

Resource Summary Report

Generated by [nidm-terms](#) on Sep 23, 2026

BioMart Project

RRID:SCR_002987

Type: Tool

Proper Citation

BioMart Project (RRID:SCR_002987)

Resource Information

URL: <http://www.biomart.org>

Proper Citation: BioMart Project (RRID:SCR_002987)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 4, 2023. Platform provides free software and data services to international scientific community in order to foster scientific collaboration and facilitate scientific discovery process. Project adheres to open source philosophy that promotes collaboration and code reuse.

Synonyms: BioMart software

Resource Type: data access protocol, data or information resource, portal, project portal, software resource, web service

Defining Citation: [PMID:21930506](#), [PMID:19144180](#)

Keywords: biology, data, management, data mining, search, descriptive, graphical, application, perl, java, gold standard

Funding: Breast Cancer Campaign Tissue Bank ;
Center for Genome Regulation ;
Center for Mathematical Modelling ;
European Molecular Biology Laboratory ;
NSF NRF 2013M3A6A4043695;
Sandra Ibarra Foundation for Cancer ;
Spanish Government ;
U.S. Department of Energy ;
Wellcome Trust

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: BioMart Project

Resource ID: SCR_002987

Alternate IDs: nif-0000-30184

License: GNU Lesser General Public License

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260919T195506+0000

Ratings and Alerts

No rating or validation information has been found for BioMart Project.

No alerts have been found for BioMart Project.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 295 mentions in open access literature.

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

Yang L, et al. (2026) Transcription factor ATF3 aggravates kidney fibrosis by maintaining the state of histone H3 lysine 27 acetylation. Chinese medical journal, 139(2), 253.

Aggrey-Fynn JE, et al. (2026) Epigenetic context defines the transcriptional activity of canonical and noncanonical NF- κ B signaling in pancreatic cancer. Cell death discovery, 12(1).

Tollenaere A, et al. (2026) Mechanisms of gene regulation by SRCAP and H2A.Z. Nature communications, 17(1).

Zhang Y, et al. (2026) Stem cell control in the lung by an autocrine injury-activated Igf complex. Science (New York, N.Y.), 392(6795), eadt1310.

Cassel R, et al. (2025) FUS Mislocalization Rewires a Cortical Gene Network to Drive Cognitive and Behavioral Impairment in ALS. medRxiv : the preprint server for health sciences.

Liakos A, et al. (2025) Cockayne syndrome B protein is implicated in transcription and associated chromatin dynamics in homeostatic and genotoxic conditions. Aging cell, 24(1), e14341.

Megat S, et al. (2025) CREB3 gain of function variants protect against ALS. Nature communications, 16(1), 2942.

Ji P, et al. (2025) Single-cell delineation of the microbiota-gut-brain axis: Probiotic intervention in Chd8 haploinsufficient mice. *Cell genomics*, 5(2), 100768.

Wang Y, et al. (2024) Genome-Wide Detection of Copy Number Variations and Their Potential Association with Carcass and Meat Quality Traits in Pingliang Red Cattle. *International journal of molecular sciences*, 25(11).

Yuan H, et al. (2024) Unveiling the Influence of Copy Number Variations on Genetic Diversity and Adaptive Evolution in China's Native Pig Breeds via Whole-Genome Resequencing. *International journal of molecular sciences*, 25(11).

Liang B, et al. (2024) Two mutations at KRT74 and EDAR synergistically drive the fine-wool production in Chinese sheep. *Journal of advanced research*, 57, 1.

Niu Y, et al. (2024) Targeting the intestinal circadian clock by meal timing ameliorates gastrointestinal inflammation. *Cellular & molecular immunology*, 21(8), 842.

Belay S, et al. (2024) Anthropogenic events and responses to environmental stress are shaping the genomes of Ethiopian indigenous goats. *Scientific reports*, 14(1), 14908.

Pons G, et al. (2023) Analysis of Cancer Genomic Amplifications Identifies Druggable Collateral Dependencies within the Amplicon. *Cancers*, 15(6).

Townes FW, et al. (2023) Nonnegative spatial factorization applied to spatial genomics. *Nature methods*, 20(2), 229.

Xu C, et al. (2023) Genome-Wide Detection and Analysis of Copy Number Variation in Anhui Indigenous and Western Commercial Pig Breeds Using Porcine 80K SNP BeadChip. *Genes*, 14(3).

Wu X, et al. (2023) Mutation in Polycomb repressive complex 2 gene OsFIE2 promotes asexual embryo formation in rice. *Nature plants*, 9(11), 1848.

Clasen F, et al. (2023) Systematic diet composition swap in a mouse genome-scale metabolic model reveals determinants of obesogenic diet metabolism in liver cancer. *iScience*, 26(2), 106040.

Vetters J, et al. (2023) Canonical IRE1 function needed to sustain vigorous natural killer cell proliferation during viral infection. *iScience*, 26(12), 108570.

Taghizadeh S, et al. (2022) Genome-wide identification of copy number variation and association with fat deposition in thin and fat-tailed sheep breeds. *Scientific reports*, 12(1), 8834.