

Resource Summary Report

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Animal Genome Size Database

RRID:SCR_007551

Type: Tool

Proper Citation

Animal Genome Size Database (RRID:SCR_007551)

Resource Information

URL: <http://www.genomesize.com>

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Description: Comprehensive catalogue of animal genome size data. Haploid DNA contents (C-values, in picograms) are available for 4972 species (3231 vertebrates and 1741 non-vertebrates) based on 6518 records from 669 published sources. Data may be submitted directly to the database or reprints and notifications of new papers may be sent to database curation staff.

Abbreviations: Genomesize

Resource Type: catalog, data or information resource, data repository, database, service resource, storage service resource

Defining Citation: [PMID:17090588](#)

Keywords: genome size, haploid dna, non-vertebrate, vertebrate, genome structure, comparative biodiversity, sequencing, genome, genomic, FASEB list

Funding: Natural Sciences and Engineering Research Council of Canada

Availability: Data taken from the database must not be reproduced in published lists, Online databases, Or other such formats, Nor redistributed without permission. The information is provided solely for personal and academic use., Please cite, The community can contribute to this resource

Resource Name: Animal Genome Size Database

Resource ID: SCR_007551

Alternate IDs: nif-0000-02548, r3d100012517

Alternate URLs: <https://doi.org/10.17616/R3R782>, <https://doi.org/10.17616/R3R782>

Record Creation Time: 20220129T080242+0000

Record Last Update: 20260905T132614+0000

Ratings and Alerts

No rating or validation information has been found for Animal Genome Size Database.

No alerts have been found for Animal Genome Size Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 190 mentions in open access literature.

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

Guirao-Rico S, et al. (2026) ERGA-CBP chromosome-level genome assembly of the blind scorpion *Belisarius xambeui* Simon, 1879 (Belisariidae, Scorpiones), a singular scorpion in Europe. *Open research Europe*, 6, 53.

Baeza JA, et al. (2025) Insight Into the Nuclear and Mitochondrial Genome of the Caribbean King Crab *Maguimithrax spinosissimus* (Crustacea: Brachyura: Mithracidae) to Support Fisheries Management and Conservation Initiatives. *Ecology and evolution*, 15(7), e71619.

Han S, et al. (2025) High-quality chromosome-level genome assembly of the whitespotted conger (*Conger myriaster*). *Scientific data*, 12(1), 626.

Ichikawa K, et al. (2025) CGC1, a new reference genome for *Caenorhabditis elegans*. *Genome research*, 35(8), 1902.

Marino A, et al. (2025) Effective population size does not explain long-term variation in genome size and transposable element content in animals. *eLife*, 13.

Baeza JA, et al. (2025) Assembly of Mitochondrial Genomes Using Nanopore Long-Read Technology in Three Sea Chubs (Teleostei: Kyphosidae). *Molecular ecology resources*, 25(1), e14034.

Christensen KA, et al. (2025) Masu salmon species complex relationships and sex chromosomes revealed from analyses of the masu salmon (*Oncorhynchus masou masou*) genome assembly. *G3 (Bethesda, Md.)*, 15(2).

Souza LHB, et al. (2025) New Insights into the Sex Chromosome Evolution of the Common Barker Frog Species Complex (Anura, Leptodactylidae) Inferred from Its Satellite DNA Content. *Biomolecules*, 15(6).

Neiman M, et al. (2025) Variation in nuclear genome size in a freshwater snail model system featuring a recent whole-genome duplication. *Royal Society open science*, 12(6), 250171.

Rios-Carlos H, et al. (2024) Genomic Gigantism is not Associated with Reduced Selection Efficiency in Neotropical Salamanders. *Journal of molecular evolution*, 92(4), 371.

Drozdova PB, et al. (2024) Lake Baikal amphipods and their genomes, great and small. *Vavilovskii zhurnal genetiki i selektsii*, 28(3), 317.

Bista B, et al. (2024) De novo genome assemblies of two cryptodiran turtles with ZZ/ZW and XX/XY sex chromosomes provide insights into patterns of genome reshuffling and uncover novel 3D genome folding in amniotes. *Genome research*, 34(10), 1553.

Kawato S, et al. (2024) Integrase-associated niche differentiation of endogenous large DNA viruses in crustaceans. *Microbiology spectrum*, 12(1), e0055923.

Póti Á, et al. (2024) Mutational profile of the regenerative process and de novo genome assembly of the planarian *Schmidtea polychroa*. *Nucleic acids research*, 52(4), 1779.

Rives N, et al. (2024) Diverse origins of near-identical antifreeze proteins in unrelated fish lineages provide insights into evolutionary mechanisms of new gene birth and protein sequence convergence. *bioRxiv : the preprint server for biology*.

Fernández P, et al. (2024) A 160 Gbp fork fern genome shatters size record for eukaryotes. *iScience*, 27(6), 109889.

Grishanin A, et al. (2024) ?Chromatin diminution as a tool to study some biological problems. *Comparative cytogenetics*, 18, 27.

Deng Y, et al. (2024) A high heterozygosity genome assembly of *Aedes albopictus* enables the discovery of the association of PGANT3 with blood-feeding behavior. *BMC genomics*, 25(1), 336.

Rives N, et al. (2024) Diverse Origins of Near-Identical Antifreeze Proteins in Unrelated Fish Lineages Provide Insights Into Evolutionary Mechanisms of New Gene Birth and Protein Sequence Convergence. *Molecular biology and evolution*, 41(9).

Decena-Segarra LP, et al. (2024) Transposable Element Diversity and Activity Patterns in Neotropical Salamanders. *Molecular biology and evolution*, 41(11).