Resource Summary Report

Generated by dkNET on Apr 28, 2025

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: database, software resource, data or information resource

Defining Citation: PMID:22102585

Funding:

Availability: Open unspecified license, Acknowledgement requested

Resource Name: GenomeView

Resource ID: SCR_012968

Alternate IDs: OMICS_00913

Record Creation Time: 20220129T080313+0000

Record Last Update: 20250428T053729+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 34 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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

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.

Gentekaki E, et al. (2017) Extreme genome diversity in the hyper-prevalent parasitic eukaryote Blastocystis. PLoS biology, 15(9), e2003769.

De Schutter K, et al. (2017) Evolutionary relationships and expression analysis of EUL domain proteins in rice (Oryza sativa). Rice (New York, N.Y.), 10(1), 26.