

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

biomaRt

RRID:SCR_019214

Type: Tool

Proper Citation

biomaRt (RRID:SCR_019214)

Resource Information

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

Proper Citation: biomaRt (RRID:SCR_019214)

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 application, software resource, data processing software, data analysis software

Defining Citation: [PMID:16082012](#)

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

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: 20260728T043558+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 2638 mentions in open access literature.

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

Yang R, et al. (2026) Population structure and genome-wide association study of body conformation traits of two native goat breeds in China. *Animal bioscience*, 39(1), 250334.

Riley SE, et al. (2026) In vivo screen reveals specific roles of Hippo pathway components in development and regeneration. *Life science alliance*, 9(3).

Apodiakou A, et al. (2026) SNRK3.15 Is a Crucial Component of the Sulfur Deprivation Response in *Arabidopsis thaliana*. *Plant direct*, 10(1), e70132.

Siadat SA, et al. (2026) The possibility of prognostic and functional values of the 8q24 and 20q13 chromosomal bands in colorectal cancer. *Molecular biology research communications*, 15(1), 3.

Tam SB, et al. (2026) A role for the cholinergic neuron circadian clock in RNA metabolism and mediating neurodegeneration. *Life science alliance*, 9(3).

Park J, et al. (2026) A robust pleiotropy method with applications to lipid traits and to inflammatory bowel disease subtypes with sample overlap. *HGG advances*, 7(1), 100501.

Huang C, et al. (2026) The High-Altitude Adaptation Characteristics of Microbiota-Host Cross-Talk in Yak Gastrointestinal Track. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(1), e14862.

Bendre SV, et al. (2026) Cholesterol efflux protein, ABCA1, supports anticancer functions of myeloid immune cells. *Science advances*, 12(1), eadx5490.

Gonzalez-Lozano MA, et al. (2025) EndoMAP.v1 charts the structural landscape of human early endosome complexes. *Nature*, 643(8070), 252.

Mu H, et al. (2025) Methionine intervention induces PD-L1 expression to enhance the immune checkpoint therapy response in MTAP-deleted osteosarcoma. *Cell reports. Medicine*, 6(3), 101977.

Lall D, et al. (2025) An organ-chip model of sporadic ALS using iPSC-derived spinal cord motor neurons and an integrated blood-brain-like barrier. *Cell stem cell*, 32(7), 1139.

DiRusso JA, et al. (2025) Sex-specific expression and function of TRIM28 during mouse primordial germ differentiation. *iScience*, 28(10), 113474.

Kobayashi H, et al. (2025) Neuro-Mesenchymal Interaction Mediated by a α 2-Adrenergic Nerve Growth Factor Feedforward Loop Promotes Colorectal Cancer Progression. *Cancer discovery*, 15(1), 202.

Lu Y, et al. (2025) Intrahepatic Microbial Heterogeneity in Multifocal Hepatocellular Carcinoma and Its Association with Host Genomic and Transcriptomic Alterations. *Cancer discovery*, 15(8), 1630.

Hu K, et al. (2025) Development and Application of MiMouse, a Comprehensive Genomic Profiling Panel for Credentialing Mouse Tumor Models. *Cancer research communications*, 5(10), 1910.

Chawla Y, et al. (2025) Lactate metabolism in clonal plasma cells and its therapeutic implications in multiple myeloma patients with elevated serum LDH levels. *Cancer & metabolism*, 13(1), 9.

Chung DC, et al. (2025) CD103⁺CD56⁺ ILCs Are Associated with an Altered CD8⁺ T-cell Profile within the Tumor Microenvironment. *Cancer immunology research*, 13(4), 527.

Gao Y, et al. (2025) Multimodal analyses reveal genes driving electrophysiological maturation of neurons in the primate prefrontal cortex. *Neuron*, 113(15), 2490.

Yang J, et al. (2025) Insights into human melanocyte development and characteristics through pluripotent stem cells combined with single-cell sequencing. *iScience*, 28(5), 112373.

Smith JD, et al. (2025) Genomic Signatures of Poor Prognosis in Merkel Cell Carcinoma: A Single-Institution Prospective Study. *Molecular cancer research : MCR*.