

Resource Summary Report

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GenomeView

RRID:SCR_012968

Type: Tool

Proper Citation

GenomeView (RRID:SCR_012968)

Resource Information

URL: <http://genomeview.org/>

Proper Citation: GenomeView (RRID:SCR_012968)

Description: A next-generation stand-alone genome browser and editor initiated in the BSB group at VIB and currently developed at Broad Institute.

Abbreviations: GenomeView

Resource Type: data or information resource, database, software resource

Defining Citation: [PMID:22102585](#)

Resource Name: GenomeView

Resource ID: SCR_012968

Alternate IDs: OMICS_00913

Record Creation Time: 20220129T080313+0000

Record Last Update: 20260919T195235+0000

Ratings and Alerts

No rating or validation information has been found for GenomeView.

No alerts have been found for GenomeView.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 36 mentions in open access literature.

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

Zeng T, et al. (2025) Multisite long-read sequencing reveals the early contributions of somatic structural variations to HBV-related hepatocellular carcinoma tumorigenesis. *Genome research*, 35(4), 671.

Zakerzade R, et al. (2025) Diversification and recurrent adaptation of the synaptonemal complex in *Drosophila*. *PLoS genetics*, 21(1), e1011549.

Rabelo-Araujo JVDS, et al. (2025) Phylogeny, structural patterns, and polymorphisms in *Dyckia* spp. from the Espinhaço mountain range based on complete chloroplast genome. *Frontiers in plant science*, 16, 1549351.

Ji M, et al. (2023) A nuclear receptor HR96-related gene underlies large trans-driven differences in detoxification gene expression in a generalist herbivore. *Nature communications*, 14(1), 4990.

Ma X, et al. (2021) Improved chromosome-level genome assembly and annotation of the seagrass, *Zostera marina* (eelgrass). *F1000Research*, 10, 289.

Joubert M, et al. (2021) Expression of several *Phytophthora cinnamomi* putative RxLRs provides evidence for virulence roles in avocado. *PloS one*, 16(7), e0254645.

Goldberger O, et al. (2021) Wisdom of the crowds: A suggested polygenic plan for small-RNA-mediated regulation in bacteria. *iScience*, 24(10), 103096.

Bourdareau S, et al. (2021) Histone modifications during the life cycle of the brown alga *Ectocarpus*. *Genome biology*, 22(1), 12.

De Vos S, et al. (2021) The genome of the extremophile *Artemia* provides insight into strategies to cope with extreme environments. *BMC genomics*, 22(1), 635.

Greenhalgh R, et al. (2020) Genome streamlining in a minute herbivore that manipulates its host plant. *eLife*, 9.

Cauz-Santos LA, et al. (2020) A Repertory of Rearrangements and the Loss of an Inverted Repeat Region in *Passiflora* Chloroplast Genomes. *Genome biology and evolution*, 12(10), 1841.

Stokes JM, et al. (2020) A Deep Learning Approach to Antibiotic Discovery. *Cell*, 180(4), 688.

Klopper M, et al. (2020) A landscape of genomic alterations at the root of a near-untreatable tuberculosis epidemic. *BMC medicine*, 18(1), 24.

Cuello C, et al. (2019) A systems biology approach uncovers a gene co-expression network associated with cell wall degradability in maize. *PloS one*, 14(12), e0227011.

Arun A, et al. (2019) Convergent recruitment of TALE homeodomain life cycle regulators to direct sporophyte development in land plants and brown algae. *eLife*, 8.

Mignerot L, et al. (2019) A key role for sex chromosomes in the regulation of parthenogenesis in the brown alga *Ectocarpus*. *PLoS genetics*, 15(6), e1008211.

Snoeck S, et al. (2018) Transcriptomic Plasticity in the Arthropod Generalist *Tetranychus urticae* Upon Long-Term Acclimation to Different Host Plants. *G3 (Bethesda, Md.)*, 8(12), 3865.

Munhoz CF, et al. (2018) A gene-rich fraction analysis of the *Passiflora edulis* genome reveals highly conserved microsyntenic regions with two related Malpighiales species. *Scientific reports*, 8(1), 13024.

Mikhailov KV, et al. (2017) Genomic Survey of a Hyperparasitic Microsporidian *Amphiamblys* sp. (Metchnikovellidae). *Genome biology and evolution*, 9(3), 454.

Sarilar V, et al. (2017) Genome sequence of the type strain CLIB 1764T (= CBS 14374T) of the yeast species *Kazachstania saulgeensis* isolated from French organic sourdough. *Genomics data*, 13, 41.