

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/>

Proper Citation: genomation (RRID:SCR_003435)

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

Defining Citation: [PMID: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

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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 58 mentions in open access literature.

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

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.

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).

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.

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.

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.

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

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.

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.

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.

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.

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

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.

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.

Andrade-Brito DE, et al. (2023) Neuronal-specific methylome and hydroxymethylome analysis reveal replicated and novel loci associated with alcohol use disorder. *medRxiv : the preprint server for health sciences*.

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.

Barbosa IAM, et al. (2023) Cancer lineage-specific regulation of YAP responsive elements revealed through large-scale functional epigenomic screens. *Nature communications*, 14(1), 3907.

Hoguin A, et al. (2023) The model diatom *Phaeodactylum tricornutum* provides insights into the diversity and function of microeukaryotic DNA methyltransferases. *Communications biology*, 6(1), 253.

Lo EKW, et al. (2023) Comprehensive DNA Methylation Analysis Indicates That Pancreatic Intraepithelial Neoplasia Lesions Are Acinar-Derived and Epigenetically Primed for Carcinogenesis. *Cancer research*, 83(11), 1905.