

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. Equipment 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., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16, 2025.

Synonyms: Genomics Core Facility

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

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

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

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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 22 mentions in open access literature.

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

Mazan-Bury A, et al. (2026) MLK4 orchestrates macrophage-induced triple-negative breast cancer invasion and ECM remodeling via enhanced paracrine signaling and NF- κ B-MMP axis activation. *Cell death & disease*, 17(1).

Popek M, et al. (2026) Astrocytic TCF7L2 Impacts Brain Osmoregulation and Restricts Neuronal Excitability. *Glia*, 74(2), e70103.

Mierzejewski B, et al. (2026) CD146 + interstitial cells contribute to the dystrophic skeletal muscle phenotype in vitro. *Scientific reports*, 16(1).

Dawidziak DM, et al. (2026) Human FASTK preferentially binds single-stranded and G-rich RNA. *The FEBS journal*, 293(3), 729.

Korsak S, et al. (2026) RepliSage: a stochastic graph-based framework for 3D chromatin modeling across the cell cycle. *Nucleic acids research*, 54(12).

Crucitti-Thoo RM, et al. (2026) Comparing Aquatic Environmental DNA, Microscopy and Sedimentary DNA to Investigate Cyanobacterial Community Dynamics Across a Trophic Gradient. *Microbial ecology*.

Brouze M, et al. (2025) DIS3L, cytoplasmic exosome catalytic subunit, is essential for development but not cell viability in mice. *RNA (New York, N.Y.)*, 31(5), 646.

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.

Santaeufemia S, et al. (2025) Transcriptomics Reveals an Energy-Saving Metabolic Switch in an Extremophilic Red Microalga *Cyanidioschyzon merolae* Under Nickel Stress. *International journal of molecular sciences*, 26(10).

Wang C, et al. (2025) UBA2A regulates seed dormancy and the stability of chromatin-retained DOG1 messenger RNA. *Journal of integrative plant biology*, 67(12), 3109.

Krawczyk PS, et al. (2025) Re-adenylation by TENT5A enhances efficacy of SARS-CoV-2 mRNA vaccines. *Nature*, 641(8064), 984.

Buka K, et al. (2025) Improved cohesin HiChIP protocol and bioinformatic analysis for robust detection of chromatin loops and stripes. *Communications biology*, 8(1), 437.

Drazkowska K, et al. (2025) Effective recognition of double-stranded RNA does not require activation of cellular inflammation. *Science advances*, 11(15), eads6498.

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.

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.

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

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.

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.

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.