

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 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, project portal, software resource, web service, portal, data or information resource

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

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

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

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: 20260731T042644+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 284 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

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.

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*.

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.

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

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.

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

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.

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

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

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

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

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.

O'Callaghan A, et al. (2022) BASiCS workflow: a step-by-step analysis of expression variability using single cell RNA sequencing data. *F1000Research*, 11, 59.

Ta AC, et al. (2022) Temporal and spatial transcriptomic dynamics across brain development in *Xenopus laevis* tadpoles. *G3 (Bethesda, Md.)*, 12(1).

Kilian M, et al. (2022) T-cell Receptor Therapy Targeting Mutant Capicua Transcriptional Repressor in Experimental Gliomas. *Clinical cancer research : an official journal of the American Association for Cancer Research*, 28(2), 378.

Liu X, et al. (2022) A single-nucleotide mutation within the TBX3 enhancer increased body size in Chinese horses. *Current biology : CB*, 32(2), 480.

Chai H, et al. (2022) Defining the characteristics of interferon-alpha-stimulated human genes: insight from expression data and machine learning. *GigaScience*, 11.

Yuan C, et al. (2021) A global analysis of CNVs in Chinese indigenous fine-wool sheep populations using whole-genome resequencing. *BMC genomics*, 22(1), 78.

Elsadany M, et al. (2021) Transcriptional Analysis of Nuclear-Encoded Mitochondrial Genes in Eight Neurodegenerative Disorders: The Analysis of Seven Diseases in Reference to Friedreich's Ataxia. *Frontiers in genetics*, 12, 749792.

Clemens Z, et al. (2021) The biphasic and age-dependent impact of *klotho* on hallmarks of aging and skeletal muscle function. *eLife*, 10.