

Resource Summary Report

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CLC Main Workbench

RRID:SCR_000354

Type: Tool

Proper Citation

CLC Main Workbench (RRID:SCR_000354)

Resource Information

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

Proper Citation: CLC Main Workbench (RRID:SCR_000354)

Description: A suite of software for DNA, RNA and protein sequence data analysis. The software allows for the analysis and visualization of Sanger sequencing data as well as gene expression analysis, molecular cloning, primer design, phylogenetic analyses, and sequence data management.

Abbreviations: CLC Main Workbench

Resource Type: software resource, software toolkit

Keywords: sequencing, analysis, cloning, data, management, molecular, gene, genome, dna, rna

Availability: Restricted

Resource Name: CLC Main Workbench

Resource ID: SCR_000354

Alternate IDs: OMICS_01813

License: Commercial license

Record Creation Time: 20220129T080201+0000

Record Last Update: 20260801T191030+0000

Ratings and Alerts

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

No alerts have been found for CLC Main Workbench.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 31 mentions in open access literature.

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

Sánchez de Medina Hernández V, et al. (2025) Cross-species interactome analysis uncovers a conserved selective autophagy mechanism for protein quality control in plants. *Developmental cell*.

Höfler M, et al. (2024) Mechanical forces instruct division plane orientation of cambium stem cells during radial growth in *Arabidopsis thaliana*. *Current biology : CB*, 34(23), 5518.

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.

Knickmann J, et al. (2024) A simple method for rapid cloning of complete herpesvirus genomes. *Cell reports methods*, 4(2), 100696.

Akinyi MY, et al. (2022) A cross-sectional analysis identifies a low prevalence of *Plasmodium ovale* species infections in symptomatic and asymptomatic individuals in Kilifi county, Kenya. *Wellcome open research*, 7, 207.

Tong Y, et al. (2020) CRISPR-Cas9, CRISPRi and CRISPR-BEST-mediated genetic manipulation in streptomycetes. *Nature protocols*, 15(8), 2470.

Hansen BK, et al. (2020) Structure and Function of the Bacterial Protein Toxin Phenomycin. *Structure (London, England : 1993)*, 28(5), 528.

Döring CC, et al. (2020) The visual pigment xenopsin is widespread in protostome eyes and impacts the view on eye evolution. *eLife*, 9.

Lo LH, et al. (2020) The Protein Arginine Methyltransferase PRMT8 and Substrate G3BP1 Control Rac1-PAK1 Signaling and Actin Cytoskeleton for Dendritic Spine Maturation. *Cell reports*, 31(10), 107744.

Welgemoed T, et al. (2020) De novo Assembly of Transcriptomes From a B73 Maize Line Introgressed With a QTL for Resistance to Gray Leaf Spot Disease Reveals a Candidate Allele of a Lectin Receptor-Like Kinase. *Frontiers in plant science*, 11, 191.

Zhao J, et al. (2020) Specific depletion of the motor protein KIF5B leads to deficits in dendritic transport, synaptic plasticity and memory. *eLife*, 9.

Bongers M, et al. (2020) Adaptation of hydroxymethylbutenyl diphosphate reductase enables volatile isoprenoid production. *eLife*, 9.

Peeters S, et al. (2020) DNA Methylation Profiling and Genomic Analysis in 20 Children with Short Stature Who Were Born Small for Gestational Age. *The Journal of clinical endocrinology and metabolism*, 105(12).

Qiu H, et al. (2018) Unexpected conservation of the RNA splicing apparatus in the highly streamlined genome of *Galdieria sulphuraria*. *BMC evolutionary biology*, 18(1), 41.

Gul IS, et al. (2018) GC Content of Early Metazoan Genes and Its Impact on Gene Expression Levels in Mammalian Cell Lines. *Genome biology and evolution*, 10(3), 909.

Viana MVC, et al. (2017) Comparative genomic analysis between *Corynebacterium pseudotuberculosis* strains isolated from buffalo. *PloS one*, 12(4), e0176347.

Bakshi M, et al. (2017) *Piriformospora indica* Reprograms Gene Expression in Arabidopsis Phosphate Metabolism Mutants But Does Not Compensate for Phosphate Limitation. *Frontiers in microbiology*, 8, 1262.

Vöcking O, et al. (2017) Co-expression of xenopsin and rhabdomeric opsin in photoreceptors bearing microvilli and cilia. *eLife*, 6.

Orczyk JJ, et al. (2017) Female rat transcriptome response to infraorbital nerve transection differs from that of males: RNA-seq. *The Journal of comparative neurology*, 525(1), 140.

Ei PW, et al. (2016) Molecular Strain Typing of *Mycobacterium tuberculosis*: a Review of Frequently Used Methods. *Journal of Korean medical science*, 31(11), 1673.