

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

Fit-Hi-C

RRID:SCR_027917

Type: Tool

Proper Citation

Fit-Hi-C (RRID:SCR_027917)

Resource Information

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

Proper Citation: Fit-Hi-C (RRID:SCR_027917)

Description: Software tool for assigning statistical confidence estimates to chromosomal contact maps produced by genome-wide genome architecture assays such as Hi-C.

Resource Type: source code, software application, software resource

Keywords: assigning statistical confidence estimates, chromosomal contact maps, genome-wide, genome architecture assays, Hi-C

Availability: Free, Available for download, Freely available

Resource Name: Fit-Hi-C

Resource ID: SCR_027917

License: MIT license

Record Creation Time: 20260204T060344+0000

Record Last Update: 20260815T183311+0000

Ratings and Alerts

No rating or validation information has been found for Fit-Hi-C.

No alerts have been found for Fit-Hi-C.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

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

Yu L, et al. (2026) Impaired cohesin loading disrupts pancreatic differentiation by Polycomb-driven chromatin rewiring and loop collapse. *Communications biology*, 9(1).

Xiao Y, et al. (2022) Chromatin conformation of human oral epithelium can identify orofacial cleft missing functional variants. *International journal of oral science*, 14(1), 43.

Feng D, et al. (2022) Chromatin organizer SATB1 controls the cell identity of CD4+ CD8+ double-positive thymocytes by regulating the activity of super-enhancers. *Nature communications*, 13(1), 5554.

Wu HJ, et al. (2021) Topological isolation of developmental regulators in mammalian genomes. *Nature communications*, 12(1), 4897.