

Resource Summary Report

Generated by [RRID](#) on Aug 31, 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: 20260829T182807+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 [RRID](#) .

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.