

Resource Summary Report

Generated by [ASWG](#) on Aug 2, 2026

Ensembl Genome Browser

RRID:SCR_013367

Type: Tool

Proper Citation

Ensembl Genome Browser (RRID:SCR_013367)

Resource Information

URL: <http://Mar2008.archive.ensembl.org>

Proper Citation: Ensembl Genome Browser (RRID:SCR_013367)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on March 17,2022. Genome databases for vertebrates and other eukaryotic species. Analysis and annotation maintained on current data.Distribution of analysis to other bioinformatics laboratories. Ensembl concentrates on vertebrate genomes, but other groups have adapted system for use with plant and fungal genomes (see Powered by Ensembl list on website).

Resource Type: data or information resource, database

Funding: European Bioinformatics Institute ;
Wellcome Trust Sanger Institute

Availability: THIS RESOURCE IS NO LONGER IN SERVICE.

Resource Name: Ensembl Genome Browser

Resource ID: SCR_013367

Alternate IDs: nif-0000-30518

Alternate URLs: <http://uswest.ensembl.org/index.html>

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260801T191021+0000

Ratings and Alerts

No rating or validation information has been found for Ensembl Genome Browser.

No alerts have been found for Ensembl Genome Browser.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1179 mentions in open access literature.

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

De Paolis V, et al. (2025) An antisense-long-noncoding-RNA modulates p75NTR expression levels during neuronal polarization. *iScience*, 28(1), 111566.

Lee SY, et al. (2025) Exploring the importance of predicted camel NRAP exon 4 for environmental adaptation using a mouse model. *Animal genetics*, 56(1), e13490.

Raffle J, et al. (2025) Identification of novel genetic variants associated with feline cardiomyopathy using targeted next-generation sequencing. *Scientific reports*, 15(1), 3871.

Honarpour A, et al. (2025) The First Evidence for the Role of ACVR2A Gene Fetal Genotype in Preeclampsia Susceptibility. *Molecular genetics & genomic medicine*, 13(2), e70069.

Trastulli G, et al. (2025) Sample Tracking Tool: A Comprehensive Approach Based on OpenArray Technology and R Scripting for Genomic Sample Monitoring. *Diagnostics (Basel, Switzerland)*, 15(2).

Lim B, et al. (2025) Cell deconvolution-based integrated time-series network of whole blood transcriptome reveals systemic antiviral activities and cell-specific immunological changes against PRRSV infection. *Veterinary research*, 56(1), 19.

Xu QZ, et al. (2025) Chromosome-level genome assembly and single-cell analysis unveil molecular mechanisms of arm regeneration in the ophiuroid *Ophiura sarsii vadicola*. *Genome biology*, 26(1), 82.

Li S, et al. (2025) Atlas of expression of acyl CoA binding protein/diazepam binding inhibitor (ACBP/DBI) in human and mouse. *Cell death & disease*, 16(1), 134.

Deebani A, et al. (2025) Knockdown of zebrafish tmem242 enhances the production of ROS that signals to increase f9a expression resulting in DIC-like condition. *Scientific reports*, 15(1), 3058.

Sun K, et al. (2025) Aberrant expression of PYGB as a potential therapeutic target and its associations with immune cell infiltration in lung cancer. *Frontiers in immunology*, 16, 1536248.

Niayale R, et al. (2025) Molecular characterization and expression of Spata22 in testes of the sterile male cattle-yak. *Veterinary and animal science*, 29, 100471.

Abuzahra M, et al. (2025) A novel p.127Val>Ile single nucleotide polymorphism in the MTNR1A gene and its relation to litter size in Thin-tailed Indonesian ewes. *Animal bioscience*, 38(2), 209.

DeMeis JD, et al. (2025) Long G4-rich enhancers target promoters via a G4 DNA-based mechanism. *Nucleic acids research*, 53(2).

Kontou D, et al. (2025) Adaptation in a keystone grazer under novel predation pressure. *Proceedings. Biological sciences*, 292(2039), 20241935.

Kasitipradit K, et al. (2025) Sex-specific effects of prenatal bisphenol A exposure on transcriptome-interactome profiles of autism candidate genes in neural stem cells from offspring hippocampus. *Scientific reports*, 15(1), 2882.

Ali A, et al. (2025) Chromosome level genome assembly and annotation of the Swanson rainbow trout homozygous line. *Scientific data*, 12(1), 345.

Grobbelaar J, et al. (2025) Longitudinal assessment of DNA recovery from post-mortem whole blood stored in EDTA, sodium fluoride/potassium oxalate and additive-free tubes. *International journal of legal medicine*, 139(2), 495.

Rolfs LA, et al. (2025) myh9b is a critical non-muscle myosin II encoding gene that interacts with myh9a and myh10 during zebrafish development in both compensatory and redundant pathways. *G3 (Bethesda, Md.)*, 15(1).

Peng J, et al. (2025) Integrated transcriptomic hypothalamic-pituitary-ovarian axis network analysis reveals the role of energy availability on egg production in layers. *Animal nutrition (Zhongguo xu mu shou yi xue hui)*, 20, 66.

Bibi H, et al. (2025) Molecular and computational analysis of a novel pathogenic variant in emopamil-binding protein (EBP) involved in cholesterol biosynthetic pathway causing a rare male EBP disorder with neurologic defects (MEND syndrome). *Molecular biology reports*, 52(1), 101.