

Resource Summary Report

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Ensembl Genomes

RRID:SCR_006773

Type: Tool

Proper Citation

Ensembl Genomes (RRID:SCR_006773)

Resource Information

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

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Description: Database portal offering integrated access to genome-scale data from non-vertebrate species of scientific interest, developed using the Ensembl genome annotation and visualization platform. Ensembl Genomes consists of five sub-portals (for bacteria, protists, fungi, plants and invertebrate metazoa) designed to complement the availability of vertebrate genomes in Ensembl. Many of the databases supporting the portal have been built in close collaboration with the scientific community - essential for maintaining the accuracy and usefulness of the resource. A common set of user interfaces (which include a graphical genome browser, FTP, BLAST search, a query optimized data warehouse, programmatic access, and a Perl API) is provided for all domains. Data types incorporated include annotation of (protein and non-protein coding) genes, cross references to external resources, and high throughput experimental data (e.g. data from large scale studies of gene expression and polymorphism visualized in their genomic context). Additionally, extensive comparative analysis has been performed, both within defined clades and across the wider taxonomy, and sequence alignments and gene trees resulting from this can be accessed through the site.

Synonyms: Ensembl Genomes: Extending Ensembl across the taxonomic space, EnsemblGenomes, Ensembl Genome

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

Defining Citation: [PMID:24163254](#), [PMID:19884133](#)

Keywords: genome, gold standard, bio.tools, FASEB list

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Resource Name: Ensembl Genomes

Resource ID: SCR_006773

Alternate IDs: r3d100011197, OMICS_01648, nlx_65207, biotools:ensembl_genomes

Alternate URLs: https://bio.tools/ensembl_genomes, <https://doi.org/10.17616/R3MW6M>

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260801T042626+0000

Ratings and Alerts

No rating or validation information has been found for Ensembl Genomes.

No alerts have been found for Ensembl Genomes.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 276 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Chen L, et al. (2025) Genomic and Cis-Regulatory Basis of a Plastic C3-C4 Photosynthesis in *Eleocharis Baldwinii*. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(32), e15681.

Goldman OV, et al. (2025) Mosquito Cell Atlas: A single-nucleus transcriptomic atlas of the adult *Aedes aegypti* mosquito. *bioRxiv : the preprint server for biology*.

Rutaganira FU, et al. (2025) A stress-responsive p38 signaling axis in choanoflagellates. *RSC chemical biology*, 6(6), 891.

Wu J, et al. (2025) Genome-wide identification and expression analysis of the class III peroxidase gene family in *Medicago sativa*. *BMC plant biology*, 25(1), 1717.

Stanciu A, et al. (2025) Personalized ctDNA detection and genomic profiling in the NeoRHEA Study. *NPJ breast cancer*, 11(1), 137.

Grätz C, et al. (2025) Extracellular vesicle-associated transcriptomic and proteomic biomarkers show in vitro potential for vandetanib treatment monitoring in anaplastic thyroid cancer. *Scientific reports*, 15(1), 32464.

Yang H, et al. (2025) Identification, characterization, and expression profiling of the bHLH gene family in *Beta vulgaris*. *BMC plant biology*, 25(1), 1744.

Tamburino R, et al. (2025) Genotype-specific transcriptomic response to drought stress in potato cultivars modulated by microbial biostimulants. *BMC plant biology*, 25(1), 1777.

Morales AE, et al. (2025) Bat genomes illuminate adaptations to viral tolerance and disease resistance. *Nature*, 638(8050), 449.

Nicolas L, et al. (2025) The serine palmitoyl transferase of plant pathogenic fungi: a promising new target for the development of novel crop protection solutions†. *Pest management science*, 81(10), 6567.

Goldman OV, et al. (2025) A single-nucleus transcriptomic atlas of the adult *Aedes aegypti* mosquito. *Cell*, 188(25), 7267.

Sharafshah A, et al. (2025) Pharmacoepigenomics in Personalized Medicine: A Hypothesis-Generating Approach to Introduce CpG-PGx SNPs as New Candidates for a Systematic Insight into Genomic-Epigenomic-Phenomic-Pharmacogenomics (G-E-Ph-PGx) Axis. *Journal of personalized medicine*, 15(12).

Pan J, et al. (2024) Genome-wide characterization of TCP family and their potential roles in abiotic stress resistance of oat (*Avena sativa* L.). *Frontiers in plant science*, 15, 1382790.

Subramani PG, et al. (2024) Conserved role of hnRNPL in alternative splicing of epigenetic modifiers enables B cell activation. *EMBO reports*, 25(6), 2662.

Li X, et al. (2024) Genome-wide identification of the wall-associated kinase gene family and their expression patterns under various abiotic stresses in soybean (*Glycine max* (L.) Merr). *Frontiers in plant science*, 15, 1511681.

He A, et al. (2024) Genome-wide identification and expression analysis of the SPL gene family and its response to abiotic stress in barley (*Hordeum vulgare* L.). *BMC genomics*, 25(1), 846.

Wang Z, et al. (2024) TIM-4 increases the proportion of CD4+CD25+FOXP3+ regulatory T cells in the pancreatic ductal adenocarcinoma microenvironment by inhibiting IL-6 secretion. *Cancer medicine*, 13(17), e70110.

Sun R, et al. (2024) Chromosome-level genome assembly and annotation of a potential model organism *Gossypium arboreum* ZB-1. *Scientific data*, 11(1), 620.

Fu Y, et al. (2024) Perturbation of METTL1-mediated tRNA N7- methylguanosine modification induces senescence and aging. *Nature communications*, 15(1), 5713.

Waman VP, et al. (2024) Predicting human and viral protein variants affecting COVID-19 susceptibility and repurposing therapeutics. *Scientific reports*, 14(1), 14208.