

Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

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: 20260905T132538+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 [PRECISE-TBI](#) .

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.

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).

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

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.

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.

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.