

Resource Summary Report

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CES Genome Quebec Core Facility

RRID:SCR_017703

Type: Tool

Proper Citation

CES Genome Quebec Core Facility (RRID:SCR_017703)

Resource Information

URL: <https://cesgq.com/>

Proper Citation: CES Genome Quebec Core Facility (RRID:SCR_017703)

Description: Core for full DNA and RNA analysis services. Canada's largest integrated provider of sequencing, genotyping and biochips services. Offers scientific community around the world genomic services in support of research in human health, agrifood, forestry and sustainable development.

Synonyms: Genome Quebec Center of Expertise and Services

Resource Type: access service resource, core facility, service resource

Keywords: DNA, RNA, analysis, service, core, Canada, sequencing, genotyping, biochip

Availability: Open

Resource Name: CES Genome Quebec Core Facility

Resource ID: SCR_017703

Alternate IDs: ABRF_115, SCR_017718

Record Creation Time: 20220129T080336+0000

Record Last Update: 20260912T200400+0000

Ratings and Alerts

No rating or validation information has been found for CES Genome Quebec Core Facility.

No alerts have been found for CES Genome Quebec Core Facility.

Data and Source Information

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Clerissi C, et al. (2023) A core of functional complementary bacteria infects oysters in Pacific Oyster Mortality Syndrome. *Animal microbiome*, 5(1), 26.

Wang M, et al. (2023) Genome-Wide DNA Methylation and Transcriptome Integration Associates DNA Methylation Changes with Bovine Subclinical Mastitis Caused by *Staphylococcus chromogenes*. *International journal of molecular sciences*, 24(12).

Iqbal I, et al. (2023) Interaction and association analysis of malting related traits in barley. *PloS one*, 18(4), e0283763.

Smith SR, et al. (2022) A chromosome-anchored genome assembly for Lake Trout (*Salvelinus namaycush*). *Molecular ecology resources*, 22(2), 679.

Carrier A, et al. (2022) Design and validation of a 63K genome-wide SNP-genotyping platform for caribou/reindeer (*Rangifer tarandus*). *BMC genomics*, 23(1), 687.

Ibeagha-Awemu EM, et al. (2021) Whole Genome Methylation Analysis Reveals Role of DNA Methylation in Cow's Ileal and Ileal Lymph Node Responses to *Mycobacterium avium* subsp. *paratuberculosis* Infection. *Frontiers in genetics*, 12, 797490.

Sauriol A, et al. (2020) Modeling the Diversity of Epithelial Ovarian Cancer through Ten Novel Well Characterized Cell Lines Covering Multiple Subtypes of the Disease. *Cancers*, 12(8).