

Resource Summary Report

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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: database, data or information resource

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: r3d100011198, nif-0000-33714

Record Creation Time: 20220129T080203+0000

Record Last Update: 20260805T044014+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 37 mentions in open access literature.

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

Han B, et al. (2025) Evolutionarily diverse caveolins share a common structural framework built around amphipathic disks. *The Journal of cell biology*, 224(9).

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

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

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.

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.

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

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

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.

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

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

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.

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.

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

Pace RM, et al. (2016) Composition and genomic organization of arthropod Hox clusters. *EvoDevo*, 7, 11.

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

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.