Resource Summary Report

Generated by ASWG on May 3, 2025

Ensembl Protists

RRID:SCR_013154
Type: Tool

Proper Citation

Ensembl Protists (RRID:SCR_013154)

Resource Information

URL: http://protists.ensembl.org

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Description: The Ensembl Genomes project produces genome databases for important species from across the taxonomic range, using the Ensembl software system. Five sites are now available, one of which is Ensembl Protists, which houses protists species. Sponsors: EnsembProtists is a project run by EMBL - EBI to maintain annotation on selected genomes, based on the software developed in the Ensembl project developed jointly by the EBI and the Wellcome Trust Sanger Institute.

Synonyms: EnsemblProtists

Resource Type: database, data or information resource

Keywords: database, genome, protist, software, specie, taxonomic

Funding:

Resource Name: Ensembl Protists

Resource ID: SCR_013154

Alternate IDs: nif-0000-33712

Record Creation Time: 20220129T080314+0000

Record Last Update: 20250503T060348+0000

Ratings and Alerts

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

No alerts have been found for Ensembl Protists.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 27 mentions in open access literature.

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

Dyer SC, et al. (2025) Ensembl 2025. Nucleic acids research, 53(D1), D948.

Dias HM, et al. (2024) THI1 Gene Evolutionary Trends: A Comprehensive Plant-Focused Assessment via Data Mining and Large-Scale Analysis. Genome biology and evolution, 16(10).

Vo NNT, et al. (2024) Transcription factor binding specificities of the oomycete Phytophthora infestans reflect conserved and divergent evolutionary patterns and predict function. BMC genomics, 25(1), 710.

Wu Y, et al. (2023) A Whole-Genome Assembly for Hyaloperonospora parasitica, A Pathogen Causing Downy Mildew in Cabbage (Brassica oleracea var. capitata L.). Journal of fungi (Basel, Switzerland), 9(8).

Yates AD, et al. (2022) Ensembl Genomes 2022: an expanding genome resource for non-vertebrates. Nucleic acids research, 50(D1), D996.

García-Catalán S, et al. (2021) Ca2+-regulated mitochondrial carriers of ATP-Mg2+/Pi: Evolutionary insights in protozoans. Biochimica et biophysica acta. Molecular cell research, 1868(7), 119038.

Xu JJ, et al. (2021) A unique flavoenzyme operates in ubiquinone biosynthesis in photosynthesis-related eukaryotes. Science advances, 7(50), eabl3594.

Jaijyan DK, et al. (2020) Establishment of a stable transfection method in Babesia microti and identification of a novel bidirectional promoter of Babesia microti. Scientific reports, 10(1), 15614.

Balestra AC, et al. (2020) A divergent cyclin/cyclin-dependent kinase complex controls the atypical replication of a malaria parasite during gametogony and transmission. eLife, 9.

Howe KL, et al. (2020) Ensembl Genomes 2020-enabling non-vertebrate genomic research. Nucleic acids research, 48(D1), D689.

Miroliubova TS, et al. (2020) Polyphyletic origin, intracellular invasion, and meiotic genes in the putatively asexual agamococcidians (Apicomplexa incertae sedis). Scientific reports, 10(1), 15847.

Lin X, et al. (2020) Divergent Evolution of PcF/SCR74 Effectors in Oomycetes Is Associated with Distinct Recognition Patterns in Solanaceous Plants. mBio, 11(3).

Dunker F, et al. (2020) Oomycete small RNAs bind to the plant RNA-induced silencing complex for virulence. eLife, 9.

Mandalasi M, et al. (2020) A terminal ?3-galactose modification regulates an E3 ubiquitin ligase subunit in Toxoplasma gondii. The Journal of biological chemistry, 295(27), 9223.

Bilir Ö, et al. (2019) Small RNA inhibits infection by downy mildew pathogen Hyaloperonospora arabidopsidis. Molecular plant pathology, 20(11), 1523.

Majda S, et al. (2019) Intraspecific Variation in Protists: Clues for Microevolution from Poteriospumella lacustris (Chrysophyceae). Genome biology and evolution, 11(9), 2492.

Matsubayashi M, et al. (2019) Novel Characteristics of Mitochondrial Electron Transport Chain from Eimeria tenella. Genes, 10(1).

Rujirawat T, et al. (2018) Probing the Phylogenomics and Putative Pathogenicity Genes of Pythium insidiosum by Oomycete Genome Analyses. Scientific reports, 8(1), 4135.

Fraschka SA, et al. (2018) Comparative Heterochromatin Profiling Reveals Conserved and Unique Epigenome Signatures Linked to Adaptation and Development of Malaria Parasites. Cell host & microbe, 23(3), 407.

Silva Pereira S, et al. (2018) UDP-glycosyltransferase genes in trypanosomatid genomes have diversified independently to meet the distinct developmental needs of parasite adaptations. BMC evolutionary biology, 18(1), 31.