

Resource Summary Report

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Oregon State University Center for Quantitative Life Sciences Core Facility

RRID:SCR_018373

Type: Tool

Proper Citation

Oregon State University Center for Quantitative Life Sciences Core Facility
(RRID:SCR_018373)

Resource Information

URL: <http://cqls.oregonstate.edu/>

Proper Citation: Oregon State University Center for Quantitative Life Sciences Core Facility (RRID:SCR_018373)

Description: Formerly Center for Genome Research and Biocomputing Core Facility. Functions and facilities include services in genomics, functional genomics, genotyping and imaging. Biocomputing facilities with computing infrastructure, which includes managed cloud and shared resources, data analyses and training are customized to individual needs, including genome assembly and annotation, analysis of RNAseq, GBS, and metagenomics data, and GPU-enabled deep learning analyses.

Abbreviations: CQLS

Synonyms: CGRB, Center for Genome Research and Biocomputing

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

Keywords: Genome, genomic, functional genomic, genotyping, imaging, biocomputing, data analysis, training, core facility, ABRF, ABRF

Availability: Open

Resource Name: Oregon State University Center for Quantitative Life Sciences Core Facility

Resource ID: SCR_018373

Alternate IDs: ABRF_856

Alternate URLs: <https://coremarketplace.org/?FacilityID=856>

Record Creation Time: 20220129T080340+0000

Record Last Update: 20260801T042815+0000

Ratings and Alerts

No rating or validation information has been found for Oregon State University Center for Quantitative Life Sciences Core Facility.

No alerts have been found for Oregon State University Center for Quantitative Life Sciences Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Padgitt-Cobb LK, et al. (2023) An improved assembly of the "Cascade" hop (*Humulus lupulus*) genome uncovers signatures of molecular evolution and refines time of divergence estimates for the Cannabaceae family. *Horticulture research*, 10(2), uhac281.

Kirchoff NS, et al. (2022) Gut Microbial Composition of Pacific Salmonids Differs across Oregon River Basins and Hatchery Ancestry. *Microorganisms*, 10(5).