

# Helicobacter pylori Resistance

VS-HPR0116PHRUO\*

End-to-end NGS solution for sequencing *Helicobacter pylori* and its antimicrobial resistance mutations through targeted amplicon sequencing.

Designed for routine labs and optimized for efficiency, robustness, and seamless implementation.

## Technology

Amplicon-based targeted enrichment. Ensuring **high sensitivity** and reproducibility with low DNA input.

## Workflow

- 01 Enrichment and indexing
- 02 Pooling
- 03 Sequencing
- 04 Bioinformatic analysis with V-Xplora

Total workflow time:

~4 hours

## Performance characteristics

- **Culture-free identification** directly from gastric biopsy or stool samples.
- Simultaneous detection of multiple **resistance-associated mutations**.
- **Low DNA input** requirements.
- Multiplex processing of **up to 16 samples**.
- **Reduced hands-on time** through a streamlined workflow.

## Reagents and format

- **Lyophilized, pre-dispensed** reagents.
- **Ready-to-use** format.
- **One-tube protocol** for enrichment and indexing.

## Platform compatibility

- Designed for **short-read sequencing** technologies.
- Validated on **Illumina platforms** and **AVITI™** (Element Biosciences).
- Compatibility with **other platforms** (e.g., MGI) may require additional **library conversion** steps.

## Targeted regions

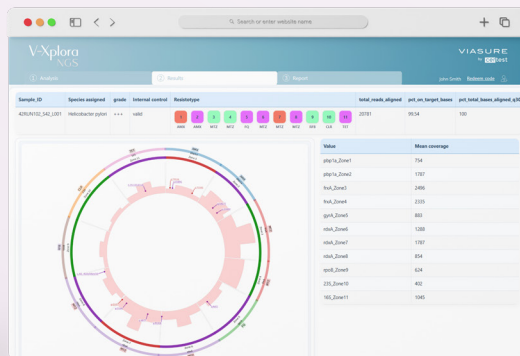
Antibiotic	Gene	Key Mutations
<b>Clarithromycin</b>	23S rRNA	A2143G, A2142G, A2142C
<b>Fluoroquinolones</b>	gyrA	N87K/I, D91N/Y/G
<b>Metronidazole</b>	rdxA / frxA	Truncating and frameshift mutations
<b>Amoxicillin</b>	pbp1A	S414R, T556S, N562Y
<b>Tetracycline</b>	16S rRNA	A965T + G966T + A967C
<b>Rifabutin</b>	rpoB	Non-synonymous mutations

## Data analysis

Using **VIASURE V-Xplora** software:

- ✓ FASTQ-to-report workflow
- ✓ Automated variant detection and interpretation
- ✓ Use of curated databases and predefined pipelines
- ✓ Standardized report generation
- ✓ Visualization tools for data exploration

No  
bioinformatics  
expertise  
required



*Circos-based resistome visualization across the genome.*