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Sequencing open chromatin of single cell nuclei: snATAC-seq V.2

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Protocol status: Working

We use this protocol and it's working

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Abstract

Protocol for applying the TN5-based ATAC-seq method to the analysis of the chromatin of single cell nuclei isolated from brain tissue, as performed within the Center for Epigenomics of the Mouse Brain Atlas (CEMBA) and in coordination with the BRAIN Initiative Cell Census Network (BICCN).

Attachments



PDF

[Ren_Lab_snATACseq_CE](#)

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116KB

