

Resource Summary Report

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genomation

RRID:SCR_003435

Type: Tool

Proper Citation

genomation (RRID:SCR_003435)

Resource Information

URL: <https://bioconductor.org/packages/genomation/>

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Description: Software R package for simplifying common tasks in genomic feature analysis. Toolkit to summarize, annotate and visualize genomic intervals. Provides functions for reading BED and GFF files as GRanges objects, summarizing genomic features over predefined windows so users can make average enrichment of features over defined regions or produce heatmaps. Can annotate given regions with other genomic features such as exons, introns and promoters.

Abbreviations: genomation

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Defining Citation: [PMID:25417204](https://pubmed.ncbi.nlm.nih.gov/25417204/)

Keywords: genome, genomic interval, genomic feature analysis, GRanges objects, annotate given regions, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: genomation

Resource ID: SCR_003435

Alternate IDs: biotools:genomation, OMICS_02306

Alternate URLs: <https://github.com/al2na/genomation>, <https://github.com/BIMSBbioinfo/genomation>, <https://bio.tools/genomation>

Old URLs: <http://al2na.github.io/genomation/>

License: Artistic License

Record Creation Time: 20220129T080219+0000

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Ratings and Alerts

No rating or validation information has been found for genomation.

No alerts have been found for genomation.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 62 mentions in open access literature.

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

Heredia-Negrón F, et al. (2026) Building epigenetic risk scores of opioid use disorder: Insights from human postmortem brain data. Translational psychiatry, 16(1), 62.

González-González NL, et al. (2026) Infants exposed to maternal type 1 diabetes: intrauterine epigenetic modifications and neurological development. Frontiers in endocrinology, 17, 1759949.

Huang S, et al. (2026) Uncovering functional variants using a high-efficiency PE3-based screening platform. Science advances, 12(23), eady7359.

Lefebvre V, et al. (2026) Micropropagation of Cannabis sativa: genetic and epigenetic stability assessment over multiple generations. Journal of cannabis research, 8(1).

Kohwi Y, et al. (2025) Genome organization by SATB1 binding to base-unpairing regions (BURs) provides a scaffold for SATB1-regulated gene expression. eLife, 14.

McGregor BA, et al. (2025) Deciphering motor dysfunction and microglial activation in mThy1-?-synuclein mice: a comprehensive study of behavioral, gene expression, and methylation changes. Frontiers in molecular neuroscience, 18, 1544971.

Farkas D, et al. (2025) Short-term transcriptional memory and association-forming ability of tomato plants in response to ultrasound and drought stress stimuli. Plant signaling & behavior, 20(1), 2556982.

Wang S, et al. (2025) Engineering of BZ transposase and transposon donor vector for enhanced efficiency and safety in gene delivery applications. Nucleic acids research, 53(18).

Phan MHQ, et al. (2025) Conservation of regulatory elements with highly diverged sequences across large evolutionary distances. *Nature genetics*, 57(6), 1524.

Zimmann F, et al. (2025) Retinitis pigmentosa-linked mutations impair the snRNA unwinding activity of SNRNP200 and reduce pre-mRNA binding of PRPF8. *Cellular and molecular life sciences : CMLS*, 82(1), 103.

Bensberg M, et al. (2025) Exposing the DNA methylation-responsive compartment of the leukaemic genome in T-ALL cell lines support its potential as a novel therapeutic target in T-ALL. *Clinical epigenetics*, 17(1), 114.

Frank LE, et al. (2025) Epigenetic Changes Associated with the Progression of Prion Disease in Syrian Hamsters (*Mesocricetus auratus*). *Research square*.

Ochmann MT, et al. (2024) A novel hyperactive variant of the Sleeping Beauty transposase facilitates non-viral genome engineering. *Molecular therapy. Nucleic acids*, 35(4), 102381.

Zhou J, et al. (2024) Integrative analysis of the methylome and transcriptome of tomato fruit (*Solanum lycopersicum* L.) induced by postharvest handling. *Horticulture research*, 11(6), uhae095.

Diaby M, et al. (2024) A Naturally Active Spy Transposon Discovered from the Insect Genome of *Colletes gigas* as a Promising Novel Gene Transfer Tool. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 11(29), e2400969.

Andrade-Brito DE, et al. (2024) Neuronal-specific methylome and hydroxymethylome analysis reveal significant loci associated with alcohol use disorder. *Frontiers in genetics*, 15, 1345410.

Sajjanar B, et al. (2024) Genome-wide DNA methylation profiles regulate distinct heat stress response in zebu (*Bos indicus*) and crossbred (*Bos indicus* × *Bos taurus*) cattle. *Cell stress & chaperones*, 29(4), 603.

Hossain MN, et al. (2024) Cold exposure impacts DNA methylation patterns in cattle sperm. *Frontiers in genetics*, 15, 1346150.

Zhao Y, et al. (2023) Model-based characterization of the equilibrium dynamics of transcription initiation and promoter-proximal pausing in human cells. *Nucleic acids research*, 51(21), e106.

Straube J, et al. (2023) Cre recombinase expression cooperates with homozygous FLT3 internal tandem duplication knockin mouse model to induce acute myeloid leukemia. *Leukemia*, 37(4), 741.