

## TECHNOLOGY/BUSINESS OPPORTUNITY

### DETECTION AND IDENTIFICATION OF NUCLEIC ACID SUBSEQUENCES IN A COMPLEX MIXTURE

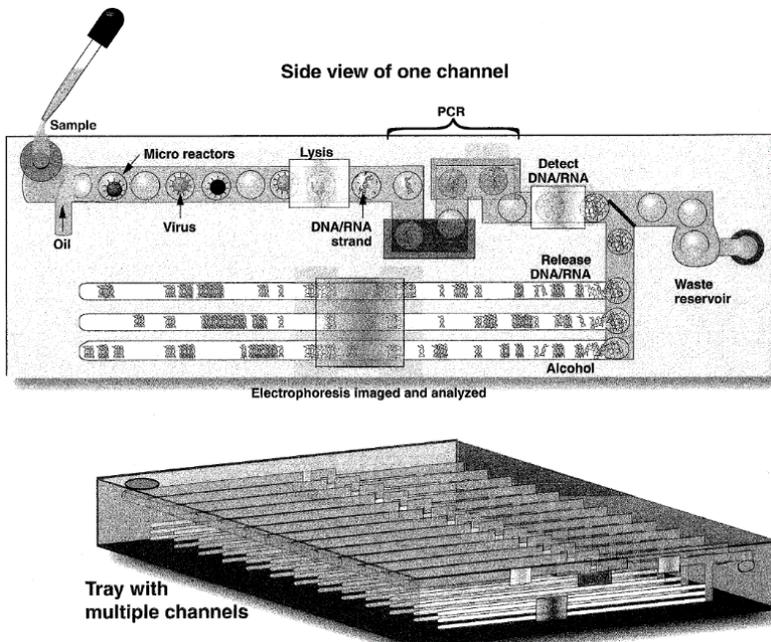
#### Opportunity

Lawrence Livermore National Laboratory (LLNL), operated by the Lawrence Livermore National Security (LLNS), LLC under contract no. DE-AC52-07NA27344 (Contract 44) with the U.S. Department of Energy (DOE), is offering the opportunity to secure a license to exercise patent rights for commercializing its detection and identification of nucleic acid subsequences in a complex mixture technology.

#### Background

There are trillions of unique microorganisms on this planet and identifying and analyzing specific viruses, pathogens, or other microorganisms in clinical or environmental samples can be challenging. Culturing viruses and certain other microorganisms for differentiation analysis is difficult. Few, if any, repeated sequences between microorganism genomes indicates fickle lineage between species and confounds the limited information available on, say, viral and other pathogen backgrounds. Metagenomics has been beneficial in providing metagenomic libraries, however, many metagenomic sequences have no homologues present in their databases, a key identifying factor for organisms. Improving the ability to identify and differentiate between organism families plays a key part in epidemic preparation and response.

#### Description



LLNL researchers have invented a system for identifying all known and unknown pathogenic or non-pathogenic organisms in a sample. This invention takes a complex sample and generates droplets from it. The droplets consist of sub-nanoliter volume reactors which contain the organism sized particles. A lysis device lyses the organisms and releases the nucleic acids. An amplifier then magnifies the quantity of available nucleic acids. Then, a fractionator liberates the nucleic acids from the droplets. Finally, a parallel analyzer identifies all the known and unknown

pathogen or non-pathogenic organisms in the complex sample. This device functions with DNA or RNA samples.

## Advantages

- Speedy and accurate detection and identification of organisms
- Parallel analyzer is compact for clinical, field, or research purposes
- Device can function with small sample sizes

## Potential Applications

- Identification and detection of pathogens which contain nucleic acid signatures such as spores, bacteria, and viruses
- Identification and monitoring of outbreaks of infectious diseases including emerging or unknown pathogens
- Detection of host or microbial and viral DNA or RNA in biological clinical samples

## Development Status

LLNL currently holds patent [8,338,166](#) "Sorting, amplification, detection, and identification of nucleic acid subsequences in a complex mixture" for this technology (LLNL internal # IL-11652).

Please visit the IPO website at <https://ipo.llnl.gov/resources> for more information on working with LLNL and the industrial partnering and technology transfer process.

Note: **THIS IS NOT A PROCUREMENT.** Companies interested in commercializing LLNL's detection and identification of nucleic acid subsequences in a complex mixture technology should provide a written statement of interest, which includes the following:

1. Company Name and address.
2. The name, address, and telephone number of a point of contact.
3. A description of corporate expertise and facilities relevant to commercializing this technology.

Written responses should be directed to:

Lawrence Livermore National Laboratory

Innovation and Partnerships Office

P.O. Box 808, L-795

Livermore, CA 94551-0808

Attention: FBO 438-19

Please provide your written statement within thirty (30) days from the date this announcement is published to ensure consideration of your interest in commercializing LLNL's detection and identification of nucleic acid subsequences in a complex mixture technology.