

Resource Summary Report

Generated by [kravitz2](#) on Jul 30, 2026

[ggbio](#)

RRID:SCR_003313

Type: Tool

Proper Citation

ggbio (RRID:SCR_003313)

Resource Information

URL: <http://www.bioconductor.org/packages/release/bioc/html/ggbio.html>

Proper Citation: ggbio (RRID:SCR_003313)

Description: An R package for extending the grammar of graphics for genomic data. The graphics are designed to answer common scientific questions, in particular those often asked of high throughput genomics data. All core Bioconductor data structures are supported, where appropriate. The package supports detailed views of particular genomic regions, as well as genome-wide overviews. Supported overviews include ideograms and grand linear views. High-level plots include sequence fragment length, edge-linked interval to data view, mismatch pileup, and several splicing summaries.

Synonyms: ggbio - Visualization tools for genomic data

Resource Type: software resource

Defining Citation: [PMID:22937822](#)

Keywords: standalone software, unix/linux, mac os x, windows, r, infrastructure, visualization, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: ggbio

Resource ID: SCR_003313

Alternate IDs: biotools:ggbio, OMICS_04660

Alternate URLs: <http://www.tengfei.name/ggbio/>, <https://bio.tools/ggbio>

Record Creation Time: 20220129T080218+0000

Record Last Update: 20260725T190538+0000

Ratings and Alerts

No rating or validation information has been found for ggbio.

No alerts have been found for ggbio.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Kariyayama H, et al. (2025) Hagfish olfactory repertoire illuminates lineage-specific diversification of olfaction in basal vertebrates. *iScience*, 28(12), 114118.

Cunha-Ferreira IC, et al. (2024) Impact of *Paenibacillus elgii* supernatant on screening bacterial strains with potential for biotechnological applications. *Engineering microbiology*, 4(3), 100163.

Ugolini M, et al. (2024) Transcription bodies regulate gene expression by sequestering CDK9. *Nature cell biology*, 26(4), 604.

Velásquez-Zapata V, et al. (2024) Diverse epistatic effects in barley-powdery mildew interactions localize to host chromosome hotspots. *iScience*, 27(10), 111013.

Salahudeen AA, et al. (2023) Functional screening of amplification outlier oncogenes in organoid models of early tumorigenesis. *Cell reports*, 42(11), 113355.

Cox LS, et al. (2023) Blimp-1 and c-Maf regulate Il10 and negatively regulate common and unique proinflammatory gene networks in IL-12 plus IL-27-driven T helper-1 cells. *Wellcome open research*, 8, 403.

Swaney MH, et al. (2022) Cobamide Sharing Is Predicted in the Human Skin Microbiome. *mSystems*, 7(5), e0067722.

Yokobayashi S, et al. (2021) Inherent genomic properties underlie the epigenomic heterogeneity of human induced pluripotent stem cells. *Cell reports*, 37(5), 109909.

McDonald MM, et al. (2021) Osteoclasts recycle via osteomorphs during RANKL-stimulated bone resorption. *Cell*, 184(5), 1330.

Miller ME, et al. (2020) Increased virulence of *Puccinia coronata* f. sp. *avenae* populations through allele frequency changes at multiple putative Avr loci. *PLoS genetics*, 16(12), e1009291.

Spencer S, et al. (2019) Loss of the interleukin-6 receptor causes immunodeficiency, atopy, and abnormal inflammatory responses. *The Journal of experimental medicine*,

216(9), 1986.

Albert FW, et al. (2018) Genetics of trans-regulatory variation in gene expression. *eLife*, 7.

Koh W, et al. (2016) Dynamic ASXL1 Exon Skipping and Alternative Circular Splicing in Single Human Cells. *PloS one*, 11(10), e0164085.

Böttcher R, et al. (2016) Human PDE4D isoform composition is deregulated in primary prostate cancer and indicative for disease progression and development of distant metastases. *Oncotarget*, 7(43), 70669.