

# Resource Summary Report

Generated by T1D on Aug 1, 2026

## ChiCMaxima

RRID:SCR\_018178

Type: Tool

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### Proper Citation

ChiCMaxima (RRID:SCR\_018178)

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### Resource Information

**URL:** <https://github.com/yousra291987/ChiCMaxima>

**Proper Citation:** ChiCMaxima (RRID:SCR\_018178)

**Description:** Pipeline for analyzing and identification of chromatin loops in CHi-C promoters data. Used to capture Hi-C visualization and interaction calling.

**Resource Type:** data access protocol, service resource, production service resource, software resource, web service, analysis service resource

**Defining Citation:** [PMID:31118054](#)

**Keywords:** Chromatin loop, CHi-C promoter, data, Hi-C visualization, interaction calling, data, analysis, bio.tools

**Availability:** Free, Freely available

**Resource Name:** ChiCMaxima

**Resource ID:** SCR\_018178

**Alternate IDs:** biotools:ChiCMaxima

**Alternate URLs:** <https://bio.tools/ChiCMaxima>

**License:** GNU General Public License v2.0

**Record Creation Time:** 20220129T080339+0000

**Record Last Update:** 20260801T042814+0000

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### Ratings and Alerts

No rating or validation information has been found for ChiCMaxima.

No alerts have been found for ChiCMaxima.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#) .

Recoules L, et al. (2022) The histone variant macroH2A1.1 regulates RNA polymerase II-paused genes within defined chromatin interaction landscapes. Journal of cell science, 135(7).

Ben Zouari Y, et al. (2019) ChiCMaxima: a robust and simple pipeline for detection and visualization of chromatin looping in Capture Hi-C. Genome biology, 20(1), 102.