

Resource Summary Report

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OHSU Massively Parallel Sequencing Shared Resource Core Facility

RRID:SCR_009984

Type: Tool

Proper Citation

OHSU Massively Parallel Sequencing Shared Resource Core Facility
(RRID:SCR_009984)

Resource Information

URL: <https://www.ohsu.edu/research-cores/massively-parallel-sequencing-shared-resource-mpssr>

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Description: As of January 1, 2024, the Integrated Genomics Laboratory is one shared resource comprising the former Massively Parallel Sequencing Shared Resource, the Gene Profiling Shared Resource, and the DNA Services Core. Please be aware that the reorganization is an ongoing process, particularly regarding our iLab integration. Provides RNA-sequencing for gene expression analysis, DNA resequencing for single nucleotide polymorphism discovery, DNA resequencing for copy number variation discovery, ChIP-sequencing for promoter analysis, DNA methylation analysis, De novo sequencing for unique genomes, Sequence capture service. Offers sequencing including genome resequencing, transcriptome analysis, miRNA analysis, and promoter analysis via ChIP-seq.

Abbreviations: MPSSR

Synonyms: OHSU Massively Parallel Sequencing Shared Resource

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

Keywords: RNA-sequencing for gene expression analysis, DNA resequencing for single nucleotide polymorphism discovery, DNA resequencing for copy number variation discovery, ChIP-sequencing for promoter analysis, DNA methylation analysis, De novo sequencing for unique genomes, USEDit

Resource Name: OHSU Massively Parallel Sequencing Shared Resource Core Facility

Resource ID: SCR_009984

Alternate IDs: nlx_156453, SCR_018868

Old URLs: <http://ohsu.eagle-i.net/i/0000012b-5a48-0b10-62b8-f47280000000>

Record Creation Time: 20220129T080256+0000

Record Last Update: 20260912T200325+0000

Ratings and Alerts

No rating or validation information has been found for OHSU Massively Parallel Sequencing Shared Resource Core Facility.

No alerts have been found for OHSU Massively Parallel Sequencing Shared Resource Core Facility.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Pandita R, et al. (2026) Azacytidine restores T cell function in AML by modulating DNA methylation. bioRxiv : the preprint server for biology.

English IA, et al. (2025) Myc and Kras cooperate in adult acinar cells to drive phenotypic heterogeneity, metastasis, and therapeutic resistance in a novel pancreatic cancer mouse model. bioRxiv : the preprint server for biology.

Li Z, et al. (2024) HER2 heterogeneity and treatment response-associated profiles in HER2-positive breast cancer in the NCT02326974 clinical trial. The Journal of clinical investigation, 134(7).

Danoff JS, et al. (2024) A Common OXTR Risk Variant Alters Regulation of Gene Expression by DNA Hydroxymethylation in Pregnant Human Myometrium. Reproductive sciences (Thousand Oaks, Calif.), 31(10), 3132.

Shipman A, et al. (2024) Defects in Exosome Biogenesis Are Associated with Sensorimotor Defects in Zebrafish vps4a Mutants. The Journal of neuroscience : the official journal of the Society for Neuroscience, 44(50).

Erickson T, et al. (2023) Regionalized Protein Localization Domains in the Zebrafish Hair Cell Kinocilium. Journal of developmental biology, 11(2).

Shah VM, et al. (2023) Micelle-Formulated Juglone Effectively Targets Pancreatic Cancer and Remodels the Tumor Microenvironment. *Pharmaceutics*, 15(12).

Khan MR, et al. (2023) Genome sequencing of Pakistani families with male infertility identifies deleterious genotypes in SPAG6, CCDC9, TKTL1, TUBA3C, and M1AP. *Andrology*.

Vermehren-Schmaedick A, et al. (2021) Characterization of PARP6 Function in Knockout Mice and Patients with Developmental Delay. *Cells*, 10(6).