Resource Summary Report

Generated by NIF on May 4, 2025

wFleaBase

RRID:SCR_006018
Type: Tool

Proper Citation

wFleaBase (RRID:SCR_006018)

Resource Information

URL: http://wfleabase.org/

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Description: wFleaBase provides gene and genomic information for species of the genus Daphnia - commonly known as the water flea. It contains the genome of Daphnia pulex and other species, including bulk data files, and all gene pages, plus genomics tools including microsatellites, cDNA, Cosmid and BAC libraries, GSS and ESTs, and microarrays. It also contains maps of the Daphnia genome, and genome annotation tools. The freshwater crustacean Daphnia is a model system for ecology, evolution and the environmental sciences. The rapidly growing genomic data for this organism is stimulating interdisciplinary research to understand the complex interplay between genome structure, gene expression, individual fitness, and population-level responses to chemical contaminants and environmental change.wFleaBase includes data from all species of the genus, yet the primary species are D. pulex and D. magna, because of the broad set of genomic tools that have already been developed for these animals. A complete sequence for Daphnia pulex is now available at this site. Please observe this Data release policy. The data is a first characterization of the crustacean genome, which was made possible by the U.S. Department of Energy (DOE) Joint Genome Institute (JGI) in collaboration with the Daphnia Genomics Consortium (DGC) whose members were funded by the National Science Foundation. Category: Genomics Databases (non-vertebrate) Subcategory: Invertebrate genome databases

Synonyms: wFleaBase

Resource Type: database, data or information resource

Keywords: FASEB list

Funding:

Resource Name: wFleaBase

Resource ID: SCR_006018

Alternate IDs: nif-0000-03642

Record Creation Time: 20220129T080233+0000

Record Last Update: 20250503T055809+0000

Ratings and Alerts

No rating or validation information has been found for wFleaBase.

No alerts have been found for wFleaBase.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 65 mentions in open access literature.

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

Chaturvedi A, et al. (2023) The hologenome of Daphnia magna reveals possible DNA methylation and microbiome-mediated evolution of the host genome. Nucleic acids research, 51(18), 9785.

Ebert D, et al. (2022) Daphnia as a versatile model system in ecology and evolution. EvoDevo, 13(1), 16.

Kong WL, et al. (2022) Development of transcriptomics-based growth rate indices in two model eukaryotes and relevance to metatranscriptomics datasets. Molecular ecology resources, 22(7), 2627.

Oliver A, et al. (2022) Phenotypic and transcriptional response of Daphnia pulicaria to the combined effects of temperature and predation. PloS one, 17(7), e0265103.

Brasseur MV, et al. (2022) Impacts of multiple anthropogenic stressors on the transcriptional response of Gammarus fossarum in a mesocosm field experiment. BMC genomics, 23(1), 816.

Ameline C, et al. (2021) A Two-Locus System with Strong Epistasis Underlies Rapid Parasite-Mediated Evolution of Host Resistance. Molecular biology and evolution, 38(4), 1512.

Bento G, et al. (2020) An alternative route of bacterial infection associated with a novel resistance locus in the Daphnia-Pasteuria host-parasite system. Heredity, 125(4), 173.

Schwarzenberger A, et al. (2020) Toward Disentangling the Multiple Nutritional Constraints Imposed by Planktothrix: The Significance of Harmful Secondary Metabolites and Sterol Limitation. Frontiers in microbiology, 11, 586120.

Kowal K, et al. (2020) Identification of Mitochondrial DNA (NUMTs) in the Nuclear Genome of Daphnia magna. International journal of molecular sciences, 21(22).

Coucheron DH, et al. (2019) MicroRNAs in Daphnia magna identified and characterized by deep sequencing, genome mapping and manual curation. Scientific reports, 9(1), 15945.

Duki? M, et al. (2019) How clonal are clones? A quest for loss of heterozygosity during asexual reproduction in Daphnia magna. Journal of evolutionary biology, 32(6), 619.

Street SM, et al. (2019) The role of nuclear receptor E75 in regulating the molt cycle of Daphnia magna and consequences of its disruption. PloS one, 14(8), e0221642.

Lindeman LC, et al. (2019) Epigenetic, transcriptional and phenotypic responses in two generations of Daphnia magna exposed to the DNA methylation inhibitor 5-azacytidine. Environmental epigenetics, 5(3), dvz016.

Ravindran SP, et al. (2019) Daphnia stressor database: Taking advantage of a decade of Daphnia '-omics' data for gene annotation. Scientific reports, 9(1), 11135.

Abehsera S, et al. (2018) CPAP3 proteins in the mineralized cuticle of a decapod crustacean. Scientific reports, 8(1), 2430.

Rivetti C, et al. (2018) Tryptophan hydroxylase (TRH) loss of function mutations induce growth and behavioral defects in Daphnia magna. Scientific reports, 8(1), 1518.

Cordes MHJ, et al. (2018) Evolutionary dynamics of origin and loss in the deep history of phospholipase D toxin genes. BMC evolutionary biology, 18(1), 194.

Kakaley EK, et al. (2017) Agonist-mediated assembly of the crustacean methyl farnesoate receptor. Scientific reports, 7, 45071.

Marco HG, et al. (2017) Characterisation and pharmacological analysis of a crustacean G protein-coupled receptor: the red pigment-concentrating hormone receptor of Daphnia pulex. Scientific reports, 7(1), 6851.

Roncalli V, et al. (2017) A deep transcriptomic resource for the copepod crustacean Labidocera madurae: A potential indicator species for assessing near shore ecosystem health. PloS one, 12(10), e0186794.