

Resource Summary Report

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D-GENIES

RRID:SCR_018967

Type: Tool

Proper Citation

D-GENIES (RRID:SCR_018967)

Resource Information

URL: <http://dgenies.toulouse.inra.fr/>

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Description: Open source software package developed in Python and JavaScript. Standalone and web application tool performing large genome alignments and generating interactive dot plots. Designed to compare two genomes. Used to sort query sequences along reference, zoom in plot and download several image, alignment or sequence files. Allows to display dot plots from other aligners by uploading their PAF or MAF alignment file.

Synonyms: Dot plot large GENomes in an Interactive, Efficient and Simple way

Resource Type: image analysis software, web application, alignment software, software application, software resource, data processing software, standalone software

Defining Citation: [PMID:29888139](#)

Keywords: bio.tools

Availability: Free, Available for download, Freely available

Resource Name: D-GENIES

Resource ID: SCR_018967

Alternate IDs: biotools:d-genies

Alternate URLs: <https://github.com/genotoul-bioinfo/dgenies>, <https://bio.tools/d-genies>

License: GNU General Public License

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260801T190621+0000

Ratings and Alerts

No rating or validation information has been found for D-GENIES.

No alerts have been found for D-GENIES.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 46 mentions in open access literature.

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

Johns J, et al. (2026) A near chromosome-level assembly of the serpentine endemic columbine, *Aquilegia eximia*. *The Journal of heredity*, 117(1), 85.

Xin H, et al. (2025) Jan and mini-Jan, a model system for potato functional genomics. *Plant biotechnology journal*, 23(4), 1243.

Shukla HG, et al. (2025) Genetic variation in recalcitrant repetitive regions of the *Drosophila melanogaster* genome. *Genome research*, 35(9), 2023.

Han H, et al. (2025) A telomere-to-telomere phased genome of an octoploid strawberry reveals a receptor kinase conferring anthracnose resistance. *GigaScience*, 14.

Dowling CA, et al. (2025) FT-like genes in *Cannabis* and hops: sex specific expression and copy-number variation may explain flowering time variation. *BMC genomics*, 26(1), 930.

Pégaré M, et al. (2025) QTL detection and genomic prediction for resistance to anthracnose in alfalfa (*Medicago sativa*). *The plant genome*, 18(3), e70085.

Adhikari TB, et al. (2025) Genomic insights and comparative analysis of *Colletotrichum* species associated with anthracnose fruit rot and crown rot of strawberry in North Carolina. *Frontiers in microbiology*, 16, 1515894.

Nakandala U, et al. (2025) Characterizing the structural variations in the genome of the mandarin variety, IrM2, induced by gamma irradiation. *Plant biotechnology journal*, 23(9), 3814.

Belinchon-Moreno J, et al. (2025) Nuclear and organelle genome assemblies of 5 *Cucumis melo* L. accessions, Ananas, Canton, PI 414723, Vedrantaïs, and Zhimali, belonging to diverse botanical groups. *G3 (Bethesda, Md.)*, 15(7).

Tanaka T, et al. (2025) Reference-based chromosome-scale assembly of Japanese barley (*Hordeum vulgare* ssp. *vulgare*) cultivar Hayakiso 2. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(4).

Arai H, et al. (2025) Single-cell genome analysis of a feminizing Wolbachia in Eurema butterflies reveals a shared origin with male-killing Wolbachia. *Microbial genomics*, 11(11).

Tizabi D, et al. (2025) Nanopore Sequencing of Amoebophrya Species Reveals Novel Collection of Bacteria Putatively Associated With *Karlodinium veneficum*. *Genome biology and evolution*, 17(3).

Hesson JC, et al. (2025) A chromosomal reference genome sequence for the northern house mosquito, *Culex pipiens form pipiens*, Linnaeus, 1758. *Wellcome open research*, 10, 107.

Liu J, et al. (2024) Deep R-gene discovery in HLB resistant wild Australian limes uncovers evolutionary features and potentially important loci for hybrid breeding. *Frontiers in plant science*, 15, 1503030.

Xin H, et al. (2024) Jan and mini-Jan, a model system for potato functional genomics. *bioRxiv : the preprint server for biology*.

Wongdontree P, et al. (2024) Oxidative stress is intrinsic to staphylococcal adaptation to fatty acid synthesis antibiotics. *iScience*, 27(4), 109505.

Perrier A, et al. (2024) Maternal inheritance of functional centrioles in two parthenogenetic nematodes. *Nature communications*, 15(1), 6042.

González-Prendes R, et al. (2024) Long-read de novo assembly of the red-legged partridge (*Alectoris rufa*) genome. *Scientific data*, 11(1), 908.

Sato M, et al. (2024) Chromosomal DNA sequences of the Pacific saury genome: versatile resources for fishery science and comparative biology. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 31(2).

Cuello C, et al. (2024) The Madagascar palm genome provides new insights on the evolution of Apocynaceae specialized metabolism. *Heliyon*, 10(6), e28078.