Resource Summary Report

Generated by RRID on Apr 9, 2025

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, portal, web service, data or information resource, software resource, project portal

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: 20250409T060229+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 281 mentions in open access literature.

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

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.

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.

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.

Livernois AM, et al. (2021) Heat stress and immune response phenotype affect DNA methylation in blood mononuclear cells from Holstein dairy cows. Scientific reports, 11(1), 11371.

Gutierrez-Quiceno L, et al. (2021) A proteomic network approach resolves stage-specific molecular phenotypes in chronic traumatic encephalopathy. Molecular neurodegeneration, 16(1), 40.

Lopez D, et al. (2021) Early transcriptional response to gravistimulation in poplar without phototropic confounding factors. AoB PLANTS, 13(1), plaa071.

Zhu C, et al. (2021) Genome wide association study for the identification of genes associated with tail fat deposition in Chinese sheep breeds. Biology open, 10(5).