

Resource Summary Report

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CLC Genomics Server

RRID:SCR_017396

Type: Tool

Proper Citation

CLC Genomics Server (RRID:SCR_017396)

Resource Information

URL: <https://www.qiagenbioinformatics.com/products/clc-genomics-server/>

Proper Citation: CLC Genomics Server (RRID:SCR_017396)

Description: Commercially available software tool for high throughput sequencing analysis, designed for use on central compute cluster or server. Can handle data volumes beyond capacity of desktop systems and manages submission of many jobs via its own queuing system or through submission of jobs to third party grid scheduler.

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

Keywords: high, throughput, sequencing, analysis, data

Availability: Restricted

Resource Name: CLC Genomics Server

Resource ID: SCR_017396

Record Creation Time: 20220129T080335+0000

Record Last Update: 20260803T040749+0000

Ratings and Alerts

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

No alerts have been found for CLC Genomics Server.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Azhar G, et al. (2025) Differential microRNA profiling of the Marshallese population in Arkansas reveals a higher association with chronic diseases. *PloS one*, 20(8), e0329321.

Serrano-Gonzalo I, et al. (2025) Expression Profiles of Exosomal miRNAs in Gaucher Patients and Their Association With Severity of Bone Involvement. *Journal of inherited metabolic disease*, 48(4), e70061.

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.

Damiecki M, et al. (2024) Mitochondrial apolipoprotein MIC26 is a metabolic rheostat regulating central cellular fuel pathways. *Life science alliance*, 7(12).

Brochu HN, et al. (2024) A program for real-time surveillance of SARS-CoV-2 genetics. *Scientific reports*, 14(1), 20249.

Hall ET, et al. (2024) Cytoneme signaling provides essential contributions to mammalian tissue patterning. *Cell*, 187(2), 276.

N??hr-Meldgaard K, et al. (2023) Antimicrobial susceptibility testing and tentative epidemiological cut-off values for Lactobacillaceae family species intended for ingestion. *Frontiers in antibiotics*, 2, 1162636.

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

Hurtado-Navarro L, et al. (2023) NLRP3 inflammasome activation and symptom burden in KRAS-mutated CMML patients is reverted by IL-1 blocking therapy. *Cell reports. Medicine*, 4(12), 101329.

Spelat R, et al. (2022) Metabolic reprogramming and membrane glycan remodeling as potential drivers of zebrafish heart regeneration. *Communications biology*, 5(1), 1365.

Flegel J, et al. (2022) The Highly Potent AhR Agonist Picoberin Modulates Hh-Dependent Osteoblast Differentiation. *Journal of medicinal chemistry*, 65(24), 16268.

Qin Q, et al. (2022) NELL1 Regulates the Matrisome to Promote Osteosarcoma Progression. *Cancer research*, 82(15), 2734.

Wang Y, et al. (2021) The role of strigolactones in P deficiency induced transcriptional changes in tomato roots. *BMC plant biology*, 21(1), 349.

Schroeder K, et al. (2021) The Chaperonin GroESL Facilitates *Caulobacter crescentus* Cell Division by Supporting the Functions of the Z-Ring Regulators FtsA and FzIA. *mBio*, 12(3).

Negri S, et al. (2020) Human perivascular stem cells prevent bone graft resorption in osteoporotic contexts by inhibiting osteoclast formation. *Stem cells translational medicine*, 9(12), 1617.

Bowman CE, et al. (2019) Maternal Lipid Metabolism Directs Fetal Liver Programming following Nutrient Stress. *Cell reports*, 29(5), 1299.

Xu J, et al. (2019) Human perivascular stem cell-derived extracellular vesicles mediate bone repair. *eLife*, 8.

Adeyemo AA, et al. (2019) ZRANB3 is an African-specific type 2 diabetes locus associated with beta-cell mass and insulin response. *Nature communications*, 10(1), 3195.