

Resource Summary Report

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University of Luxembourg LCSB Genomics Platform Core Facility

RRID:SCR_021931

Type: Tool

Proper Citation

University of Luxembourg LCSB Genomics Platform Core Facility (RRID:SCR_021931)

Resource Information

URL: <https://www.uni.lu/lcsb-en/facilities/genomics-platform/>

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Description: Core offers next generation sequencing services. Provided sequencers include NextSeq2000 and MiSeq from Illumina, and MinION nanopore sequencer from Oxford Nanopore Technologies. Illumina sequencers allow sequencing tunable read lengths up to 300 bases of single as well as paired end runs while MinION sequencer complements by ultra long read lengths up to several hundreds of kilobases. Together this offers high flexibility for the different sequencing needs. Platform offers full service, starting with advice in experimental design up to sequencing data generation. Receiving RNA or DNA samples, sample quality check, sample shearing, library preparation, sequencing run, raw data generation and preliminary data quality control report is performed. General applications include RNA sequencing, metagenomics, small genome sequencing, targeted gene sequencing, amplicon sequencing, and HLA typing. Upon user request, sequencing platform works closely with bioinformatics platform to offer downstream data analysis. Besides wide range of standard services, platform also offers new method development.

Synonyms: , LCSB Sequencing Platform Core Facility, University of Luxembourg LCSB Sequencing Platform Core Facility, LCSB Sequencing Platform

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

Keywords: USEDit, ABRF, next generation sequencing services, NextSeq2000, MiSeq, Illumina, MinION nanopore sequencer, Oxford Nanopore Technologies

Availability: Open

Resource Name: University of Luxembourg LCSB Genomics Platform Core Facility

Resource ID: SCR_021931

Alternate IDs: ABRF_813

Alternate URLs: <https://coremarketplace.org/?FacilityID=813>

Old URLs: <http://sequencing.uni.lu>,
https://www.en.uni.lu/lcsb/services/platforms/sequencing_platform

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Record Last Update: 20260905T133423+0000

Ratings and Alerts

No rating or validation information has been found for University of Luxembourg LCSB Genomics Platform Core Facility.

No alerts have been found for University of Luxembourg LCSB Genomics Platform Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

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

Zhou Z, et al. (2026) Integrative analysis of the mouse cecal microbiome across diet, age, and weight in the diverse BXD population. *Microbiome*, 14(1).

Ding L, et al. (2026) Cell-specific transcriptomics and knockout reveal aquaporin function in grass stomatal movements. *The New phytologist*, 250(3), 1569.

Cochereau B, et al. (2026) Microbial valorisation of PET-derived terephthalic acid by *Rhizopus arrhizus*: towards plastic waste biotransformation. *Bioresource technology*, 442, 133681.

Petrov VA, et al. (2026) Resistant starch improves Parkinson's disease symptoms through restructuring of the gut microbiome and modulating inflammation. *Brain, behavior, and immunity*, 132, 106217.

Jarazo J, et al. (2026) SARS-CoV-2 Infection Induces Dopaminergic Neuronal Loss in Midbrain Organoids. *Journal of neurochemistry*, 170(5), e70486.

Tsenkova M, et al. (2025) Ketogenic diet suppresses colorectal cancer through the gut microbiome long chain fatty acid stearate. *Nature communications*, 16(1), 1792.

Chemla A, et al. (2025) Parkinson's disease mutant Miro1 causes mitochondrial dysfunction and dopaminergic neuron loss. *Brain : a journal of neurology*.

Ali M, et al. (2025) Temporal transcriptomic changes in the THY-Tau22 mouse model of tauopathy display cell type- and sex-specific differences. *Acta neuropathologica communications*, 13(1), 93.

Esser SP, et al. (2025) Differential Expression of Core Metabolic Functions in Candidatus Altiarchaeum Inhabiting Distinct Subsurface Ecosystems. *Environmental microbiology reports*, 17(3), e70096.

Delogu F, et al. (2024) Forecasting the dynamics of a complex microbial community using integrated meta-omics. *Nature ecology & evolution*, 8(1), 32.

Scicchitano D, et al. (2024) A 15-day pilot biodiversity intervention with horses in a farm system leads to gut microbiome rewilding in 10 urban Italian children. *One health* (Amsterdam, Netherlands), 19, 100902.

Talavera And??jar B, et al. (2024) Exploring environmental modifiers of LRRK2-associated Parkinson's disease penetrance: An exposomics and metagenomics pilot study on household dust. *Environment international*, 194, 109151.

Xu X, et al. (2023) Characterization of MdMYB68, a suberin master regulator in russeted apples. *Frontiers in plant science*, 14, 1143961.

de Nies L, et al. (2023) Altered infective competence of the human gut microbiome in COVID-19. *Microbiome*, 11(1), 46.

Soriano-Baguet L, et al. (2023) Pyruvate dehydrogenase fuels a critical citrate pool that is essential for Th17 cell effector functions. *Cell reports*, 42(3), 112153.

Delbrouck C, et al. (2023) Formate promotes invasion and metastasis in reliance on lipid metabolism. *Cell reports*, 42(9), 113034.

de Nies L, et al. (2022) Evolution of the murine gut resistome following broad-spectrum antibiotic treatment. *Nature communications*, 13(1), 2296.