# Biomedical, Virus and Bacteria-related Microbial Research Panels

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| **my Baits Expert Respiratory Virus Kits** | Expert Respiratory Virus Kit, with individual modules - List of modules: Adenovirus (15+*), Bocavirus (3), Chickenpox (1), Coronavirus Human (4), Coronavirus Non-human (60), EBV (2), Enterovirus (8), Influenza A (7), Influenza B (1), Influenza C (1), Measles (1), MERS (1), Metapneumovirus (6), Mumps (1), Orthopneumovirus / RSV (7), Parainfluenza (4), Parechovirus (6), Rhinovirus (38), Roseola (4), SARS (1), SARS-CoV-2 (6) myBaits Expert Respiratory Virus Kit, precombined all-modules | Hybridisation capture panels for sequencing genome-scale data from common human-relevant respiratory viruses (DNA or RNA)<br><br>Available as a single module for 20+ virus groups or individual probe sets per group. | Sequencing respiratory viruses (e.g., SARS-CoV-2, Influenza, RSV)<br><br>Detecting and characterising genomic diversity/function of specific pathogen species/strains<br><br>Profiling microbial communities in complex substrates (e.g., faeces, wastewater, soil)<br><br>Studying viral evolution, transmission dynamics, and co-infections<br><br>Public health surveillance and disease tracking/monitoring | Low-abundance targets in complex samples (e.g., host-dominated DNA/RNA)<br><br>Degraded or trace DNA/RNA from FFPE, wastewater, or ancient samples<br><br>Need for strain-level resolution and variant detection<br><br>Cost-effective sequencing for large sample sets<br><br>Flexible panels that can be customised or scaled | High enrichment rates (many orders of magnitude) even from degraded samples<br><br>Customisable designs for specific pathogens or gene families<br><br>Efficient sequencing from complex backgrounds (e.g., human, environmental, faecal)<br><br>Bioinformatics support and optional lab services via myReads | Identification of coinfections<br><br>Detection of novel pathogens<br><br>Public health surveillance outbreak tracing<br><br>Monitoring viral evolution<br><br>Waste-water based epidemiology |

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| **AMR Community Panels** | "Resistome" – Antimicrobial Resistance Genes (ARG) enrichment panel<br>"AMR–Cap" – Antimicrobial Resistance Gene enrichment panel | Targeted enrichment panels for antimicrobial resistance genes (ARGs) from CARD and PAI-DB databases<br><br>Designed for comprehensive AMR surveillance and research<br><br>Targets >3,500 AMR genes<br><br>>200-fold increase in on-target reads vs shotgun sequencing<br><br>Compatible with low-input and degraded DNA | Profiling resistance genes in clinical, environmental, and agricultural samples<br><br>Monitoring AMR trends in wastewater, natural environment, and built environment (e.g. hospitals, public transport, etc.)<br><br>Studying resistomes in complex microbial communities<br><br>Supporting outbreak investigations and surveillance programs<br><br>Developing culture-free diagnostics for high-containment pathogens | Low-abundance AMR genes in complex samples<br><br>High sequence diversity (hard for PCR/arrays)<br><br>Cost constraints for large-scale surveillance<br><br>Diverse sample types (faeces, wastewater, tissue, air filters)<br><br>Need for strain-level resolution | Compatibility with low-input and degraded DNA<br><br>Easy to update as new resistance genes are discovered<br><br>Demonstrated performance in real-world samples (e.g., wastewater, clinical surfaces) | AMR surveillance & tracking<br><br>Public Health Policy support<br><br>Drug Development<br><br>Combating superbugs,<br><br>Preserving antibiotic effectiveness |

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| **"CryptoCap" Cryptosporidium WGS catalog panel** | myBaits Expert CryptoCap WGS v2.0<br><br>o 8 Rxn (Cat# 308508.V5)<br>o 48 Rxn (Cat# 308548.V5)<br>o 96 Rxn (Cat# 308596.V5) | Hybridisation capture kit for whole-genome sequencing of **Cryptosporidium spp**, targeting six major human-infecting species. Includes ~100,000 probes tiled across ~9 Mb genomes, making hyb-cap the most efficient and cost-effective solution. | Whole-genome sequencing (WGS) of Cryptosporidium spp. from clinical and environmental samples<br><br>Population structure and genetic diversity analysis for outbreak investigations<br><br>Drug and vaccine target discovery<br><br>Mixed-species infection detection and strain typing<br><br>One Health surveillance linking human, animal, and environmental reservoirs | Extremely low DNA yield from oocysts<br><br>Mixed species & heavy background DNA<br><br>WGS without enrichment is inefficient & costly<br><br>Need for high sensitivity & specificity in complex matrices | Targets six species (C. parvum, C. hominis, C. cuniculus, C. tyzzeri, C. meleagridis, C. viatorum)<br><br>~100,000 probes for genome-wide enrichment<br><br>Compatible with standard & high-sensitivity protocols<br><br>Proven performance on faecal & environmental samples<br><br>Optional full-service workflow (library prep, sequencing, bioinformatics) | Epidemiology & outbreak tracing<br><br>Population genetics and diversity studies<br><br>Drug/vaccine target identification<br><br>mixed species infection detection<br><br>one health surveillance |