

Approaches and techniques

Antimicrobial resistance

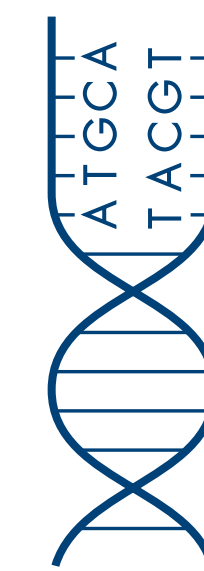
Strain typing and outbreak analysis

Microbiome profiling and functional metagenomics

Featured products and Contact information

# Microbial/Metagenomics with QIAGEN Digital Insights Solutions

  
**Tools** and **workflows**

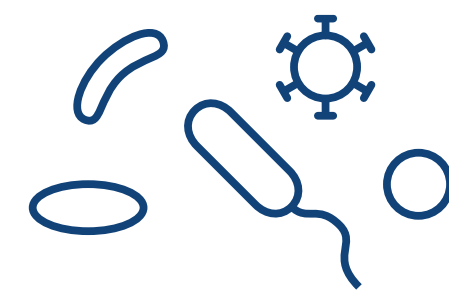


to meet a broad range of **bioinformatics** needs

for



**microbiome analysis**, isolate **characterization**,



functional **metagenomics** and **resistance identification**.



**Antimicrobial Resistance (AMR)**

**Isolates**

**Metagenomics**

**Microbiome**

## Make sense of complex microbial genomic data

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Uncover critical correlations among microbiota, its metagenome and host.

Make sense of complex metagenomic data through tools and streamlined analysis workflows for gene finding, annotation, and taxonomic and functional microbiome analyses.

Whether you're focused on **public health epidemiology**, **clinical microbiology research** or **basic microbial genomics research**, **QIAGEN Digital Insights** provides state-of-the-art tools for strain typing of **bacterial, fungal and viral** genomes.

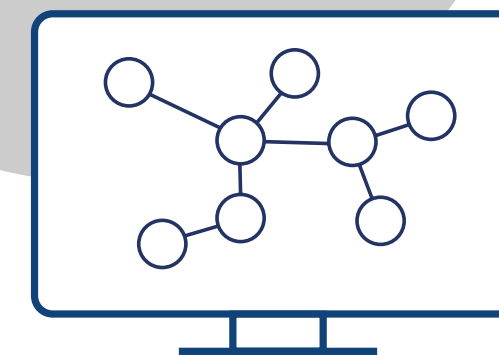
Leverage our epidemiological tool set and antimicrobial resistance database for advanced bioinformatics and genomics analyses of antimicrobial resistance (AMR) genes and markers.

### Microbial/Metagenomics tools and applications:

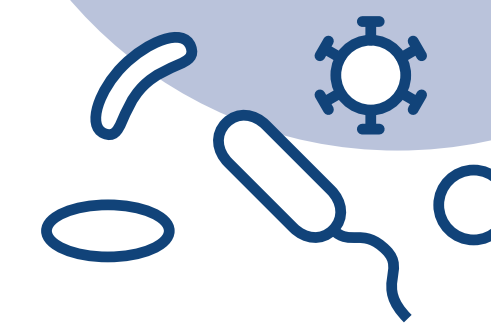
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To support you in the fight against the **worldwide** threat of emerging **antimicrobial resistant (AMR) pathogens**, a comprehensive set of tools and databases designed to work together are **readily available for download and immediate use**.

