Resource Summary Report

Generated by NIF on May 15, 2025

biomaRt

RRID:SCR_019214
Type: Tool

Proper Citation

biomaRt (RRID:SCR_019214)

Resource Information

URL: https://bioconductor.org/packages/biomaRt/

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Description: Software package that integrates BioMart data resources with data analysis software in Bioconductor. Can annotate range of gene or gene product identifiers including Entrez Gene and Affymetrix probe identifiers with information such as gene symbol, chromosomal coordinates, Gene Ontology and OMIM annotation. Enables retrieval of genomic sequences and single nucleotide polymorphism information, which can be used in data analysis.

Synonyms: biomaRt v 2.42.1

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

Defining Citation: PMID:16082012

Keywords: BioMart databases, Bioconductor, data analysis, BioMart data integration, gene annotation, gene product identifiers annotation, gene symbol retrival, chromosomal coordinates retrival, genomic sequence retrival, nucleotide polimorphism information, , bio.tools

Funding:

Availability: Free, Available for download, Freely available

Resource Name: biomaRt

Resource ID: SCR_019214

Alternate IDs: biotools:biomart

Alternate URLs: https://bio.tools/biomart

License: Artistic-2.0

Record Creation Time: 20220129T080344+0000

Record Last Update: 20250514T061857+0000

Ratings and Alerts

No rating or validation information has been found for biomaRt.

No alerts have been found for biomaRt.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2351 mentions in open access literature.

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

Luo Y, et al. (2025) Exploring the impacts of senescence on implantation and early embryonic development using totipotent cell-derived blastoids. Journal of advanced research, 68, 115.

Barton RD, et al. (2025) A sort and sequence approach to dissect heterogeneity of response to a self-amplifying RNA vector in a novel human muscle cell line. Molecular therapy. Nucleic acids, 36(1), 102400.

Le Y, et al. (2025) Unveiling the omics tapestry of B-acute lymphoblastic leukemia: bridging genomics, metabolomics, and immunomics. Scientific reports, 15(1), 3188.

Ding Y, et al. (2025) The ortholog of human DNAJC9 promotes histone H3-H4 degradation and is counteracted by Asf1 in fission yeast. Nucleic acids research, 53(3).

Guo WT, et al. (2025) Time-Dependent Transcriptional Dynamics of Contextual Fear Memory Retrieval Reveals the Function of Dipeptidyl Peptidase 9 in Reconsolidation. Neuroscience bulletin, 41(1), 16.

McGinnis CD, et al. (2025) Acetylation of proximal cysteine-lysine pairs by alcohol metabolism. Redox biology, 79, 103462.

Weber M, et al. (2025) Transcriptomic and proteomic profiling identifies feline fibrosarcoma as clinically amenable model for aggressive sarcoma subtypes. Neoplasia (New York, N.Y.), 60, 101104.

Goodman MO, et al. (2025) Genome-wide association analysis of composite sleep health scores in 413,904 individuals. Communications biology, 8(1), 115.

Zhao Q, et al. (2025) TRIAGE: an R package for regulatory gene analysis. Briefings in bioinformatics, 26(1).

Luo H, et al. (2025) Pathogenic variants of TUBB8 cause oocyte spindle defects by disrupting with EB1/CAKP5 interactions and potential treatment targeting microtubule acetylation through HDAC6 inhibition. Clinical and translational medicine, 15(1), e70193.

Ren C, et al. (2025) Single-Cell Insights Into Cellular Response in Abdominal Aortic Occlusion-Induced Hippocampal Injury. CNS neuroscience & therapeutics, 31(1), e70154.

Paris JR, et al. (2025) The Genomic Signature and Transcriptional Response of Metal Tolerance in Brown Trout Inhabiting Metal-Polluted Rivers. Molecular ecology, 34(1), e17591.

Wang S, et al. (2025) Ferroptosis-related genes participate in the microglia-induced neuroinflammation of spinal cord injury via NF-?B signaling: evidence from integrated single-cell and spatial transcriptomic analysis. Journal of translational medicine, 23(1), 43.

Liang W, et al. (2025) Analysis of key lncRNA related to Parkinson's disease based on gene co-expression weight networks. Neurosciences (Riyadh, Saudi Arabia), 30(1), 20.

Ohri N, et al. (2025) Gene expression dynamics in fibroblasts during early-stage murine pancreatic carcinogenesis. iScience, 28(1), 111572.

Goclowski CL, et al. (2025) Galaxy as a gateway to bioinformatics: Multi-Interface Galaxy Hands-on Training Suite (MIGHTS) for scRNA-seq. GigaScience, 14.

Magnitov MD, et al. (2025) ZNF143 is a transcriptional regulator of nuclear-encoded mitochondrial genes that acts independently of looping and CTCF. Molecular cell, 85(1), 24.

Harada K, et al. (2025) Intestinal butyric acid-mediated disruption of gut hormone secretion and lipid metabolism in vasopressin receptor-deficient mice. Molecular metabolism, 91, 102072.

van Gelderen TA, et al. (2025) Gonadal miRNomes and transcriptomes in infected fish reveal sexually dimorphic patterns of the immune response. Functional & integrative genomics, 25(1), 29.

Minaeva M, et al. (2025) Specifying cellular context of transcription factor regulons for

exploring context-specific gene regulation programs. NAR genomics and bioinformatics, 7(1), lqae178.