

Rapid sample-to-sequence profiling of circulating nucleic acids (RISE-Seq)

[2026-026]



THE UNIVERSITY OF
SYDNEY

Medical technology and devices



- > TRL 4
- > Proof of concept

Problem

Current cell-free DNA workflows can create significant barriers to scalable testing:

- Multiple extraction and library-preparation steps
- Millilitre-scale sample requirements
- Turnaround times of hours to days
- Dependence on specialised infrastructure and batch processing
- Limited suitability for decentralised and point-of-care applications

These constraints can increase cost, complexity and time to sequencing across cfDNA-based diagnostics and monitoring.

Solution

This is a simplified sample-to-sequencing workflow that generates sequencing-compatible material directly from plasma and cerebrospinal fluid.

Compared with conventional cfDNA workflows, the technology offers the potential for:

- 70–90% fewer workflow steps
- 50–80% lower costs
- More than 90% reduction in time to sequencing
- μ L input vs mL-scale input
- Reduced infrastructure requirements
- Greater compatibility with automation and decentralised deployment

Early proof-of-concept studies have demonstrated analytical concordance with standard workflows

and preservation of relevant cfDNA characteristics

Intellectual Property Status

This technology is the subject of an Australian provisional patent application.

Potential Commercial Applications

The workflow could support products, platforms and services across:

- Cancer detection and disease monitoring
- Multi-cancer early detection
- Fragmentomics and sequencing-based diagnostics
- Non-invasive prenatal testing
- Transplant monitoring
- Neurological disease testing using cerebrospinal fluid
- Automated and decentralised molecular-testing platforms

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