Next Generation Sequencing

ATOM-Seq®

Discover the Unknown

GeneFirst's ATOM-Seq technology is a beautifully simple, reliable, and effective NGS tool that can help you find the unknown. It overcomes technical and clinical limitations of existing NGS methods to allow you to find the location of your target sequence and capture more of your sample.

- **Shows all integration sites, making it an ideal companion for gene therapy technologies**
- **Identifies unknown gene fusions**
- **Works well with short, fragmented material**
- **Identifies all viral integration sites**
- **Detects low abundant circulating cell free/tumour DNA**

ATOM-Seq's unique chemistry provides an advanced method for targeting and enriching specific sequences from challenging nucleic acid materials. With fewer steps and a simplified NGS library preparation workflow, ATOM-Seq also promises unparalleled ease-of-use.

Acting like a hybrid between ligation and amplicon approaches, it provides the best of both worlds using a single targeting primer to identify the location of any target sequence. It works well with damaged and highly fragmented sample material, double - or single-stranded input and ultra-short and ultra-low quantities of starting material.

ATOM-Seq offers a truly game-changing approach for NGS-based liquid biopsy testing for early cancer screening, and also eliminates sequencing errors via a proprietary method which adds both a molecular barcode and a universal priming site directly to the ends of the starting material without the need for a ligation step.

Adapter Template Oligo

Gene editing technologies

The essential companion tool for the development of gene editing systems and treatments, ATOM-Seq is perfect for the monitoring and detection of off target gene editing because it adds a universal priming site directly to the ends of the starting material meaning that edited/added sequences can be located with a single targeting primer based on the target sequence.

Finding unknown fusions

During cancer treatment, chemotherapeutic agents can cause other fusions to occur in the "sick" tumour cells. It is important to be able to detect these fusions so treatment can be adjusted to avoid the development of resistance. Unfortunately these new fusion partner is often unknown so the fusion cannot be detected using standard panels. ATOM-Seq only requires one targeting primer so is ideal for detecting uknown fusions.

Identification of viral or plasmid integration sites

The integration site of viral genetic material can have an effect on the oncogenicity of a virus. The same is also true of viral vectors carrying genetic payloads, so it is important to know if and where the virus/plasmid integrates. Because ATOM-Seq adds a universal priming site directly to the ends of the starting material, it means integrated sequences can be located with a single primer based on the target sequence.

Identification of mutations in short, fragmented material

As space is only needed for one primer binding site in the material, ATOM-Seq is ideal for sequencing small lengths of material as may be seen in highly fragmented samples. This is also particularly relevant when investigating minimal residual disease and detecting disease from liquid biopsy. ATOM-Seq is perfect for high efficiency capture of FFPE material, cfDNA testing and MRD.

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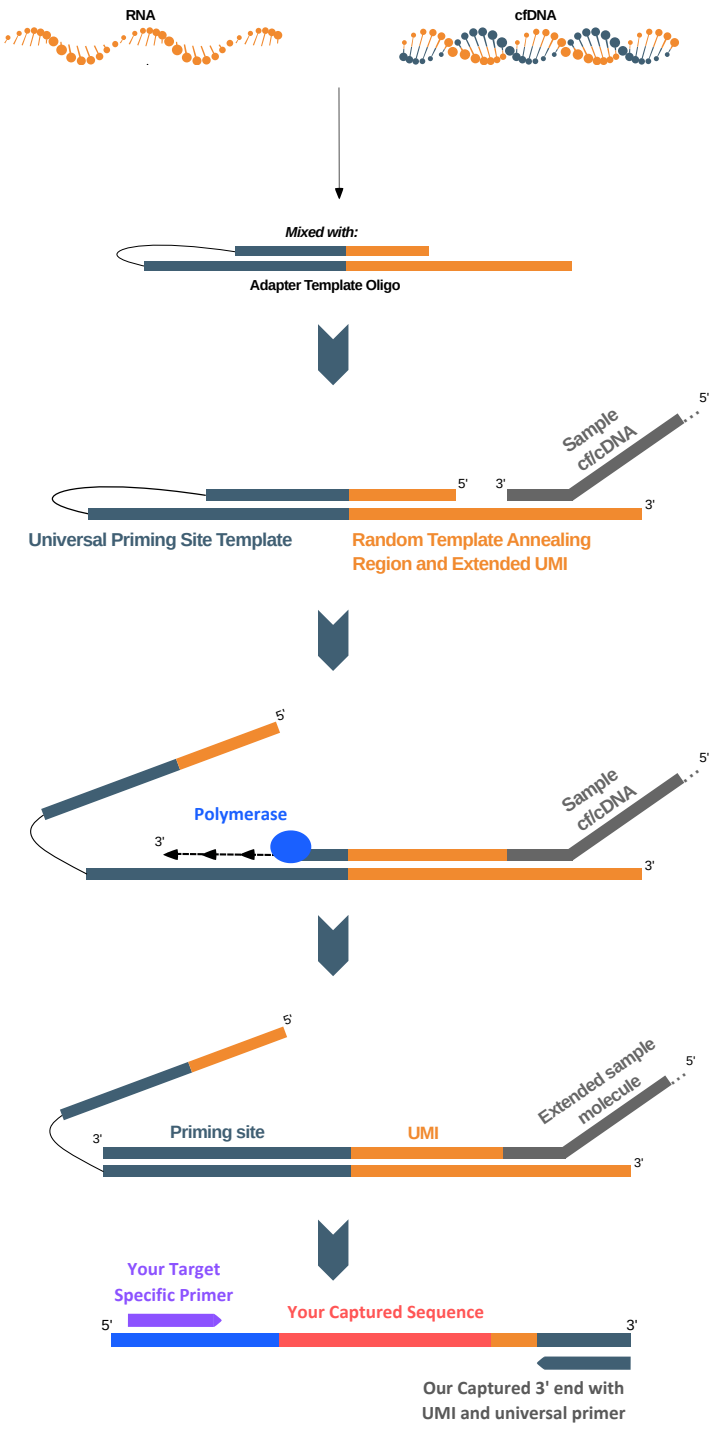
ATOM-Seq Workflow

Sample DNA (or RNA converted into cDNA) is combined with the Adapter Template Oligo. The DNA molecules anneal to the 3' end of the ATO, before 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.



genefirst

Custom Panel/Kit Development

Harness the power of ATOM-Seq for your project

ATOM-Seq has so many potential uses that much of what we do is custom development to support specific goals in pharmaceutical development, companion kits to work alongside gene therapy development, custom panel development for clinical uses and anything where you want to locate a target sequence when you don't know what else it might be attached to.

We just need a few pieces of information and we can provide details of how we can help, along with costs and developmental support.

What are you wanting to detect?

- **Integration**
- **Insertion**
- **Mutation**
- **Fusion**
- **SNPs**
- **Deletion**
- **CNV**
- **Anything else**

Material Type (RNA/DNA)

Material Source (Liquid Biopsy/FFPE/Fresh/Frozen cells or tissue)

Do you have a turnaround time/time frame for when this is required?

For Gene Therapy

- Number of sequences
- Details of sequence origin (CRISPR Edit, viral vector)
- Length of sequences

DNA Panel Size (total base pairs covered)

- Number of genes
- Number of exons

RNA Panel

- Number of conserved exons being targeted