

# Arima Library Prep Module

Generate high-quality Hi-C sequencing libraries with the Arima Library Prep Module.

The Arima-HiC+ workflow provides unparalleled access to the sequence, structure, and regulatory landscapes to identify all aspects of the 3D genome architecture. The preparation of high-quality next-generation sequencing (NGS) libraries is a critical step needed to achieve optimal results.

The Arima Library Prep Module is a robust solution that provides high complexity sequencing libraries. This module is compatible with our standard, low input, and capture HiC+ workflows. With this easy-to-use module, users can quickly generate NGS compatible libraries.

## Advantages of the Arima Library Prep Module



**Robust Performance:** Produces high yield NGS compatible libraries, with a high percentage of long-cis interactions, and minimal duplication rates



**Flexible Input:** Integrates with Arima standard, low-input, and capture-based workflows using as little as 5 ng of input DNA

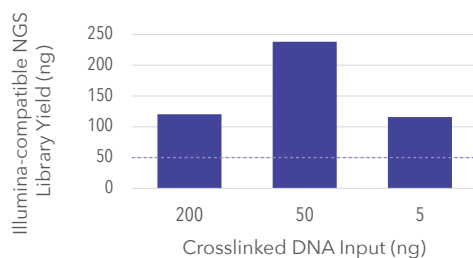


**Dependable Results:** Validated for use with most Arima workflows to produce high-quality Hi-C sequencing data ready for use in multiple types of analyses



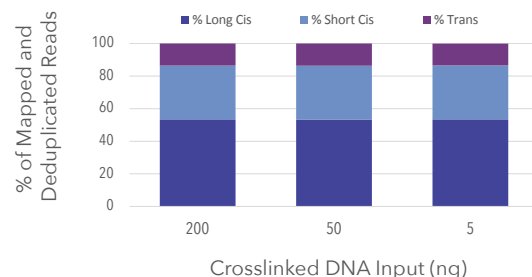
## Prepare Libraries with Confidence

The Arima Library Prep Module provides a dependable workflow step to confidently move you from prepared crosslinked DNA to sequencing and data analysis.



### High Yield Across DNA Input Ranges for Flexible Library Preparation.

The yield of this protocol was validated across a wide range of crosslinked DNA input quantities including standard input level of 200 ng, moderate input of 50 ng, and low input level of 5 ng. Across this input range high yield was achieved, well above the minimum of 50 ng of library yield (light purple line) required for sequencing.

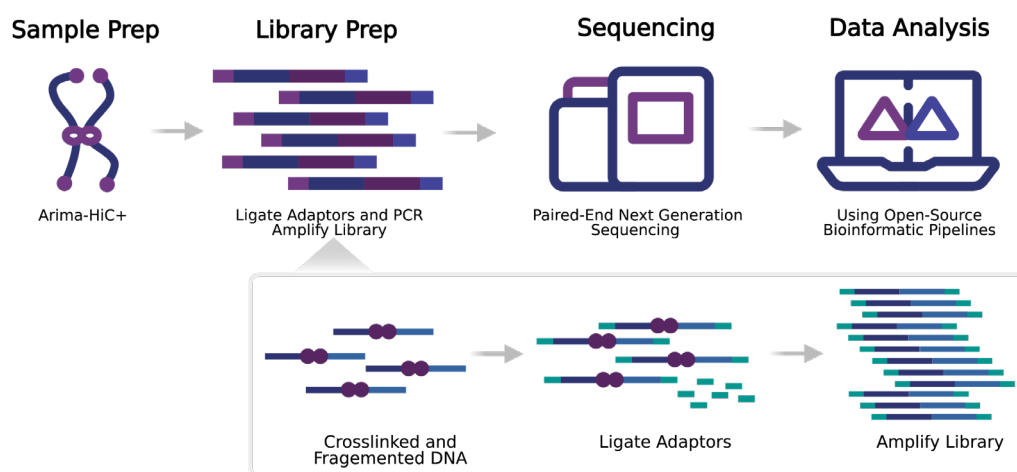


### Robust Performance Produces Data You Can Trust.

The performance of this protocol was validated across a range of crosslinked DNA input quantities from the standard input level of 200 ng to a low input level of 5 ng. The percentage of long-cis and short-cis interactions was above the analysis threshold of 70% percent, meaning this data is of sufficient quality for multiple types of analyses including calling of loops, TAD, compartment, genome assembly and structural variant detection.

# Arima Library Prep Module Workflow

The Arima Library Prep Module provides a simple, robust, and validated workflow to generate NGS libraries from proximally ligated DNA produced from Arima-HiC+ sample prep kits.



## Product List

Product	Description	Size	SKU
Arima Library Prep Module <sup>1</sup>	Reagent for constructing 16 indexed Hi-C libraries	16 rxn	A303011

Arima offers end-to-end service with all our products for most sample types.

## Specifications

<b>Input Requirements</b>	5-200 ng Arima-HiC+ crosslinked DNA
<b>Sequencing Requirements</b>	2 x 150 paired-end reads from Illumina®
<b>Yield Required for Sequencing</b>	>50 ng NGS libraries*
<b>Duplicates</b>	<1%
<b>Supported Arima Workflows**</b>	Genome-Wide HiC standard and low input (all tissue types) <sup>2</sup> Capture HiC <sup>3</sup> High Coverage HiC <sup>4</sup>

\*Performance results vary based on sample quality and purity.

\*\*Arima-HiChIP and Arima-HiC+ FFPE workflows are not currently supported.

## References

1. [User Guide: Arima Library Prep Module](#). Arima Genomics.
2. [User Guides: Arima-HiC \(various tissue-type specific protocols\)](#). Arima Genomics.
3. [User Guide: Arima Capture HiC for Mammalian Cell Lines](#). Arima Genomics.
4. [User Guides: Arima High Coverage HiC \(various tissue-type specific protocols\)](#). Arima Genomics.

Contact an Arima Genomics scientist for a quote or project consultation.