Resource Summary Report

Generated by NIF on Apr 22, 2025

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

Keywords: high, throughput, sequencing, analysis, data

Funding:

Availability: Restricted

Resource Name: CLC Genomics Server

Resource ID: SCR_017396

Record Creation Time: 20220129T080335+0000

Record Last Update: 20250422T060020+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 16 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

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.

Nøhr-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.

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

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

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 FzlA. 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.

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

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

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.