

Resource Summary Report

Generated by [ASWG](#) on Aug 26, 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: 20260821T193948+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 1199 mentions in open access literature.

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

Liang W, et al. (2026) Recognition of immunogenomic signature and prognostic value of the subtype of epithelial-mesenchymal transition in breast cancer. *Biochemistry and biophysics reports*, 45, 102456.

Heintz MM, et al. (2026) Hepatic transcriptomic responses in gravid and non-gravid rats exposed to HFPO-DA: Analyses to inform the role of maternal effects in neonatal toxicity. *PloS one*, 21(4), e0345643.

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

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.

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.

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).

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.

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.

Höyhty M, et al. (2025) Fecal microbiota and genetics in pediatric-onset orofacial granulomatosis and Crohn's disease. *Scientific reports*, 15(1), 6020.

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.

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.

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.

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).

Vermani L, et al. (2025) A Haplotype GWAS in Syndromic Familial Colorectal Cancer. *International journal of molecular sciences*, 26(2).

Heintz MM, et al. (2025) Comparison of phenotypic and transcriptomic profiles between HFPO-DA and prototypical PPAR γ , PPAR α , and cytotoxic agents in wild-type and Ppara-null mouse livers. *Toxicological sciences : an official journal of the Society of Toxicology*, 206(1), 183.

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).

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

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