

ATAC-seq is a technique used in molecular biology to assess genome-wide chromatin accessibility. In 2013, the technique was first described as an alternative advanced method for MNase-seq, FAIRE-Seq, and DNase-Seq. ATAC-seq is a faster and more sensitive analysis of the epigenome than DNase-seq or MNase-seq.

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Last update: **2024/06/07 02:59**

