

# Resource Summary Report

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## CUT&Tag with Drosophila tissues

DOI:10.17504/protocols.io.bnx5mfq6

Type: Protocol

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### Proper Citation

Kami Ahmad, Steven Henikoff 2020. CUT&Tag with Drosophila tissues. protocols.io dx.doi.org/10.17504/protocols.io.bnx5mfq6

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### Protocol Information

**URL:** <https://dx.doi.org/10.17504/protocols.io.bnx5mfq6>

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**Summary:** This is a modification of the Benchtop CUT&Tag method (dx.doi.org/10.17504/protocols.io.bcuhiwt6) for epigenomic profiling of histone modifications and chromatin proteins in dissected Drosophila tissues. Intact unfixed tissues are permeabilized and incubated under conditions where a factor-specific antibody can infiltrate and bind a chromatin protein in situ. This antibody is then decorated with a secondary antibody, and this is used to tether a protein AG-Tn5 fusion protein loaded with sequencing adapters. Upon transposome activation by adding Mg<sup>2+</sup> ions, DNA is tagmented around the chromatin binding site. Here, dissected imaginal discs are coated with magnetic beads for handling, and about 5 imaginal discs provides high-quality data for histone modifications or for chromatin factor for which high-quality antibodies are available. The protocol is scaled for 8 samples. Performing CUT&Tag takes 2 days from larvae to sequencing-ready libraries.

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**Version:** 1

**Publication Date:** 2020

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### Data and Source Information

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