

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

Defining Citation: [PMID:23950696](#)

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

Funding: NHGRI P41 HG004059;
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NHLBI R01 HL094635

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: 20260905T132816+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 71 mentions in open access literature.

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

Srivastava S, et al. (2026) Adgrg6/Gpr126 is required for compact wall integrity and establishing trabecular identity during cardiac trabeculation. Nature communications, 17(1), 1484.

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

Sinke L, et al. (2026) Epigenome-wide association study of circulating interleukin-6 connects DNA methylation to immunometabolic and inflammatory health. Communications biology, 9(1), 242.

Tisdale G, et al. (2026) The Kinetic Intron Hypothesis. bioRxiv : the preprint server for biology.

Xie S, et al. (2026) Identification of cis-regulatory elements provides insights into tissue-specific gene regulation in the sheep genome. Nature communications, 17(1).

Zhang H, et al. (2026) XAP5 CIRCADIAN TIMEKEEPER coordinates circadian rhythms and anthocyanin biosynthesis independently of splicing. Plant physiology, 201(2).

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).

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

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

Pastor MM, et al. (2025) Rapid rewiring of an archaeal transcription factor function via flexible cis-trans interactions. *Molecular biology of the cell*, 36(7), ar86.

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.

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.

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.

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

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.

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

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).

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