**Docket #:** S24-053

# Computational Pipeline for Accelerated Identification of Disease-causing Variants with Ultra-Rapid Nanopore Genome Sequencing

Rapid whole genome nanopore sequencing and data analysis is a platform developed at Stanford that delivers genomic results quickly. Combining optimized sample preparation, nanopore-based sequencing, and automated analysis, this technology enables fast genetic diagnostics for critically ill patients.

Subsequent wet-lab workflow and new software implementation are covered under Stanford Dockets:
**S25-288**, Accelerated Sample Preparation and Processing for Ultra-Rapid Nanopore Genome Sequencing
and **S25-337**, Accelerated Computational Pipeline for Ultra-Rapid Nanopore Genome Diagnosis.

## Applications

- Whole Genome Diagnostics

## Advantages

- Fast Turnaround Time
- Comprehensive Variant Detection
- High Yield of Disease Associated Variants

## Innovators

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