

Resource Summary Report

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HomeoDB

RRID:SCR_015492

Type: Tool

Proper Citation

HomeoDB (RRID:SCR_015492)

Resource Information

URL: <http://homeodb.zoo.ox.ac.uk/>

Proper Citation: HomeoDB (RRID:SCR_015492)

Description: Database of homeobox genes in humans, mice, chickens, frogs, zebrafishes, amphioxuses, fruitflies, beetles, honeybees, and nematodes., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Resource Type: database, data or information resource

Keywords: homeobox gene, homeobox gene database, gene database

Funding: Marie Curie International Incoming Fellowship

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: HomeoDB

Resource ID: SCR_015492

Record Creation Time: 20220129T080326+0000

Record Last Update: 20260725T191211+0000

Ratings and Alerts

No rating or validation information has been found for HomeoDB.

No alerts have been found for HomeoDB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Fu X, et al. (2024) Key homeobox transcription factors regulate the development of the firefly's adult light organ and bioluminescence. *Nature communications*, 15(1), 1736.

Unneberg P, et al. (2024) Ecological genomics in the Northern krill uncovers loci for local adaptation across ocean basins. *Nature communications*, 15(1), 6297.

Mulhair PO, et al. (2023) Diversity, duplication, and genomic organization of homeobox genes in Lepidoptera. *Genome research*, 33(1), 32.

Leite DJ, et al. (2022) Genome Assembly of the Polyclad Flatworm *Prostheceraeus crozieri*. *Genome biology and evolution*, 14(9).

Zhang L, et al. (2022) The genome of an apodid holothuroid (*Chiridota heheva*) provides insights into its adaptation to a deep-sea reducing environment. *Communications biology*, 5(1), 224.

Fan Z, et al. (2021) A chromosome-level genome of the spider *Trichonephila antipodiana* reveals the genetic basis of its polyphagy and evidence of an ancient whole-genome duplication event. *GigaScience*, 10(3).

Nong W, et al. (2021) Horseshoe crab genomes reveal the evolution of genes and microRNAs after three rounds of whole genome duplication. *Communications biology*, 4(1), 83.

Jin F, et al. (2020) High-quality genome assembly of *Metaphire vulgaris*. *PeerJ*, 8, e10313.

Qu Z, et al. (2020) Genome of the four-finger threadfin *Eleutheronema tetradactylum* (Perciforms: Polynemidae). *BMC genomics*, 21(1), 726.

Nong W, et al. (2020) Jellyfish genomes reveal distinct homeobox gene clusters and conservation of small RNA processing. *Nature communications*, 11(1), 3051.

Li Y, et al. (2020) Reconstruction of ancient homeobox gene linkages inferred from a new high-quality assembly of the Hong Kong oyster (*Magallana hongkongensis*) genome. *BMC genomics*, 21(1), 713.

Li Y, et al. (2018) Sea cucumber genome provides insights into saponin biosynthesis and aestivation regulation. *Cell discovery*, 4, 29.

Treffkorn S, et al. (2018) Expression of NK cluster genes in the onychophoran *Euperipatoides rowelli*: implications for the evolution of NK family genes in nephrozoans. *EvoDevo*, 9, 17.

Szabó R, et al. (2018) Two more Posterior Hox genes and Hox cluster dispersal in echinoderms. *BMC evolutionary biology*, 18(1), 203.

Feindt W, et al. (2018) Transcriptome profiling with focus on potential key genes for wing development and evolution in *Megaloprepus caerulatus*, the damselfly species with the world's largest wings. *PloS one*, 13(1), e0189898.

Schwager EE, et al. (2017) The house spider genome reveals an ancient whole-genome duplication during arachnid evolution. *BMC biology*, 15(1), 62.

Wang S, et al. (2017) Scallop genome provides insights into evolution of bilaterian karyotype and development. *Nature ecology & evolution*, 1(5), 120.

Zhang X, et al. (2017) The sea cucumber genome provides insights into morphological evolution and visceral regeneration. *PLoS biology*, 15(10), e2003790.

Leidenroth A, et al. (2010) A family history of DUX4: phylogenetic analysis of DUXA, B, C and Duxbl reveals the ancestral DUX gene. *BMC evolutionary biology*, 10, 364.