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Multiome protocol - Stanford TMC

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bqzhao¹, Thomas Karathanos¹

¹Stanford University

Human BioMolecular Atlas Program (HuBMAP) Method Development Community
Tech. support email: Jeff.spraggins@vanderbilt.edu



Thomas Karathanos

Stanford University

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Protocol status: Working

We use this protocol and it's working

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Abstract

Overview of protocol followed for multiome (RNA-seq & ATAC-seq) experiments on intestinal samples at Stanford TMC, as part of the **Human Biomolecular Atlas Program**.



Steps

- 1 Isolate nuclei from frozen tissues and prepare for ATAC-seq following the Omni-ATAC protocol described by Corces et al.: [Link](#)
The original protocol (without the nuclei extraction from frozen tissues portion) is described in more detail here: [Link](#)
- 2  CG000338_ChromiumNextGEM_M... 4.7MB
Follow the 10x Genomics protocol for Single Cell Multiome ATAC + Gene Expression from a dissociated sample: [Link](#)

Protocol references

Corces, M., Trevino, A., Hamilton, E. *et al.* An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues. *Nat Methods* **14**, 959–962 (2017). <https://doi.org/10.1038/nmeth.4396>

10x Genomics. *Chromium Next GEM Single Cell Multiome ATAC + Gene Expression*. Rev. G, 2024, https://cdn.10xgenomics.com/image/upload/v1728078404/support-documents/CG000338_ChromiumNextGEM_Multiome_ATAC_GEX_User_Guide_RevG.pdf.pdf.