Resource Summary Report

Generated by dkNET on Apr 21, 2025

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.

Resource Type: database, data or information resource

Keywords: homeobox gene, homeobox gene database, gene database

Funding: Marie Curie International Incoming Fellowship

Availability: Open source

Resource Name: HomeoDB

Resource ID: SCR_015492

Record Creation Time: 20220129T080326+0000

Record Last Update: 20250420T015652+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 <u>dkNET</u>.

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.

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.

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

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.