

Resource Summary Report

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GenomicFeatures

RRID:SCR_016960

Type: Tool

Proper Citation

GenomicFeatures (RRID:SCR_016960)

Resource Information

URL: <http://bioconductor.org/packages/GenomicFeatures/>

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Description: Software R package for making and manipulating transcript centric annotations. Used to download the genomic locations of the transcripts, exons and cds of a given organism, from either the UCSC Genome Browser or a BioMart database.

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

Defining Citation: [PMID:23950696](#)

Keywords: making, manipulating, transcript, centric, annotation, genomic, location, exon, cds, bio.tools

Funding: NHGRI P41 HG004059;
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Availability: Free, Available for download, Freely available

Resource Name: GenomicFeatures

Resource ID: SCR_016960

Alternate IDs: biotools:genomicfeatures

Alternate URLs: <https://bio.tools/genomicfeatures>

License: Artistic v2.0

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260801T190547+0000

Ratings and Alerts

No rating or validation information has been found for GenomicFeatures.

No alerts have been found for GenomicFeatures.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 65 mentions in open access literature.

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

Sinke L, et al. (2026) DNA methylation of genes involved in lipid metabolism drives adiponectin levels and metabolic disease. *Diabetologia*, 69(1), 127.

Li BI, et al. (2025) The regulatory architecture of the primed pluripotent cell state. *Nature communications*, 16(1), 3351.

Kopell BH, et al. (2025) A study of RNA splicing and protein expression in the living human brain. *PloS one*, 20(10), e0332651.

Sinke L, et al. (2025) Tissue-specific methylomic responses to a lifestyle intervention in older adults associate with metabolic and physiological health improvements. *Aging cell*, 24(4), e14431.

Lu B, et al. (2025) Corepressor AtSDR4L and its paralog regulate hormonal and hypoxia responses in multiple Arabidopsis seed compartments. *Plant physiology*, 199(3).

Gurashi K, et al. (2025) An integrative multiparametric approach stratifies putative distinct phenotypes of blast phase chronic myelomonocytic leukemia. *Cell reports. Medicine*, 6(2), 101933.

Cruz-Granados P, et al. (2025) An ultra-rare missense variant in the KIF1B gene linked to autoinflammatory Meniere's disease. *NPJ genomic medicine*, 10(1), 42.

Rahman RU, et al. (2025) Singletrome enhances detection of long noncoding RNAs in single cell transcriptomes. *Scientific reports*, 15(1), 29542.

Nguyen JH, et al. (2025) Developmental pyrethroid exposure disrupts molecular pathways for MAP kinase and circadian rhythms in mouse brain. *Physiological genomics*, 57(4), 240.

Keenan CR, et al. (2024) Suv39h-catalyzed H3K9me3 is critical for euchromatic genome organization and the maintenance of gene transcription. *Genome research*, 34(4), 556.

Flynn JK, et al. (2024) Translocating bacteria in SIV infection are not stochastic and preferentially express cytosine methyltransferases. *Mucosal immunology*, 17(5), 1089.

Maestri S, et al. (2024) Benchmarking of computational methods for m6A profiling with Nanopore direct RNA sequencing. *Briefings in bioinformatics*, 25(2).

Xia W, et al. (2024) A low-cost, low-input method establishment for m6A MeRIP-seq. *Bioscience reports*, 44(1).

Harry-Paul YY, et al. (2024) The Evolution of Gene Expression Plasticity During Adaptation to Salt in *Chlamydomonas reinhardtii*. *Genome biology and evolution*, 16(11).

Kose C, et al. (2024) Genome-wide analysis of transcription-coupled repair reveals novel transcription events in *Caenorhabditis elegans*. *PLoS genetics*, 20(7), e1011365.

Castellano LA, et al. (2024) Dengue virus preferentially uses human and mosquito non-optimal codons. *Molecular systems biology*, 20(10), 1085.

Gautrat P, et al. (2024) Phytochrome-dependent responsiveness to root-derived cytokinins enables coordinated elongation responses to combined light and nitrate cues. *Nature communications*, 15(1), 8489.

Reggiani F, et al. (2024) BET inhibitors drive Natural Killer activation in non-small cell lung cancer via BRD4 and SMAD3. *Nature communications*, 15(1), 2567.

Carrick BH, et al. (2024) PUF partner interactions at a conserved interface shape the RNA-binding landscape and cell fate in *Caenorhabditis elegans*. *Developmental cell*, 59(5), 661.

Zhai D, et al. (2024) Reciprocal conversion between annual and polycarpic perennial flowering behavior in the Brassicaceae. *Cell*, 187(13), 3319.