

# Resource Summary Report

Generated by [RRID](#) on Aug 5, 2026

## [wFleaBase](#)

RRID:SCR\_006018

Type: Tool

### Proper Citation

wFleaBase (RRID:SCR\_006018)

### Resource Information

**URL:** <http://wfleabase.org/>

**Proper Citation:** wFleaBase (RRID:SCR\_006018)

**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

**Resource Name:** wFleaBase

**Resource ID:** SCR\_006018

**Alternate IDs:** nif-0000-03642

**Record Creation Time:** 20220129T080233+0000

**Record Last Update:** 20260805T044129+0000

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## Ratings and Alerts

No rating or validation information has been found for wFleaBase.

No alerts have been found for wFleaBase.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 65 mentions in open access literature.

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

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.

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.

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.

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.
- 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.
- 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.
- 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.
- Bento G, et al. (2017) The genetic basis of resistance and matching-allele interactions of a host-parasite system: The *Daphnia magna*-*Pasteuria ramosa* model. *PLoS genetics*, 13(2), e1006596.