Resource Summary Report

Generated by NIF on Apr 20, 2025

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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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: 20250420T014822+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 56 mentions in open access literature.

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

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.

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

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

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).

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.

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.

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.

Kose C, et al. (2023) Genome-wide transcription and repair maps of Caenorhabditis elegans. bioRxiv : the preprint server for biology.

Flemr M, et al. (2023) Mouse nuclear RNAi-defective 2 promotes splicing of weak 5' splice sites. RNA (New York, N.Y.), 29(8), 1140.

Rao A, et al. (2023) The translation initiation factor homolog eif4e1c regulates cardiomyocyte metabolism and proliferation during heart regeneration. Development (Cambridge, England), 150(20).

Rogala S, et al. (2023) The lncRNA Sweetheart regulates compensatory cardiac hypertrophy after myocardial injury in murine males. Nature communications, 14(1), 7024.

Nguyen JH, et al. (2023) Developmental pyrethroid exposure disrupts molecular pathways for circadian rhythms and MAP kinase in mouse brain. bioRxiv : the preprint server for biology.

Diener C, et al. (2023) Outside the limit: questioning the distance restrictions for cooperative miRNA binding sites. Cellular & molecular biology letters, 28(1), 8.

Antinucci M, et al. (2023) Population history modulates the fitness effects of Copy Number Variation in the Roma. Human genetics, 142(9), 1327.

Wu Y, et al. (2023) Fat mass and obesity-associated factor (FTO)-mediated N6-methyladenosine regulates spermatogenesis in an age-dependent manner. The Journal of biological chemistry, 299(6), 104783.

Chan WF, et al. (2023) Survey of activation-induced genome architecture reveals a novel enhancer of Myc. Immunology and cell biology, 101(4), 345.