genefirst

ATOM-Seq®

An Alternative to Ligation-based Workflows

Patented technology developed to address the challenges of processing limited or poor-quality clinical samples. ATOM-Seq combines the advantages and overcomes limitations of other common library preparation approaches.

Uniquely Designed for Challenging Material

Ligation-free chemistry with no DNA end-repair steps, for efficient capture of any material

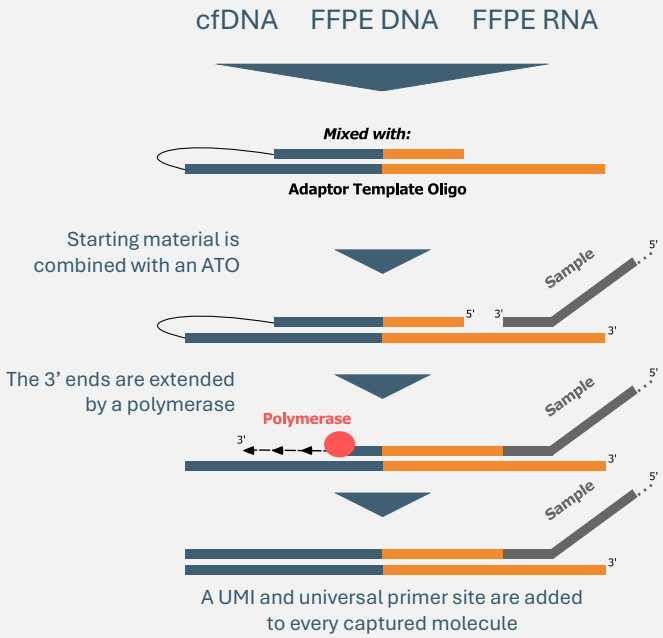
Maximum retention, minimal time, due to minimal purification steps

Capture more of your sample by capturing all single- and double-strand cDNA/DNA

Simple, single-day protocols, leveraging the inherent simplicity and efficiency of DNA polymerases

Process every sample with efficient workflows for short, degraded and low-abundance samples

ATOM-Seq Capture Chemistry



Powerful and Flexible Workflows

XCeloSeq® workflows maximise performance with patient samples and are easily implemented in any lab

Gene panels are easily customised with compatibility on all sequencing platforms including Illumina, MGI Tech, Thermo Fisher Scientific and Element Bioscience

Dynamic multiomic solutions including methylation, mutation, fragmentomics and CNV from a single sample

Comprehensively profile cancer-relevant biomarkers from the most precious patient samples

A combination of unique molecular identifiers and single primer enrichment detects even the lowest frequency signal with confidence

Workflow	Total Time (h)
cfDNA Whole Genome	4.5
cfDNA Target Enrichment	6
FFPE DNA Target Enrichment	6.5
FFPE RNA Target Enrichment	7.5

ATOM-Seq®

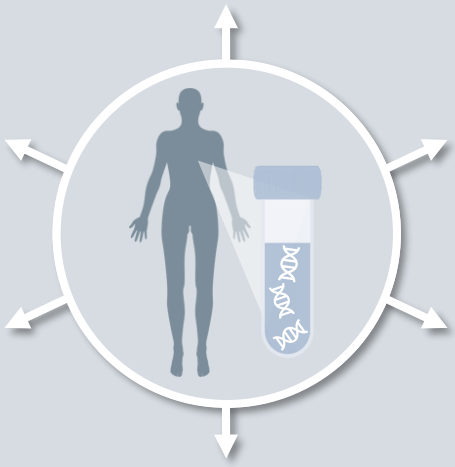
A Highly Versatile Library Preparation Chemistry

Uniquely suited to maximise information obtained from patient samples and NGS workflows

Whole-genome and targeted cell-free DNA applications from plasma and urine samples

Therapy guidance

Early cancer screening



Treatment response monitoring (tumour-informed or agnostic)

Whole-genome mutation, epigenetics and fragmentomics

Minimal residual disease (tumour-informed or agnostic)

Multiomic analysis of mutation, epigenetics and fragmentomics

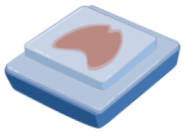
Targeted enrichment applications using poor-quality DNA and RNA from FFPE

RNA

Guides targeted therapies by identifying both **known** and **unknown** fusions

Identifies rare fusions for accurate disease classification

Calls SNVs and differential gene expression for greater sample insights



DNA

For the identification of single nucleotide variants, insertions, deletions, copy number variation, and MSI from even poor quality FFPE-preserved DNA

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