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

Defining Citation: PMID:25417204

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

Funding:

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/

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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 49 mentions in open access literature.

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

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.

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.

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.

Rabaglino MB, et al. (2022) In vitro- and in vivo-produced male dairy calves show molecular differences in the hepatic and muscular energy regulation†. Biology of reproduction, 107(4), 1113.

Patel AJ, et al. (2022) PRC2-Inactivating Mutations in Cancer Enhance Cytotoxic Response to DNMT1-Targeted Therapy via Enhanced Viral Mimicry. Cancer discovery, 12(9), 2120.

Toboz P, et al. (2022) The amino acid sensor GCN2 controls red blood cell clearance and iron metabolism through regulation of liver macrophages. Proceedings of the National Academy of Sciences of the United States of America, 119(35), e2121251119.

Revia S, et al. (2022) Histone H3K27 demethylase KDM6A is an epigenetic gatekeeper of mTORC1 signalling in cancer. Gut, 71(8), 1613.

Farooq Z, et al. (2022) The amino acid sensor GCN2 suppresses terminal oligopyrimidine (TOP) mRNA translation via La-related protein 1 (LARP1). The Journal of biological chemistry, 298(9), 102277.

Sturgill D, et al. (2022) Protocol for base resolution mapping of ac4C using RedaC:T-seq. STAR protocols, 3(4), 101858.

Wang W, et al. (2021) Impact of Epigenomic Hypermethylation at TP53 on Allogeneic Hematopoietic Cell Transplantation Outcomes for Myelodysplastic Syndromes. Transplantation and cellular therapy, 27(8), 659.e1.

Hoguin A, et al. (2021) Genome-wide analysis of allele-specific expression of genes in the model diatom Phaeodactylum tricornutum. Scientific reports, 11(1), 2954.