Resource Summary Report

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University of Warsaw Center of New Technologies Genomics Core Facility

RRID:SCR_022718
Type: Tool

Proper Citation

University of Warsaw Center of New Technologies Genomics Core Facility (RRID:SCR_022718)

Resource Information

URL: https://cent.uw.edu.pl/en/core-facilities/genomics-core-facility/

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Description: Core is dedicated to analysis of RNA and DNA sequence, structure and interactions in biological and biochemical processes.Specializes in Genomics, Metagenomics, Transcriptomics, Epigenomics, Interactomics, Oncogenomics, Structural Genomics and other fields. Equippment includes NovaSeq 6000, NextSeq 500 and MiSeq next generation sequencing systems and instruments for fractionation, quality and quantity assessment. Services include consultation and assistance, preparation of libraries from DNA (WGS, WES, Amp-seq, ATAC-Seq, ChIP-seq etc.) and RNA (different fractions: mRNA-seq, mRNA-seq, total RNA-seq, miRNA-seq, RIP-seq etc.), sequence custom libraries and conduct bioinformatic analysis.

Synonyms: Genomics Core Facility

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

Keywords: USEDit, ABRF, RNA and DNA sequence, preparation of libraries from DNA and RNA, Genomics, Metagenomics, Transcriptomics, Epigenomics, Interactomics, Oncogenomics, Structural Genomics,

Funding:

Availability: open

Resource Name: University of Warsaw Center of New Technologies Genomics Core Facility

Resource ID: SCR_022718

Alternate IDs: ABRF_1520

Alternate URLs: https://coremarketplace.org/?FacilityID=1520&citation=1

Record Creation Time: 20220901T050155+0000

Record Last Update: 20250517T060515+0000

Ratings and Alerts

No rating or validation information has been found for University of Warsaw Center of New Technologies Genomics Core Facility.

No alerts have been found for University of Warsaw Center of New Technologies Genomics Core Facility.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Czarnocka-Cieciura A, et al. (2025) Comprehensive analysis of poly(A) tails in mouse testes and ovaries using Nanopore Direct RNA Sequencing. Scientific data, 12(1), 43.

Janecki DM, et al. (2024) LINE-1 mRNA 3' end dynamics shape its biology and retrotransposition potential. Nucleic acids research.

Zalewska M, et al. (2024) A newly identified IncY plasmid from multi-drug-resistant Escherichia coli isolated from dairy cattle feces in Poland. Microbiology spectrum, 12(8), e0087724.

Brouze M, et al. (2024) TENT5-mediated polyadenylation of mRNAs encoding secreted proteins is essential for gametogenesis in mice. Nature communications, 15(1), 5331.

Rydzanicz M, et al. (2024) Mutation in the mitochondrial chaperone TRAP1 leads to autism with more severe symptoms in males. EMBO molecular medicine, 16(11), 2976.

Zalewska M, et al. (2024) The IncC and IncX1 resistance plasmids present in multi-drug resistant Escherichia coli strains isolated from poultry manure in Poland. Environmental science and pollution research international, 31(35), 47727.

Hollender M, et al. (2024) Single-cell genomics revealed Candidatus Grellia alia sp. nov. as an endosymbiont of Eutreptiella sp. (Euglenophyceae). Protist, 175(2), 126018.

Nguyen NL, et al. (2024) Taxonomic and abundance biases affect the record of marine eukaryotic plankton communities in sediment DNA archives. Molecular ecology resources, 24(8), e14014.

W??yk M, et al. (2023) Rare A360T Mutation Alters GSK3?(Ser9) Binding in the Cytosolic Loop of Presenilin 1, Influencing ?-Catenin Nuclear Localization and Pro-Death Gene Expression in Alzheimer's Disease Case. International journal of molecular sciences, 24(23).

Mierzejewski B, et al. (2023) Coding and noncoding RNA profile of human heterotopic ossifications - Risk factors and biomarkers. Bone, 176, 116883.