Next Generation Sequencing

XCeloSeq® Myeloid Fusion Kit

Highlights

- Unrivalled Library Complexity - powered by ATOM-Seq® capture technology
- Developed for liquid biopsy samples
- Fusion-Agnostic Targeted Enrichment - A single target-specific primer allows detection of both known and unknown fusions
- Rapid Protocol With High Sample Retention – Minimal bead purification and hands on time

Our XCeloSeq® Myeloid Fusion Kit employs our patented ATOM-Seq technology (Adaptor Template Oligo-Mediated Sequencing), which uses a simple and elegant chemistry to capture cDNA, using the sample cDNA molecules as primers themselves, where their 3' ends are extended by a polymerase.

ATOM-Seq adds Unique Molecular Identifiers (UMIs) and universal adapter sequences directly to available 3' ends of every original sample molecule meaning that all original fragments can be captured. A universal primer is then used for rounds of linear amplification, allowing for the sequencing of both sense- and antisense-strands when the linear product is divided between two reactions thereby further improving error correction.

This unique approach is ligation free and is set apart from conventional PCR-based approaches by requiring only a single target-specific primer for enrichment. This offers numerous advantages that make ATOM-Seq particularly well suited to challenging clinical material such as RNA from preserved FFPE samples.

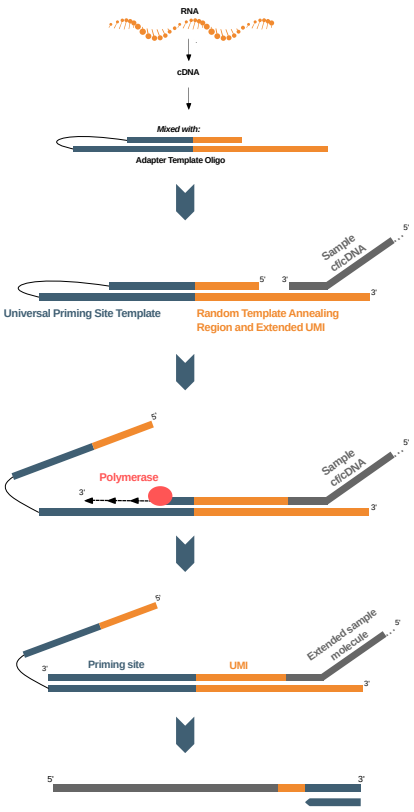
The approach employed by ATOM-Seq along with unique protocol enhancements for sensitivity, specificity, and error correction allows for the highest sample retention and capture efficiency with no compromises on sensitivity and performance.

Specifications

Up to 200 ng Input Quantity**	310 Targeting Primers*	39 Gene Targets
2.75 million Recommended Reads Per Sample	2 Hours Hands-On Time	7.25 hours Total Protocol Time

* An additional 8 control primers are included

**Higher quantities within this range will improve maximum sensitivity. When using high quality RNA, starting material should not exceed 200 ng. Cell-free RNA and total cell-free nucleic acids may be used as alternative starting materials, however fusion detection sensitivity will be lower due to cell-free RNA concentrations typically being very low, when using this material maximising starting input quantity will help ensure the best possible results.



ATOM-Seq Workflow

Sample RNA is converted into cDNA. The cDNA is combined with the Adapter Template Oligo. The DNA molecules anneal to the 3' end of the ATO and a polymerase extends the original molecule, using the ATO sequence as a template to add a Unique Molecular Identifier (UMI) and a universal priming site to the end of the captured molecule.

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Summary

The Myeloid Fusion Kit is powered by our ATOM-Seq chemistry and is for use with RNA extracted from liquid biopsy blood samples or FFPE. This kit is designed to provide comprehensive coverage of conserved fusion partners across 39 genes. When used in conjunction with XCeloSeq Unique Dual Indexing Sets, these allow for the enrichment of nucleic acids to generate high quality, high-complexity next-generation sequencing libraries suitable for use with Illumina® next-generation sequencing (NGS) instruments.

Ordering Information

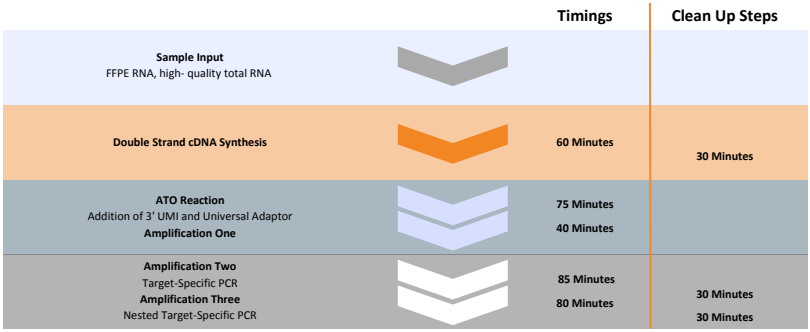
Product	No. of Samples	Catalog No.
XCeloSeq® Myeloid Fusion Kit	8	SEQ017

Learn more

For more information including the protocol please visit www.genefirst.com

Further Information

Dunwell TL, Dailey SC, et al. Adaptor Template Oligo-Mediated Sequencing (ATOM-Seq) is a new ultra-sensitive UMI-based NGS library preparation technology for use with cfDNA and cfRNA. Sci Rep. 2021 Feb 4;11(1):3138. doi: 10.1038/s41598-021-82737-9. PMID: 33542447; PMCID: PMC7862664.



XCeloSeq® Myeloid Fusion Kit Workflow.

ABL1	CHIC2	ETV6	IKZF3	MECOM	MYC	NUP214	PDGFRB	RBM15	SETD2
BCR	CREBBP	FGFR1	JAK2	MLLT10	MYH11	NUP98	PICALM	ROS1	TCF3
CBFB	CSF1R	GLIS2	KAT6A	MLLT4	NF1	PDCD1LG2	PML	RUNX1	TFG
CHD1	ERG	IKZF1	KMT2A	MRTFA	NOTCH1	PDGFRA	RARA	RUNX1T1	

XCeloSeq® Myeloid Fusion Kit Assay Targets.

Doc No: LIT1490v3.0

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