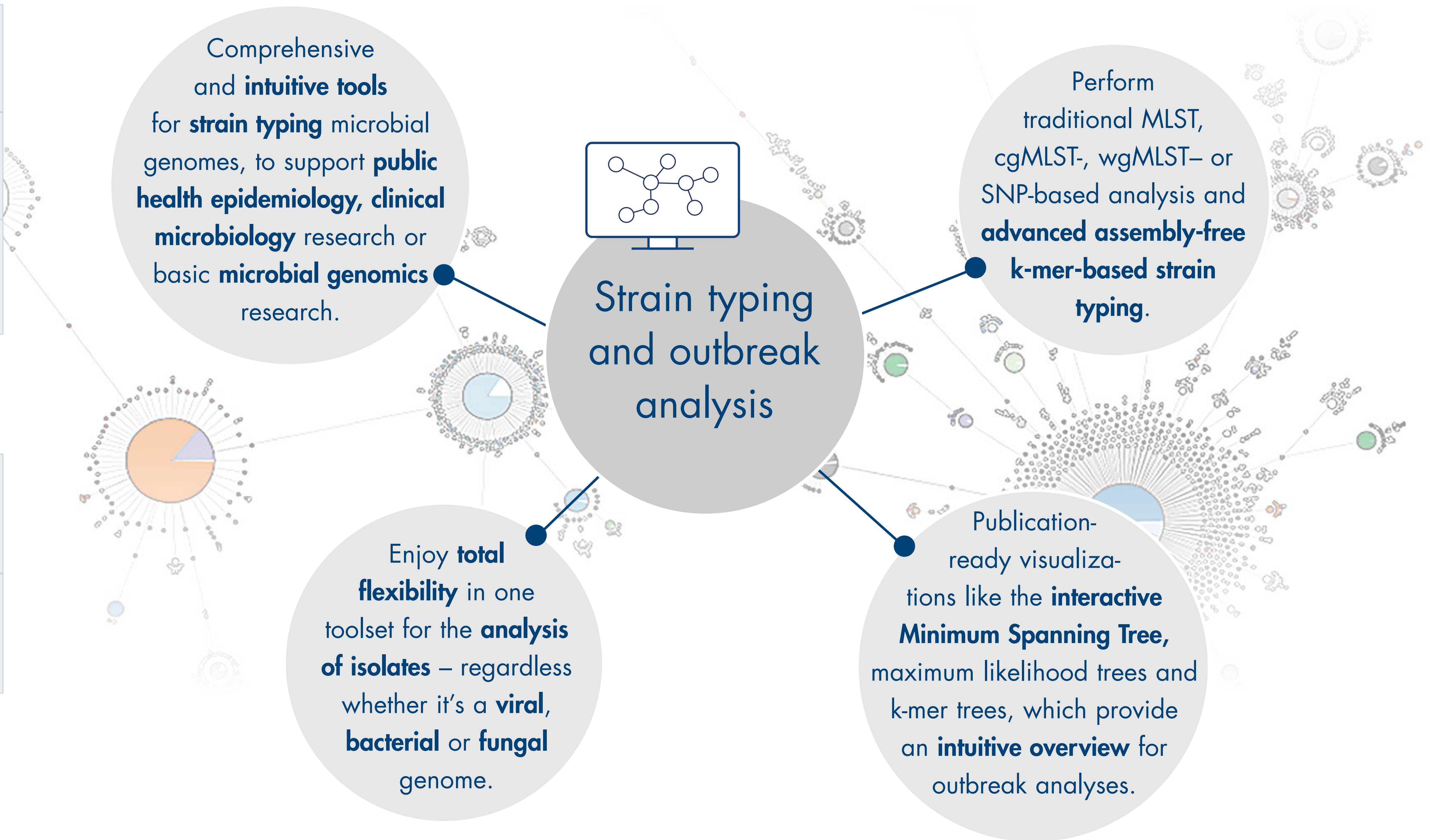
## Antimicrobial resistance

The tools **specifically developed for AMR** include those for analysis of:

- Assembled isolate **genomes or metagenomes**
- Tools for the **assembly-free detection of AMR markers** directly from your **FASTQ** data

Access to a **variety** of public and privately curated **AMR databases** enhances the ability to **characterize your data**.

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Unparalleled options for analysis of both **amplicon/OTU** and **whole metagenome sequencing** data.

Microbiome profiling and functional metagenomics

Access **innovative tools** for binning of contigs from **de novo assemblies**, important for **identifying plasmids** and other genomes from **unknown** species.

A fully integrated solution for:

- **16S/ITS microbiome profiling**
- **Shotgun metagenomics** profiling
  - **Metagenomics assembly**
  - **Automated gene finding**
  - Annotation with **BLAST** or **DIAMOND**

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## Featured products:

The products mentioned here are intended for molecular biology applications. They are not intended for the diagnosis, prevention or treatment of a disease. For up-to-date licensing information and product-specific disclaimers, see the respective product website. Further information can be requested from [TS-Bioinformatics@qiagen.com](mailto:TS-Bioinformatics@qiagen.com) or by contacting sales at [bioinformaticssales@qiagen.com](mailto:bioinformaticssales@qiagen.com).

Learn more at <https://digitalinsights.qiagen.com/microbial-genomics>.

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