

# 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:** 20260815T182316+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 317 mentions in open access literature.

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

Wang Y, et al. (2026) Haplotype-resolved genome assembly of the colored calla lily (*Zantedeschia elliottiana*) provides new insights into the evolution of the family Araceae. *Molecular horticulture*, 6(1), 12.

Zhou Z, et al. (2026) Pan-3D Genome Analysis Reveals the Roles of Structural Variation in Chicken Chromatin Architectures, Domestication and Production Traits. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(24), e20068.

Ng HL, et al. (2026) BCR::ABL1-Induced Enhancer Reprogramming Uncovers Hypersensitivity of Ph+B-ALL Cells to Enhancer-Targeting Drugs. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(25), e17231.

Rouco R, et al. (2026) Temporal constraints on enhancer usage shape the regulation of limb gene transcription. *Nature communications*, 17(1), 5.

Chen Q, et al. (2026) ADNP missense variant p.C687R disrupts chromatin regulation and GABAergic differentiation in Helsmoortel-Van der Aa syndrome. *Molecular autism*, 17(1).

Zeng Z, et al. (2026) Three Near telomere-to-telomere Genomes for *Gardenia jasminoides*. *Scientific data*, 13(1).

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.

Niu Y, et al. (2026) Chromosome-level genome assembly of the blackchin tilapia (*Sarotherodon melanotheron*). *Scientific data*, 13(1).

Cheng X, et al. (2026) Haplotype-resolved genome assembly provides insights into the unique floral scent of *Rosa rugosa* originated in China. *Molecular horticulture*, 6(1).

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.

Zhao Q, et al. (2026) Multi-omics analyses of *Dracocephalum moldavica* L. reveal two flavonoid glycosyltransferases in tilianin biosynthesis. *BMC genomics*, 27(1), 208.

Lei FL, et al. (2026) Chromosome-level genome assembly of *Nemipterus japonicus* based on PacBio sequencing and Hi-C technology. *Scientific data*, 13(1), 218.

Zhao M, et al. (2026) Genome Assembly Revealed MdZAT5 Coordinates Anthocyanin Biosynthesis in Apple Fruit Peel and Flesh by Interacting With MdHY5. *Plant*

biotechnology journal, 24(3), 1655.

Hu L, et al. (2026) High-Resolution Genomic Resources for Trait Mapping and Precision Breeding for Adzuki Bean (*Vigna angularis*). *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 13(4), e07157.

Tan X, et al. (2026) AP-1 promotes oncogenic transcription in lung cancer cells by bridging promoter-enhancer interactions. *Cancer gene therapy*, 33(3), 301.

Zhang Y, et al. (2026) Multi-omics and functional analyses in *Aesculus wilsonii* elucidate the biosynthetic pathways of moretane- and oleanane-type triterpenoids. *Plant communications*, 7(4), 101715.

Li J, et al. (2026) A telomere-to-telomere genome assembly for *Cyperus difformis*. *Scientific data*, 13(1), 257.

Kong H, et al. (2026) Functional characterization of a multi-cancer risk locus on chromosome band 2q33.1 near CASP8. *bioRxiv* : the preprint server for biology.

Jiang K, et al. (2026) Telomere-to-telomere-level genome assembly and annotation of the Zi goose *Anser cygnoides*. *Scientific data*, 13(1).

Wang P, et al. (2026) Telomere-to-telomere gap-free genome assembly of the *Opsariichthys evolans* (Cypriniformes: Cyprinidae). *Scientific data*, 13(1), 263.