Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 27, 2025

ChromasPro

RRID:SCR_000229
Type: Tool

Proper Citation

ChromasPro (RRID:SCR_000229)

Resource Information

URL: http://technelysium.com.au/?page_id=27

Proper Citation: ChromasPro (RRID:SCR_000229)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on August 31,2023. Software which is able to assemble data from 454 and Illumina next-generation sequencers, with up to 100,000 sequences if 2 Gb RAM is available.

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

Keywords: genome, sequence, dna, assemble, data, illumina, next gen sequence, next generation

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: ChromasPro

Resource ID: SCR_000229

Alternate IDs: OMICS_01808

License: Licenses for purchase. Options for packages of licenses or single-user installations. Acceptance of license terms allows for use of software for up to 30 days, after which payment must be made to the vendor.

Record Creation Time: 20220129T080200+0000

Record Last Update: 20250426T055408+0000

Ratings and Alerts

No rating or validation information has been found for ChromasPro.

No alerts have been found for ChromasPro.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Salehipour P, et al. (2023) CRISPR-Based Fluorescent Reporter (CBFR) Assay for Sensitive, Specific, Inexpensive, and Visual Detection of a Specific EGFR Exon 19 Deletion in NSCLC. Molecular biotechnology, 65(5), 807.

Gattoni G, et al. (2022) Genomic study and lipidomic bioassay of Leeuwenhoekiella parthenopeia: A novel rare biosphere marine bacterium that inhibits tumor cell viability. Frontiers in microbiology, 13, 1090197.

Testini C, et al. (2019) Myc-dependent endothelial proliferation is controlled by phosphotyrosine 1212 in VEGF receptor-2. EMBO reports, 20(11), e47845.

Diawara I, et al. (2018) Analysis of amino acid motif of penicillin-binding proteins 1a, 2b, and 2x in invasive Streptococcus pneumoniae nonsusceptible to penicillin isolated from pediatric patients in Casablanca, Morocco. BMC research notes, 11(1), 632.

Alari V, et al. (2018) Generation of the Rubinstein-Taybi syndrome type 2 patient-derived induced pluripotent stem cell line (IAIi001-A) carrying the EP300 exon 23 stop mutation c.3829A?>?T, p.(Lys1277*). Stem cell research, 30, 175.

Pawlik A, et al. (2016) Purification and characterization of laccase from Sinorhizobium meliloti and analysis of the lacc gene. International journal of biological macromolecules, 92, 138.

Clemente A, et al. (2015) Increased STAT3 phosphorylation on CD27(+) B-cells from common variable immunodeficiency disease patients. Clinical immunology (Orlando, Fla.), 161(2), 77.

Amer S, et al. (2015) Molecular characterization of Echinococcus granulosus sensu lato from farm animals in Egypt. PloS one, 10(3), e0118509.

Tongo M, et al. (2015) Near full-length HIV type 1M genomic sequences from Cameroon : Evidence of early diverging under-sampled lineages in the country. Evolution, medicine, and public health, 2015(1), 254.

Okeke MI, et al. (2014) Molecular characterization and phylogenetics of Fennoscandian cowpox virus isolates based on the p4c and atip genes. Virology journal, 11, 119.

Tajer Mohammad Ghazvini P, et al. (2014) Isolation and Characterization of a Novel Magnetotactic Bacterium From Iran: Iron Uptake and Producing Magnetic Nanoparticles in Alphaproteobacterium MTB-KTN90. Jundishapur journal of microbiology, 7(9), e19343.

Cardoso L, et al. (2014) Molecular and histopathological detection of Hepatozoon canis in red foxes (Vulpes vulpes) from Portugal. Parasites & vectors, 7, 113.

Wang L, et al. (2013) Concurrent infections of Giardia duodenalis, Enterocytozoon bieneusi, and Clostridium difficile in children during a cryptosporidiosis outbreak in a pediatric hospital in China. PLoS neglected tropical diseases, 7(9), e2437.

Scott AP, et al. (2011) Recombination mapping of the susceptibility region for sporadic inclusion body myositis within the major histocompatibility complex. Journal of neuroimmunology, 235(1-2), 77.