

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

IGB

RRID:SCR_011792

Type: Tool

Proper Citation

IGB (RRID:SCR_011792)

Resource Information

URL: <http://bioviz.org/igb/>

Proper Citation: IGB (RRID:SCR_011792)

Description: An easy-to-use, highly customizable genome browser you can use to visualize and explore genomic data and annotations, including RNA-Seq, ChIP-Seq, tiling array data, and more.

Abbreviations: IGB

Synonyms: Integrated Genome Browser

Resource Type: software resource

Defining Citation: [PMID:19654113](#)

Keywords: genome, rna-seq, chip-seq, tiling array, browser

Availability: Free, Acknowledgement requested

Resource Name: IGB

Resource ID: SCR_011792

Alternate IDs: OMICS_00916

Record Creation Time: 20220129T080306+0000

Record Last Update: 20260725T190720+0000

Ratings and Alerts

No rating or validation information has been found for IGB.

No alerts have been found for IGB.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 336 mentions in open access literature.

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

Trendel J, et al. (2025) The human proteome with direct physical access to DNA. *Cell*, 188(16), 4424.

Bielowka AM, et al. (2025) Acute endothelial stresses identify microRNA let-7b-5p and non-coding SLC11A2 (NRAMP2/DMT1) exon as biomarkers that overlap with those detected in malignant and non-malignant diseases. *QJM : monthly journal of the Association of Physicians*, 118(9), 679.

Ghatbale P, et al. (2025) Experimental phage evolution results in expanded host ranges against antibiotic resistant *Klebsiella pneumoniae* isolates. *Nature communications*, 16(1), 9903.

Shayler DWH, et al. (2025) Identification and characterization of early human photoreceptor states and cell-state-specific retinoblastoma-related features. *eLife*, 13.

Bhandare P, et al. (2025) Phenotypic screens identify SCAF1 as critical activator of RNAPII elongation and global transcription. *Nucleic acids research*, 53(4).

Wright JL, et al. (2025) The INO80 Chromatin Remodeling Complex Regulates Histone H2A.Z Mobility and the G1-S Transition in Oligodendrocyte Precursors. *Glia*, 73(6), 1307.

Jia X, et al. (2025) *Cdh2*, a downstream target of *Hes7*, regulates somitogenesis by supporting FGF signalling. *Development (Cambridge, England)*, 152(17).

Katuwal N, et al. (2025) Leveraging illumina iSeq100 for whole genome sequencing of *Salmonella Typhi* for a resource-limited setting. *Scientific reports*, 15(1), 33034.

van Gestel J, et al. (2025) *Bacillus subtilis* in defense mode: Switch-like adaptations to protistan predation. *Proceedings of the National Academy of Sciences of the United States of America*, 122(39), e2518989122.

Arifah AQ, et al. (2025) Cas9-independent tracrRNA cytotoxicity in *Lacticaseibacillus paracasei*. *microLife*, 6, uqaf013.

Pulver C, et al. (2025) Evolutionarily recent transcription factors partake in human cell cycle regulation. *Cell genomics*, 5(8), 100923.

Pan Y, et al. (2025) Myeloid EGFR deficiency accelerates recovery from AKI via macrophage efferocytosis and neutrophil apoptosis. *Nature communications*, 16(1), 4563.

Tchio C, et al. (2025) An integrative approach prioritizes the orphan GPR61 genomic region in tissue-specific regulation of chronotype. *Sleep advances : a journal of the Sleep Research Society*, 6(2), zpaf030.

Wang LT, et al. (2025) Spike protein-induced VSIR-ISX signaling disrupts metabolic homeostasis and promotes COVID-19-related immune dysfunction. *Cell biology and toxicology*, 42(1), 2.

Cruz-Saavedra L, et al. (2025) Variation in surface protein expression leads to heterogeneous *Trypanosoma cruzi* populations during host cell infection. *Nature communications*, 16(1), 9949.

Kosovsky GY, et al. (2025) *Bos taurus* and *Bison bison* conservative retrotransposon recombination products. *Frontiers in veterinary science*, 12, 1516731.

Petrucci-Nelson T, et al. (2025) Complex Genetics and Regulatory Drivers of Hypermobility Ehlers-Danlos Syndrome: Insights from Genome-Wide Association Study Meta-analysis. *medRxiv : the preprint server for health sciences*.

Alawathugoda TT, et al. (2025) Maternal obesity alters histone modifications mediated by the interaction between EZH2 and AMPK, impairing neural differentiation in the developing embryonic brain cortex. *The Journal of biological chemistry*, 301(2), 108173.

Yu R, et al. (2025) Whole-Genome Methylation Sequencing Analysis and Functional Verification of LIM-Homeobox Family Genes in Cervical Cancer. *International journal of general medicine*, 18, 87.

King EM, et al. (2025) YTHDF1 and YTHDC1 m6A reader proteins regulate HTLV-1 tax and hbx activity. *Journal of virology*, 99(3), e0206324.