

Resource Summary Report

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CAFE

RRID:SCR_005983

Type: Tool

Proper Citation

CAFE (RRID:SCR_005983)

Resource Information

URL: <https://bitbucket.org/cob87icW6z/cafe/wiki/Home>

Proper Citation: CAFE (RRID:SCR_005983)

Description: R software package for the detection of gross chromosomal abnormalities from gene expression microarray data.

Abbreviations: CAFE

Resource Type: software resource

Defining Citation: [PMID:24451624](#)

Keywords: affymetrix, r, chromosomal abnormality, gene expression, microarray, chromosome, linux, windows

Availability: GNU General Public License, v3, Acknowledgement requested

Resource Name: CAFE

Resource ID: SCR_005983

Alternate IDs: OMICS_02245

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260801T190302+0000

Ratings and Alerts

No rating or validation information has been found for CAFE.

No alerts have been found for CAFE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 793 mentions in open access literature.

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

Dong Z, et al. (2025) Chromosome-level genome sequencing and assembly of the parasitoid wasp *Leptopilina myrica*. *Scientific data*, 12(1), 235.

Clancy SM, et al. (2025) The *Calicophoron daubneyi* genome provides new insight into mechanisms of feeding, eggshell synthesis and parasite-microbe interactions. *BMC biology*, 23(1), 11.

Krawczyk K, et al. (2025) Chromosome-scale telomere to telomere genome assembly of common crystalwort (*Riccia sorocarpa* Bisch.). *Scientific data*, 12(1), 77.

Li X, et al. (2025) Genomic Insights into Post-Domestication Expansion and Selection of Body Size in Ponies. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(16), e2413023.

Wang T, et al. (2025) Multiomics analysis provides insights into musk secretion in muskrat and musk deer. *GigaScience*, 14.

Feng H, et al. (2025) Genome and Tissue-Specific Transcriptome of the Tropical Milkweed (*Asclepias curassavica*). *Plant direct*, 9(3), e70031.

La Torre R, et al. (2025) A chromosome-level genome assembly of the Peruvian Algarrobo (*Neltuma pallida*) provides insights on its adaptation to its unique ecological niche. *G3* (Bethesda, Md.), 15(2).

Ma J, et al. (2025) Tumor Microenvironment-responsive Nanocatalyst for Targeted Chemodynamic Cancer Therapy. *Advanced healthcare materials*, 14(22), e2501746.

Wang ZF, et al. (2025) Chromosome-scale assemblies of three *Ormosia* species: repetitive sequences distribution and structural rearrangement. *GigaScience*, 14.

Fan BL, et al. (2025) Analysis of gene expansion and defense-related genes in *Anacardiaceae* family from an evolutionary aspect. *Frontiers in plant science*, 16, 1638044.

Sun M, et al. (2025) Haplotype-resolved, gap-free genome assemblies provide insights into the divergence between Asian and European pears. *Nature genetics*, 57(8), 2040.

Zhou Y, et al. (2025) Telomere-to-telomere genome and resequencing of 231 individuals reveal evolution, genomic footprints in Asian icefish, *Protosalanx chinensis*. *GigaScience*, 14.

Song WL, et al. (2025) Telomere-to-telomere genome assembly and 3D chromatin architecture of *Centella asiatica* insight into evolution and genetic basis of triterpenoid saponin biosynthesis. *Horticulture research*, 12(5), uhaf037.

Zhang J, et al. (2025) Evolution of HD-ZIP transcription factors and their function in cabbage leafy head formation. *Frontiers in plant science*, 16, 1583110.

Olvera-Vazquez SG, et al. (2025) Comprehensive Annotation of Olfactory and Gustatory Receptor Genes and Transposable Elements Revealed Their Evolutionary Dynamics in Aphids. *Molecular biology and evolution*, 42(12).

Wang J, et al. (2025) Comparative genomics, integrated with single-cell sequencing and genetic analyses, reveal roles of transcription factor AP2-M2 in asexual replication of *Babesia* parasite. *PLoS pathogens*, 21(11), e1013699.

Castellano KR, et al. (2025) Genome Assembly of a Living Fossil, the Atlantic Horseshoe Crab *Limulus polyphemus*, Reveals Lineage-Specific Whole-Genome Duplications, Transposable Element-Based Centromeres, and a ZW Sex Chromosome System. *Molecular biology and evolution*, 42(2).

Zhang F, et al. (2025) Comparative Genomic Analysis Across Multiple Species to Identify Candidate Genes Associated with Important Traits in Chickens. *Genes*, 16(6).

Wang J, et al. (2025) Resolving floral development dynamics using genome and single-cell temporal transcriptome of *Dendrobium devonianum*. *Plant biotechnology journal*, 23(8), 2997.

Schwarz EM, et al. (2025) Genomes of the entomopathogenic nematode *Steinernema hermaphroditum* and its associated bacteria. *Genetics*, 231(3).