

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 access protocol, data or information resource, 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, biotools:ensembl_genomes, nlx_65207

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

Record Creation Time: 20220129T080238+0000

Record Last Update: 20260821T193803+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 320 mentions in open access literature.

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

Gu A, et al. (2026) Differential gene expression to heat stress drives thermotolerance, pathogenicity, and reproduction in Fusarium head blight pathogens: from transcriptomic profiling to functional validation. BMC plant biology, 26(1).

Katanski CD, et al. (2026) A transfer RNA inosine modification drives genome-wide synonymous recoding across human commensal bacterial families. PNAS nexus, 5(6), pgag187.

Ren Y, et al. (2026) Genome-Wide Analysis Identifies ScTCP6 as a Stress Responsive Gene in Rye. Current issues in molecular biology, 48(3).

Tsai CH, et al. (2026) Phyling: phylogenetic inference from annotated genomes. G3 (Bethesda, Md.), 16(5).

Santin A, et al. (2026) NPF2 is involved in intracellular pH regulation and ion balance in the diatom Phaeodactylum tricornutum. The New phytologist, 250(6), 3885.

Chen L, et al. (2026) Root-associated protein prediction using a protein large language model and hypergraph convolutional networks. Scientific reports, 16(1), 4876.

Zhou Y, et al. (2026) Genome-wide identification and gene expression analysis of AhNHXs in peanut. BMC plant biology, 26(1).

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.

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.

Yang W, et al. (2025) Prognostic model for predicting recurrence-free survival in hepatocellular carcinoma using integrated analysis of single-cell RNA-sequencing and bulk RNA-sequencing. *Oncology letters*, 30(5), 537.

Kitano J, et al. (2025) Functional mutations in the thyroid-stimulating hormone receptor in natural stickleback populations at sites identical to human disease-causing mutations. *BMC ecology and evolution*, 25(1), 98.

Zhang HB, et al. (2025) Knockdown of PVT1 inhibits cell proliferation in luminal and basal-like breast cancer subtypes by activating LATS2/Hippo signaling pathway. *World journal of surgical oncology*, 23(1), 289.

Braun J, et al. (2025) Contrasting Effects of SARS-CoV-2 Vaccination vs. Infection on Antibody and TCR Repertoires. *bioRxiv : the preprint server for biology*.

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.

Chen H, et al. (2025) A systematic analysis of the network of lncRNAs and mRNAs regulated by TP53 and TP53 mutants with hotspot mutations. *Scientific reports*, 15(1), 27223.