Resource Summary Report

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GenPipes

RRID:SCR_016376
Type: Tool

Proper Citation

GenPipes (RRID:SCR_016376)

Resource Information

URL: https://bitbucket.org/mugqic/genpipes/src/master/

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Description: Software for genomics and bioinformatics analysis. GenPipes includes several python pipelines that cover many genomics applications, such as RNASeq, ChIPSeq, DNASeq, WGBS, HiC, Metagenomics, PacBio assembly, etc.

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

Keywords: workflow, management, system, genomics, bioinformatics, rnaseq, chipseq, dnaseq, hic, metagenomics, WGBS, PacBio, Assembly, C3G

Funding:

Availability: Free, Available for download, Tutorial available

Resource Name: GenPipes

Resource ID: SCR_016376

Alternate URLs: http://www.computationalgenomics.ca/tutorials/

License: GNU GPLv3

Record Creation Time: 20220129T080330+0000

Record Last Update: 20250422T055929+0000

Ratings and Alerts

No rating or validation information has been found for GenPipes.

No alerts have been found for GenPipes.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 13 mentions in open access literature.

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

Naderi S, et al. (2025) Within-host genetic diversity of SARS-CoV-2 across animal species. Virus evolution, 11(1), veae117.

Jessa S, et al. (2024) FOXR2 targets LHX6+/DLX+ neural lineages to drive CNS neuroblastoma. Cancer research.

Hughes CHK, et al. (2023) Steroidogenic factor 1 (SF-1; Nr5a1) regulates the formation of the ovarian reserve. Proceedings of the National Academy of Sciences of the United States of America, 120(32), e2220849120.

Rahimi S, et al. (2023) Capturing sex-specific and hypofertility-linked effects of assisted reproductive technologies on the cord blood DNA methylome. Clinical epigenetics, 15(1), 82.

Ragamin A, et al. (2022) De novo TRPV4 Leu619Pro variant causes a new channelopathy characterised by giant cell lesions of the jaws and skull, skeletal abnormalities and polyneuropathy. Journal of medical genetics, 59(3), 305.

Sahinyan K, et al. (2022) Application of ATAC-Seq for genome-wide analysis of the chromatin state at single myofiber resolution. eLife, 11.

Lambrot R, et al. (2021) Whole-genome sequencing of H3K4me3 and DNA methylation in human sperm reveals regions of overlap linked to fertility and development. Cell reports, 36(3), 109418.

Chaouch A, et al. (2021) Histone H3.3 K27M and K36M mutations de-repress transposable elements through perturbation of antagonistic chromatin marks. Molecular cell, 81(23), 4876.

Costa MO, et al. (2020) Putting the microbiota to work: Epigenetic effects of early life antibiotic treatment are associated with immune-related pathways and reduced epithelial necrosis following Salmonella Typhimurium challenge in vitro. PloS one, 15(4), e0231942.

Chen CCL, et al. (2020) Histone H3.3G34-Mutant Interneuron Progenitors Co-opt PDGFRA for Gliomagenesis. Cell, 183(6), 1617.

Costa MO, et al. (2020) Swine dysentery disease mechanism: Brachyspira hampsonii impairs the colonic immune and epithelial repair responses to induce lesions. Microbial pathogenesis, 148, 104470.

Khazaei S, et al. (2020) H3.3 G34W Promotes Growth and Impedes Differentiation of Osteoblast-Like Mesenchymal Progenitors in Giant Cell Tumor of Bone. Cancer discovery, 10(12), 1968.

Bourgey M, et al. (2019) GenPipes: an open-source framework for distributed and scalable genomic analyses. GigaScience, 8(6).