Cell-free DNA Enrichment Workflow

NGS library preparation workflows for capturing and enriching cell-free DNA from plasma and urine

Uniquely designed for challenging material

- Simple, ligation-free approach with no DNA end-repair
- Captures all single- and double-strand DNA
- Captures short and degraded material
- Efficient with low input quantities

genefirst

- Single primer enrichment to maximise capture regardless of DNA breakpoint
- Unique molecular identifies for error suppression
- Minimal bead purification steps



Minimal residual disease and cancer screening



ATOM-Seq's efficient capture of cell-free DNA makes it ideal for detecting any low frequency genetic signature from plasma or urine samples

Identifying rare low level tumour mutations

Track disease response

Monitoring residual disease



Detect even the rarest clinical signatures with confidence, using both UMIs and unique error-reducing workflow optimisations



Maximum retention, minimal time, due to minimal purification steps



Get more from your patient sample by capturing all cfDNA and enriching targets using a single primer



ATOM-Seq[®]

Total Cell-Free DNA Capture Workflow

NGS library preparation workflows for capturing all cell-free DNA for genetic and epigenetic analysis

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Workflow benefits



Higher complexity libraries as all starting material can be captured



Process poor quality samples with resilient workflows able to process even the lowest quality sample

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Flexible workflows for

- Whole genome mutation
- Whole genome methylation
- High-GC whole genome
- Whole-sample sequencing (e.g. sample purity testing)



Get **more from methylation analysis** with linear amplifications, making the workflows resistant to DNA damage

| Product Code | Product Name |
|--------------|---|
| SEQ001 | XCeloSeq cfDNA Library Preparation Kit |
| SEQ004 | XCeloSeq Methyl-cfDNA Library Preparation Kit |

Cell-free DNA Enrichment Workflow



Total cfDNA Capture Workflow

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