# **Resource Summary Report**

Generated by NIF on May 16, 2025

# **Ensembl Metazoa**

RRID:SCR\_000800

Type: Tool

## **Proper Citation**

Ensembl Metazoa (RRID:SCR\_000800)

#### **Resource Information**

URL: http://metazoa.ensembl.org/index.html

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**Description:** Ensembl Genomes project produces genome databases for important species from across taxonomic range, using Ensembl software system. Five sites are now available, one of which is Ensembl Metazoa, which houses metazoan species.

Synonyms: EnsemblMetazoa

Resource Type: data or information resource, database

**Defining Citation:** PMID:21785142

Keywords: database, genome, metazoan, software, specie, taxonomic, FASEB list

Funding: EMBL - EBI

Resource Name: Ensembl Metazoa

Resource ID: SCR\_000800

Alternate IDs: nif-0000-33714

**Record Creation Time:** 20220129T080203+0000

**Record Last Update:** 20250507T055911+0000

## **Ratings and Alerts**

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

No alerts have been found for Ensembl Metazoa.

### **Data and Source Information**

Source: SciCrunch Registry

## **Usage and Citation Metrics**

We found 36 mentions in open access literature.

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

Ocampo Daza D, et al. (2018) Evolution of the growth hormone, prolactin, prolactin 2 and somatolactin family. General and comparative endocrinology, 264, 94.

Wragg D, et al. (2018) Autosomal and Mitochondrial Adaptation Following Admixture: A Case Study on the Honeybees of Reunion Island. Genome biology and evolution, 10(1), 220.

Parreira B, et al. (2018) Persistence of the ABCC6 genes and the emergence of the bony skeleton in vertebrates. Scientific reports, 8(1), 6027.

Grandchamp A, et al. (2018) Synchronous birth is a dominant pattern in receptor-ligand evolution. BMC genomics, 19(1), 611.

Pan PL, et al. (2018) A comprehensive omics analysis and functional survey of cuticular proteins in the brown planthopper. Proceedings of the National Academy of Sciences of the United States of America, 115(20), 5175.

Camiolo S, et al. (2018) corseq: fast and efficient identification of favoured codons from next generation sequencing reads. PeerJ, 6, e5099.

Wang T, et al. (2017) Changes in the neuropeptide content of Biomphalaria ganglia nervous system following Schistosoma infection. Parasites & vectors, 10(1), 275.

Anderson FE, et al. (2017) Phylogenomic analyses of Crassiclitellata support major Northern and Southern Hemisphere clades and a Pangaean origin for earthworms. BMC evolutionary biology, 17(1), 123.

Athrey G, et al. (2017) Chemosensory gene expression in olfactory organs of the anthropophilic Anopheles coluzzii and zoophilic Anopheles quadriannulatus. BMC genomics, 18(1), 751.

Attwood MM, et al. (2017) Highly diversified expansions shaped the evolution of membrane bound proteins in metazoans. Scientific reports, 7(1), 12387.

Hultqvist G, et al. (2017) Emergence and evolution of an interaction between intrinsically disordered proteins. eLife, 6.

Vlahovic I, et al. (2017) Regular Higher Order Repeat Structures in Beetle Tribolium castaneum Genome. Genome biology and evolution, 9(10), 2668.

Yin C, et al. (2016) InsectBase: a resource for insect genomes and transcriptomes. Nucleic acids research, 44(D1), D801.

Zhou QZ, et al. (2016) BmncRNAdb: a comprehensive database of non-coding RNAs in the silkworm, Bombyx mori. BMC bioinformatics, 17(1), 370.

Zolfaghari Emameh R, et al. (2016) Innovative molecular diagnosis of Trichinella species based on ?-carbonic anhydrase genomic sequence. Microbial biotechnology, 9(2), 172.

Sharma A, et al. (2016) Protein Translation Enzyme lysyl-tRNA Synthetase Presents a New Target for Drug Development against Causative Agents of Loiasis and Schistosomiasis. PLoS neglected tropical diseases, 10(11), e0005084.

Hoy MA, et al. (2016) Genome Sequencing of the Phytoseiid Predatory Mite Metaseiulus occidentalis Reveals Completely Atomized Hox Genes and Superdynamic Intron Evolution. Genome biology and evolution, 8(6), 1762.

Yu H, et al. (2016) Genome-wide identification and characterization of long intergenic noncoding RNAs and their potential association with larval development in the Pacific oyster. Scientific reports, 6, 20796.

Baa-Puyoulet P, et al. (2016) ArthropodaCyc: a CycADS powered collection of BioCyc databases to analyse and compare metabolism of arthropods. Database: the journal of biological databases and curation, 2016.

Yue JX, et al. (2016) The evolution of genes encoding for green fluorescent proteins: insights from cephalochordates (amphioxus). Scientific reports, 6, 28350.