



## PUBLICATIONS

# Pathogen Detection

Using Products From Standard BioTools

**Shrestha, S. et al. “High-throughput microfluidic quantitative PCR system for the simultaneous detection of antibiotic resistance genes and bacterial and viral pathogens in wastewater.” *Environmental Research* 255 (2024): 119156.**

**Objective:** Simultaneously quantify antibiotic resistance genes (ARGs) in wastewater using high-throughput qPCR to understand the relationship between pathogens and antibiotic resistance in environmental waters.

### Highlights

- HT-qPCR system capable of concurrently assessing 14 distinct assays.
- qPCR assays can be modified to rapidly adjust to emerging and reemerging infectious diseases and ARGs.
- All qPCR assays exhibited high performance with  $R^2 \geq 0.978$  and efficiencies ranging from 90.5% to 117.7%.
- Fifty-six percent of samples were positive for norovirus genogroup II, 67% were positive for *Salmonella* spp. and *Campylobacter jejuni* and 36% were positive for *Campylobacter coli*.
- Insights from this study suggest the importance of a high-throughput qPCR system for wastewater-based epidemiology studies.

**Malla, B. et al. “Application of a high-throughput quantitative PCR system for simultaneous monitoring of SARS-CoV-2 variants and other pathogenic viruses in wastewater.” *Science of the Total Environment* 853 (2022): 158659.**

**Objective:** Rapid pathogen detection in wastewater for community monitoring in Japan.

### Highlights

- Simultaneously detect 22 targets in one run.
- Targets: SARS-CoV-2, key variants and epidemiologically relevant viruses such as InfA, NoV-G1, NoV-GII, EnV, RVA and Aiv-1

**Buelow, E. et al. “Hospital discharges in urban sanitation systems: long-term monitoring of wastewater resistome and microbiota in relationship to their eco-exposome.” *Water Research X* 7 (2020): 100045.**

**Objective:** Develop an approach to assess wastewater for ARGs and microbial communities.

### Highlights

- Hospital and urban wastewater antimicrobial resistance (AMR) genes were stable over time.
- Hospital wastewater contains significantly higher loads of ARGs and AMR.
- AMR data shows no risk of increased spread when processing mixed wastewater samples.

All applications that were performed using IFCs on the Biomark™ HD or Juno™ instruments can be performed on the **Biomark X9™ System for High-Throughput Genomics.**



**Berry, I.M. et al. “Genomic surveillance of SARS-CoV-2 in US military compounds in Afghanistan reveals multiple introductions and outbreaks of Alpha and Delta variants.” *BMC Genomics* 23 (2022): 513.**

**Objective:** Sequence and analyze SARS-CoV-2 samples collected from personnel at major military compounds in Afghanistan.

**Highlights**

- Sequencing and phylogenetic analyses found 16-plus independent introductions of Alpha and Delta SARS-CoV-2 in four isolated compounds in Afghanistan during April and May 2021.
- Four of these introductions resulted in spread within and between compounds.
- In some cases, Alpha and Delta outbreaks occurred simultaneously.

**Michelet, L. et al. “High-throughput screening of tick-borne pathogens in Europe.” *Frontiers in Cellular and Infection Microbiology* 4 (2014): 103.**

**Objective:** Develop a panel to detect and assess the prevalence of common and rare pathogens in a high-throughput (HT) capacity.

**Highlights**

- HT method allows simultaneous detection of 25 bacterial and 12 parasitic species from ticks.
- Reliably detected expected pathogens and detected several pathogens on Danish ticks for the first time.
- Method can be customized quickly to monitor emerging diseases.

**Coudray-Meunier, C. et al. “A novel high-throughput method for molecular detection of human pathogenic viruses using a nanofluidic real-time PCR system.” *PLoS One* 11 (2016): e0147832.**

**Objective:** Develop a high-throughput, cost-effective method for monitoring 19 human enteric pathogens associated with food/waterborne diseases.

**Highlights**

- Standard BioTools™ microfluidic-based integrated fluidic circuits (IFCs) produced similar results to conventional qPCR methods.
- All clinical samples tested were detected and results met expectations.
- Authors successfully detected instances of coinfection or multiple viral genomes per sample.



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