

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

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: 20260821T194139+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 56 mentions in open access literature.

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

Blanchard I, et al. (2026) Phylogeny-driven pangenome analysis uncovers the genomic landscape of domesticated and wild *Armeniaca* species. *Horticulture research*, 13(7), uhag104.

Arai H, et al. (2026) Linking genomic variation in *Spiroplasma* endosymbionts to male production and male-killing in the pea aphid. *BMC genomics*, 27(1).

Nawae W, et al. (2026) Genome Assembly of Three Shrub Mangroves in the Genus *Acanthus* Reveals Two Polyploidy Events and Expansion of Genes Linked to Root Adaptation in Coastal Habitats. *GigaScience*, 15.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

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

Chen YZ, et al. (2026) Whole-Genome Sequencing of Pathogenic *Nigrospora musae* ST1 Causing Leaf Spot Disease in *Idesia polycarpa*. *Journal of fungi* (Basel, Switzerland), 12(3).

Denis H, et al. (2026) Contrasting population structures of reef-building corals and their algal symbionts inform adaptive potential across the western Pacific. *Current biology : CB*, 36(11), 2808.

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

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),

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.

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.

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

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).

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).

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).

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.

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).