ATAC-SEQ

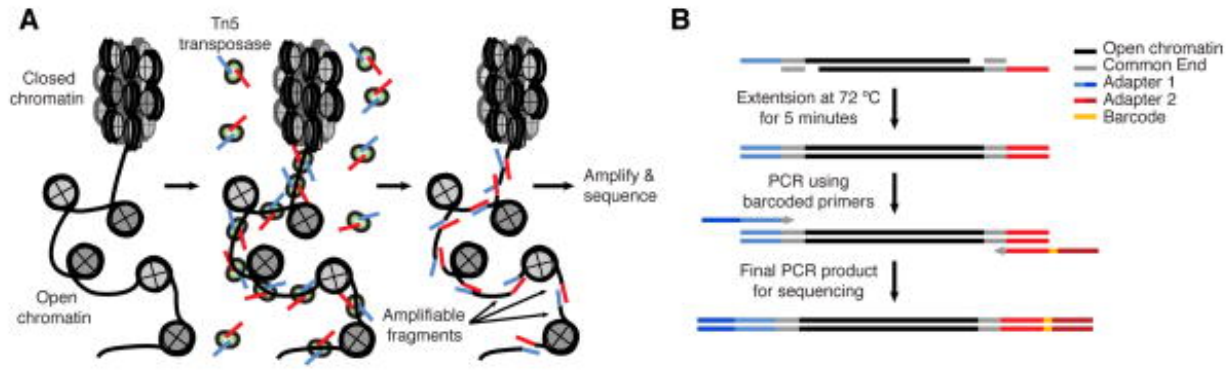
EASI-Genomics facilities have an expertise in functional genomics approaches to analyze chromatin composition and accessibility, and 3D genome organization. EASI-Genomics facilities are also expert in state-of-the-art sequencing technologies, adapted to functional genomic approaches.

MAIN APPLICATIONS

ATAC-seq, "Assay for transposase-accessible chromatin using sequencing" is routinely carried out in a variety of primary cells and immortalized cell lines to identify regions of open chromatin and identify regulatory elements across the genome (ATAC and its derivative FastATAC).

METHODOLOGICAL AND SCIENTIFIC BACKGROUND:

The method consists to simultaneously fragment and integrate sequencing adaptors into DNA with the Tn5 transposase. As the *in vitro* transposition is performed into native chromatin, transposition preferentially occurs in regions of accessible chromatin.



(A) Library preparation schematic. **(B)** Transposition results in fragmented DNA. Prior to amplification, adapters have to be completed with a 72°C extension step. During the subsequent PCR additional sequence is incorporated into the adapters, which include common sequencing ends and a sequencing barcode. (Buenrostro et al. DOI: 10.1002/0471142727.mb2129s109)

YIELD AND EXPECTED RESULTS

ATAC-seq provides similar information to that given by the well-established DNaseI-seq method, but it requires far fewer cells.

SAMPLE TECHNICAL REQUIREMENTS

DNaseI-seq is typically generated from 5.10^6 cells whereas ATAC-seq is carried out with 5,000 and 50,000 cells, making it compatible with cell-sorting.