

Resource Summary Report

Generated by [Kravitz](#) on Sep 17, 2026

Hinge

RRID:SCR_016135

Type: Tool

Proper Citation

Hinge (RRID:SCR_016135)

Resource Information

URL: <https://github.com/HingeAssembler/HINGE>

Proper Citation: Hinge (RRID:SCR_016135)

Description: Software application for long read genome assembly based on hinging. Used in long-read sequencing technologies in genome assemblies to achieve optimal repeat resolution.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [PMID:28320918](#)

Keywords: long, read, genome, assembly, hinging, sequence, optimal, repeat, resolution

Availability: Free, Available for download

Resource Name: Hinge

Resource ID: SCR_016135

Alternate IDs: OMICS_12339

Alternate URLs: <https://sources.debian.org/src/hinge/>

Record Creation Time: 20220129T080329+0000

Record Last Update: 20260912T200018+0000

Ratings and Alerts

No rating or validation information has been found for Hinge.

No alerts have been found for Hinge.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Kapoor R, et al. (2023) Infrastructure tools to support an effective Radiation Oncology Learning Health System. Journal of applied clinical medical physics, 24(10), e14127.

Dida F, et al. (2021) Empirical evaluation of methods for de novo genome assembly. PeerJ. Computer science, 7, e636.

Ahmad J, et al. (2021) Structures of synthetic nanobody-SARS-CoV-2 receptor-binding domain complexes reveal distinct sites of interaction. The Journal of biological chemistry, 297(4), 101202.

Ahmad J, et al. (2021) Structures of synthetic nanobody-SARS-CoV-2-RBD complexes reveal distinct sites of interaction and recognition of variants. Research square.

Yoshimura J, et al. (2019) Recompleting the Caenorhabditis elegans genome. Genome research, 29(6), 1009.

Kamath GM, et al. (2017) HINGE: long-read assembly achieves optimal repeat resolution. Genome research, 27(5), 747.

Rebocho AB, et al. (2017) Generation of shape complexity through tissue conflict resolution. eLife, 6.

Nolivos S, et al. (2016) MatP regulates the coordinated action of topoisomerase IV and MukBEF in chromosome segregation. Nature communications, 7, 10466.

Kumar S, et al. (2015) Evidence of niche shift and global invasion potential of the Tawny Crazy ant, Nylanderia fulva. Ecology and evolution, 5(20), 4628.