

Resource Summary Report

Generated by [PRECISE-TBI](#) on Jul 29, 2026

Mustache

RRID:SCR_026110

Type: Tool

Proper Citation

Mustache (RRID:SCR_026110)

Resource Information

URL: <https://github.com/ay-lab/mustache>

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Description: Software tool for multi-scale detection of chromatin loops from Hi-C and Micro-C contact maps in high resolutions (10kbp all the way to 500bp and even more). Used to detect chromatin loops caused by interaction of DNA segments with variable size.

Synonyms: Multi-scale Detection of Chromatin Loops from Hi-C and Micro-C Maps using Scale-Space Representation

Resource Type: software application, source code, software resource

Defining Citation: [PMID:32998764](#)

Keywords: detect chromatin loops, interaction of DNA segments, Hi-C, Micro-C, contact maps,

Funding: NIGMS R35 GM128938

Availability: Free, Available for download, Freely available

Resource Name: Mustache

Resource ID: SCR_026110

License: MIT license

Record Creation Time: 20241203T053255+0000

Record Last Update: 20260729T044632+0000

Ratings and Alerts

No rating or validation information has been found for Mustache.

No alerts have been found for Mustache.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Hamanaka K, et al. (2025) Genome sequencing provides high diagnostic yield and new etiological insights for intellectual disability and developmental delay. NPJ genomic medicine, 10(1), 60.

Goel VY, et al. (2025) Dynamics of microcompartment formation at the mitosis-to-G1 transition. Nature structural & molecular biology, 32(12), 2614.

Ege T, et al. (2025) Mapping of chromatin architecture and enhancer-promoter interactions in the cochlea. Frontiers in molecular biosciences, 12, 1683964.

Golov AK, et al. (2024) A genome-wide nucleosome-resolution map of promoter-centered interactions in human cells corroborates the enhancer-promoter looping model. eLife, 12.

Wang X, et al. (2024) A generalizable Hi-C foundation model for chromatin architecture, single-cell and multi-omics analysis across species. bioRxiv : the preprint server for biology.