobial resistances for clinical research and surveillance:

- Identifies > 170 pathogens associated with urinary tract infections
- Characterizes antimicrobial resistance of > 3700 markers associated to 18 antimicrobial classes
- Accommodates a variety of sample types
- Performs automated analysis powered by Explify UPIP Data Analysis



DETECT MORE: Multipathogen sequencing does not require cultured isolates and can be used to detect specific microbes and certain antimicrobial resistance (AMR) mutations.



Vibrio cholerae bacteria



WORKFLOW APPLICATION

Pathogen discovery

NGS is a useful approach for truly unbiased analysis of a primary sample. Shotgun DNA or RNA sequencing enables analysis of the genetic material present in complex microbial communities, such as environmental samples (e.g., wastewater), human microbiomes, and primary samples (e.g., sputum, lower respiratory aspirates).

Metagenomics and metatranscriptomics

Illumina DNA Prep

Fast, flexible library prep for microbiome discovery research and surveillance:

- Run multiple sample types, DNA or cDNA input amounts, and methods
- Access fast library prep with total turnaround time ~3.5 hours
- Apply the DRAGEN Metagenomics pipeline to perform taxonomic classification of reads and provide single sample and aggregate reporting

Illumina Stranded Total RNA Prep with Ribo-Zero™ Plus Microbiome

Fast, efficient library prep that provides robust depletion of undesirable host and pan-bacterial rRNA from complex microbial samples for microbiome analysis:

- Eliminate unwanted rRNA from bacteria in complex microbial samples for highly efficient metatranscriptomics research
- Obtain reliable results with an optimized library preparation workflow
- Simplify data analysis and visualization with the BaseSpace™ Microbiome Metatranscriptomics App



UNCOVER MORE: Comprehensively sample all genes and transcripts present in a given complex sample.



Gut microbiome



Working as one, your lab and Illumina can bring the benefits of NGS-powered microbiology and infectious disease research to everyone

How can we help you?

At Illumina, we offer technology and support to cover integrated NGS workflows — from library preparation to sequencing to data analysis to sharing. With optimized end-to-end solutions, you'll experience unrivaled accuracy, operational simplicity, and fast turnaround times.

Illumina is committed to promoting global health

Beyond product offerings, Illumina offers a wide range of educational resources, support, and training programs to enhance your research. Let's make an impact, together.

illumina®

We are always available for questions, insights, and conversation.

Visit us at [illumina.com](https://www.illumina.com).

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