Resource Summary Report

Generated by Kravitz on Sep 10, 2026

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: 20260905T132545+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 883 mentions in open access literature.

Listed below are recent publications. The full list is available at Kravitz .

Liu Z, et al. (2026) Chromosome-Level Genome and Organ-Specific Transcriptome of Alnus glutinosa Uncover Lineage-Specific Innovations in Root Nodule Symbiosis. Plant, cell & environment, 49(6), 3003.

Mu D, et al. (2026) The genome of the medicinal plant Uncaria rhynchophylla provides new insights into monoterpenoid indole alkaloid metabolism and its molecular regulatory mechanism. Molecular horticulture, 6(1), 9.

Dong H, et al. (2026) The genome of Phlebotomus chinensis, the primary vector of visceral leishmaniasis in China: insights from chromosome-level assembly and comparative analysis. Infectious diseases of poverty, 15(1), 20.

Martin SLF, et al. (2026) Haplotype-resolved chromosome-level genome assemblies of four Diamesa species reveal the genetic basis of cold tolerance and high-altitude adaptations in arctic chironomids. GigaScience, 15.

Zeng L, et al. (2026) Functional genomics reveals key gene families and molecular pathways for extreme cold survival in the khapra beetle. BMC biology, 24(1).

Labella-Ortega M, et al. (2026) Uncovering the genome evolutionary dynamics of the Mediterranean endemic palm Chamaerops humilis. BMC plant biology, 26(1).

Wang Y, et al. (2026) A chromosome level genome, as well as transcriptomes and metabolomes, insights into genome evolution and the biosynthesis of kaempferol and kaempferol derivatives in Impatiens balsamina (Balsaminaceae). Frontiers in plant science, 17, 1725789.

Li H, et al. (2026) Comparative genome analysis provides a foundation for defining salvinorin A biosynthesis in Salvia divinorum. Nature communications, 17(1).

Mao C, et al. (2026) Chromosome-level genome assembly and transcriptomes of the leaf insect Cryptophyllium westwoodii provide insights into the evolution of leaf-like masquerade. GigaScience, 15.

Yang Z, et al. (2026) Copy number evolution of conserved noncoding RNA gene families across mammals. Mammalian genome : official journal of the International Mammalian Genome Society, 37(1).

Rinke S, et al. (2026) Genomic Insights Into the Evolution of Parental Care in Weevils. Genome biology and evolution, 18(6).

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.

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.

Jones ARC, et al. (2026) Cryptocercus Genomes Expand Knowledge of Adaptations to Xylophagy and Termite Sociality. Genome biology and evolution, 18(2).

Liu H, et al. (2026) Genomics of rafting crustaceans reveals adaptation to climate change in tropical oceans. Nature communications, 17(1).

Luan Y, et al. (2026) Mechanisms of Aristolochic Acid Resistance in Specialist Butterflies and Evolutionary Insights for Potential Protective Pathways. Advanced science (Weinheim, Baden-Wurttemberg, Germany), e18072.

Zhang T, et al. (2026) Multi-omics analyses shed lights on the evolution and fruit development of Chinese raspberries (Rubus spp.). Journal of integrative plant biology, 68(4), 1032.

Liu J, et al. (2026) Molecular basis of the short- and long-term osmoregulation capability in the euryhaline unicellular eukaryote Paramecium calkinsi. mBio, 17(4), e0303225.

Wang Z, et al. (2026) Chromosome-level genome assembly of the teak defoliator Hyblaea puera Cramer (Lepidoptera: Hyblaeidae). Scientific data, 13(1).

Liu T, et al. (2026) Lineage-specific expansion and positive selection of NPC2 genes in the crab spider Ebrechtella tricuspidata and other arachnids. BMC genomics, 27(1).