

Resource Summary Report

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CLC Genomics Workbench

RRID:SCR_011853

Type: Tool

Proper Citation

CLC Genomics Workbench (RRID:SCR_011853)

Resource Information

URL: <http://www.clcbio.com/products/clc-genomics-workbench/>

Proper Citation: CLC Genomics Workbench (RRID:SCR_011853)

Description: Commercially available software for visualization and analysis of next generation sequencing data. Used for viewing, exploring, and sharing of NGS analysis results. Complete toolkit for genomics, transcriptomics, epigenomics, and metagenomics in one program.

Resource Type: software application, data processing software, data analysis software, software resource, data visualization software

Keywords: ngs, next, generation, sequencing, gene, rna, visualisation, analysis

Availability: Restricted

Resource Name: CLC Genomics Workbench

Resource ID: SCR_011853

Alternate IDs: SCR_016245, OMICS_01124

License: Commercial license

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260804T043500+0000

Ratings and Alerts

No rating or validation information has been found for CLC Genomics Workbench.

No alerts have been found for CLC Genomics Workbench.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 181 mentions in open access literature.

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

Casey-Moore MC, et al. (2025) Genomic Analysis of Rotavirus G8P[8] Strains Detected in the United States Through Active Surveillance, 2016-2017. *Viruses*, 17(9).

Mehta I, et al. (2025) Control of pili synthesis and putrescine homeostasis in *Escherichia coli*. *eLife*, 13.

Franck L, et al. (2025) Elevated hexosylceramides in Parkinson's disease cause gene upregulations in neurons mimicking responses to pathogens. *NPJ Parkinson's disease*, 11(1), 268.

Diolintzi A, et al. (2025) Novel Hyperplastic Expansion of White Adipose Tissue Underlies the Metabolically Healthy Obese Phenotype of Male LFABP Null Mice. *Cells*, 14(11).

Schmidt KG, et al. (2025) Coronavirus replicase epitopes induce cross-reactive CD8 T cell responses in SARS-CoV-2-naive people with HIV-1. *iScience*, 28(3), 111949.

Turner LA, et al. (2025) Differences in gene expression between high and low tolerance rainbow trout (*Oncorhynchus mykiss*) to acute thermal stress. *PloS one*, 20(1), e0312694.

Wang Y, et al. (2024) The Mohawk homeobox gene represents a marker and osteo-inhibitory factor in calvarial suture osteoprogenitor cells. *Cell death & disease*, 15(6), 420.

Cheng J, et al. (2024) Myeloid cells coordinately induce glioma cell-intrinsic and cell-extrinsic pathways for chemoresistance via GP130 signaling. *Cell reports. Medicine*, 5(8), 101658.

Itoh M, et al. (2024) Molecular alterations associated with pathophysiology in liver-specific ZO-1 and ZO-2 knockout mice. *Cell structure and function*, 49(2), 83.

Reeves KD, et al. (2024) Mapping the geographical distribution of the mucosa-associated gut microbiome in GI-symptomatic children with autism spectrum disorder. *American journal of physiology. Gastrointestinal and liver physiology*, 327(2), G217.

Sprenger M, et al. (2024) Small RNAs direct attack and defense mechanisms in a quorum sensing phage and its host. *Cell host & microbe*, 32(5), 727.

Kim SY, et al. (2024) Antibacterial action, proteolytic immunity, and in vivo activity of a *Vibrio cholerae* microcin. *Cell host & microbe*, 32(11), 1959.

Onuma K, et al. (2024) Bardoxolone methyl prevents metabolic dysfunction-associated steatohepatitis by inhibiting macrophage infiltration. *British journal of pharmacology*,

181(15), 2545.

Kitt EM, et al. (2023) Genotypic investigation of a rotavirus cluster at a quaternary-care pediatric hospital. *Infection control and hospital epidemiology*, 44(10), 1680.

Chapagain P, et al. (2023) Dual RNA-Seq of *Flavobacterium psychrophilum* and Its Outer Membrane Vesicles Distinguishes Genes Associated with Susceptibility to Bacterial Cold-Water Disease in Rainbow Trout (*Oncorhynchus mykiss*). *Pathogens* (Basel, Switzerland), 12(3).

Qin Q, et al. (2023) CNTNAP4 signaling regulates osteosarcoma disease progression. *NPJ precision oncology*, 7(1), 2.

Noer NK, et al. (2023) Temporal regulation of temperature tolerances and gene expression in an arctic insect. *The Journal of experimental biology*, 226(11).

Wilkening RV, et al. (2023) Identifying genetic determinants of *Streptococcus pyogenes*-host interactions in a murine intact skin infection model. *Cell reports*, 42(11), 113332.

Sadaki S, et al. (2023) Large Maf transcription factor family is a major regulator of fast type IIb myofiber determination. *Cell reports*, 42(4), 112289.

Ong ALC, et al. (2023) Acquisition of neural fate by combination of BMP blockade and chromatin modification. *iScience*, 26(10), 107887.