

Resource Summary Report

Generated by [RRID](#) on Aug 12, 2026

HiCRes

RRID:SCR_022319

Type: Tool

Proper Citation

HiCRes (RRID:SCR_022319)

Resource Information

URL: <http://hub.docker.com/r/marchalc/hicres/>

Proper Citation: HiCRes (RRID:SCR_022319)

Description: Software pipeline to estimate and predict genomic resolution of Hi-C libraries. Used for estimating and predicting HiC library resolution.

Resource Type: software application, simulation software, software resource

Defining Citation: [DOI:10.1093/nar/gkab1235](https://doi.org/10.1093/nar/gkab1235)

Keywords: Hi-C libraries, 3D chromatin interactions genome wide measurement, estimate resolution of dataset, genomic resolution

Funding: NEI ZIAEY000450;
NEI ZIAEY000546

Availability: Free, Available for download, Freely available

Resource Name: HiCRes

Resource ID: SCR_022319

Alternate URLs: <https://github.com/ClaireMarchal/HiCRes>

Record Creation Time: 20220602T050139+0000

Record Last Update: 20260812T044420+0000

Ratings and Alerts

No rating or validation information has been found for HiCRes.

No alerts have been found for HiCRes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Hartley GA, et al. (2025) Centromeric transposable elements and epigenetic status drive karyotypic variation in the eastern hoolock gibbon. Cell genomics, 5(4), 100808.