

Resource Summary Report

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HiCUP

RRID:SCR_005569

Type: Tool

Proper Citation

HiCUP (RRID:SCR_005569)

Resource Information

URL: <http://www.bioinformatics.babraham.ac.uk/projects/hicup/>

Proper Citation: HiCUP (RRID:SCR_005569)

Description: A tool for mapping and performing quality control on Hi-C data.

Abbreviations: HiCUP

Synonyms: Hi-C User Pipeline

Resource Type: software resource

Keywords: bio.tools

Resource Name: HiCUP

Resource ID: SCR_005569

Alternate IDs: OMICS_00523, biotools:hicup

Alternate URLs: <https://bio.tools/hicup>

Record Creation Time: 20220129T080231+0000

Record Last Update: 20260801T190256+0000

Ratings and Alerts

No rating or validation information has been found for HiCUP.

No alerts have been found for HiCUP.

Data and Source Information

Usage and Citation Metrics

We found 273 mentions in open access literature.

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

Wang YH, et al. (2026) Insights into dill (*Anethum graveolens*) flavor formation via integrative analysis of chromosomal-scale genome, metabolome and transcriptome. *Journal of advanced research*, 79, 847.

Wang Z, et al. (2026) Multidimensional mapping of stimulation-responsive regulatory elements and candidate causal variants in T cell activation. *Science advances*, 12(1), eady2539.

Yoshihara M, et al. (2025) Transcriptional enhancers in human neuronal differentiation provide clues to neuronal disorders. *EMBO reports*, 26(5), 1212.

Campos-Le??n K, et al. (2025) Repression of CADM1 transcription by HPV type 18 is mediated by three-dimensional rearrangement of promoter-enhancer interactions. *PLoS pathogens*, 21(1), e1012506.

Gong X, et al. (2025) Chromosome-level genome assembly of *Iodes seguinii* and its metabonomic implications for rheumatoid arthritis treatment. *The plant genome*, 18(1), e20534.

Wu Y, et al. (2025) Chromosome-scale genome assembly and annotation of *Xenocypris argentea*. *Scientific data*, 12(1), 573.

Hu M, et al. (2025) Myogenic enhancer snatching promotes adipogenic differentiation during epigenetic reprogramming mediated by lineage-specific transcription factors. *Cellular and molecular life sciences : CMLS*, 82(1), 412.

Jiang D, et al. (2025) The telomere-to-telomere genome of flowering cherry (*Prunus campanulata*) reveals genomic evolution of the subgenus *Cerasus*. *GigaScience*, 14.

Lai E, et al. (2025) Genome of root celery and population genomic analysis reveal the complex breeding history of celery. *Plant biotechnology journal*, 23(3), 946.

Da X, et al. (2025) Chromosome-level assembly of *Pseudopodoces humilis* genome: A resource for avian evolutionary studies. *Scientific data*, 12(1), 799.

Zhou C, et al. (2025) Chromosome-level genome assembly and population genomic analysis provide insights into the genetic diversity and adaption of *Schizopygopsis younghusbandi* on the Tibetan Plateau. *Integrative zoology*, 20(6), 1246.

Chen Y, et al. (2025) An improved chromosome-level genome assembly and annotation of Hong Kong catfish (*Clarias fuscus*). *Scientific data*, 12(1), 193.

Morgens DW, et al. (2025) Enhancers and genome conformation provide complex transcriptional control of a herpesviral gene. *Molecular systems biology*, 21(1), 30.

Wu SP, et al. (2025) Assessment of the Histone Mark-based Epigenomic Landscape in Human Myometrium at Term Pregnancy. *bioRxiv : the preprint server for biology*.

Bai Y, et al. (2025) Chromosome-level genome assembly and annotation of the maize weevil (*Sitophilus zeamais* Motschulsky). *Scientific data*, 12(1), 966.

Zhang Y, et al. (2025) A chromosome-level genome assembly of *Wurfbainia villosa* (Zingiberaceae). *Scientific data*, 12(1), 1490.

Sun S, et al. (2025) Analysis wheat wild relatives *Thinopyrum intermedium* and *Roegneria kamoji* genomes reveal different polyploid evolution paths. *Nature communications*, 16(1), 7693.

Wang H, et al. (2025) Telomere-to-telomere gap-free genome assembly of *Euchiloglanis kishinouyei*. *Scientific data*, 12(1), 757.

Li Q, et al. (2025) A vetiver-specific terpene synthase VzTPS9 contributes to the high attractiveness of vetiver to rice stem borer. *Proceedings of the National Academy of Sciences of the United States of America*, 122(20), e2424863122.

Xu S, et al. (2025) Chromosome-level genome assembly of *Fusarium tricinctum*, a fungal pathogen associated with root rot in alfalfa. *Scientific data*, 12(1), 1676.