

Shared RESOURCES

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NEWSLETTER



A Message from our Director of Genomics Shared Resource

Happy New Year!

I hope 2025 brings health, happiness, and success to you and your loved ones. This year marks another exciting chapter for the field of Genomics, which continues to evolve at an unprecedented pace. At the Genomics Shared Resource (GSR), we are proud to remain at the forefront of this ever-expanding discipline, leveraging cutting-edge technologies and the expertise of our team to support impactful discoveries by Roswell Park researchers. It is with great pride that I share that during the last CCSG renewal, the GSR was once again rated as **"Exceptional"**, a testament to our unwavering commitment to providing exemplary services and our dedication to supporting CCSG programs and advancing cancer research.

As the field has advanced, the GSR has continuously evolved to ensure we remain at the cutting edge of research and innovation. Recent updates include the introduction of advanced technologies such as latest high-throughput sequencing platforms, multiple methods and application of single-cell sequencing, and spatial transcriptomics. Additionally, we closely collaborate with other shared resources, such as the Biostatistics and Bioinformatics Shared Resource and the Biorepository and Laboratory Services Shared Resource, to deliver streamlined, high-throughput sample-to-data pipelines. As we embark on 2025, I am excited to announce several planned advancements to our capabilities including, **Long-Read Sequencing:** Providing enhanced genomic insights, particularly for structural variations and complex regions of the genome, and **High-Throughput Automation Systems:** Improving throughput and reducing turnaround time, ensuring more efficient service for our investigators.

The GSR is committed to supporting your research needs, and we encourage you to explore how these advancements can benefit your projects. Please feel free to reach out to me or the GSR team to discuss your goals and how we can assist you in achieving them.

With best regards



Prashant Singh, PhD
Director, Genomics Shared Resource

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Information presented in
this newsletter was current
in December 2024.

Roswell Park Shared Resources

[Bioanalytics, Metabolomics & Pharmacokinetics Shared Resource \(BMPK\)](#)

[Drug Discovery Core Shared Resource \(DDCSR\)](#)

[Health Communications Shared Resource \(HCR\)](#)

[Bioinformatics Shared Resource \(BIOINF\)](#)

[Experimental Tumor Model Shared Resource \(ETM\)](#)

[Investigational Drug Service Shared Resource \(IDS\)](#)

[Biomedical Research Informatics Shared Resource \(BRISR\)](#)

[Flow & Immune Analysis Shared Resource \(FIASR\)](#)

[Nicotine & Tobacco Product Assessment Shared Resource \(NICOTAR\)](#)

[Biorepository & Lab Services Shared Resource \(BLS\)](#)

[Gene Modulation Services Shared Resource \(GMSR\)](#)

[On-site Research Supply Center Shared Resource \(ORSC\)](#)

[Biostatistics & Statistical Genomics Shared Resource \(BSGSR\)](#)

[Gene Targeting & Transgenic Shared Resource \(GeTT\)](#)

[Scientific Editing & Research Communication Core Resource \(SERCC\)](#)

[Comparative Oncology Shared Resource \(COSR\)](#)

[Genomics Shared Resource \(GSR\)](#)

[GMP Engineering & Cell Manufacturing Facility \(GEM\)](#)

[Translational Imaging Shared Resource \(TISR\)](#)

SHARED RESOURCES HIGHLIGHTS

Bioanalytics, Matabolomics & Pharmacokinetics Shared Resource (BMPK)

The [BMPK](#) is constantly improving our technologies to help support the clinical and basic science needs at the institute. We are excited to announce that we have completed development of an assay to measure short chain fatty acids, expanded the tryptophan metabolism assay, and are working to expand the metabolite coverage in the catecholamine assays. We are also starting to develop stable isotope tracing techniques, to help support institute-wide metabolomics efforts. Further, we would like to begin to support your proteomics needs. To this end, we are in the process of acquiring an [O-Link](#), which will allow for the simultaneous measurement of up to 92 proteins at once, from very little sample. Once this has been acquired, we will hold a seminar to introduce you all to its capabilities.

As always, if you have any metabolomics needs which cannot be met by the assays we currently offer, all of which are currently listed on the [website](#), please reach out so we can work together to find a solution! We look forward to working with you and supporting your research efforts!

Genomics Shared Resource (GSR)

Long-Read Sequencing with the Oxford Nanopore PromethION 2 Solo Anticipated start date April 2025

The [GSR](#) is thrilled to announce the addition of Oxford Nanopore's PromethION 2 Solo (P2 Solo) to our genomics arsenal, enabling cutting-edge long-read sequencing capabilities in our lab. This revolutionary technology allows direct sequencing of native DNA and RNA, achieving unparalleled read lengths of over 4 Mb.

The P2 Solo is a powerful platform for addressing complex genomic questions. Its long-read capabilities make it ideal for detecting structural variants, genomic rearrangements, and phasing, as well as for identifying isoforms with high accuracy. Additionally, the ability to sequence native DNA molecules provides dual-layer insights by delivering both the DNA sequence and epigenetic information, such as DNA methylation, in a single run.



Applications in Cancer Research

The ability to accurately detect structural variants and genomic rearrangements is essential for understanding the genomic instability often associated with cancer. By resolving complex genomic regions, such as those with repetitive sequences or large insertions and deletions, researchers can uncover tumor-specific mutations, gene fusions, and copy number variations that drive cancer progression.

Furthermore, the platform's ability to simultaneously detect epigenetic modifications, such as DNA methylation, allows for deeper insights into gene regulation and tumor microenvironment dynamics. This is particularly critical for identifying biomarkers, understanding treatment resistance, and designing targeted therapies.

Enabling Single-Cell and Isoform-Level Resolution

In single-cell sequencing, the P2 Solo's long-read technology provides unparalleled resolution for capturing the full-length sequences of transcripts, making it possible to identify and characterize isoforms at the single-cell level. This capability is transformative for understanding cell-to-cell heterogeneity in complex tissues, including tumors, and for studying rare cell populations that drive disease progression or therapeutic resistance. By resolving full-length RNA molecules, researchers can accurately profile alternative splicing events and their functional implications, offering a more detailed view of transcriptomic diversity in single cells.

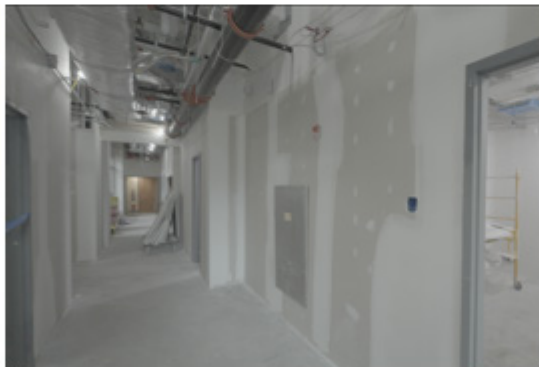
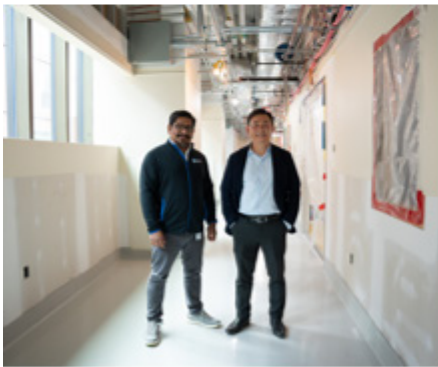
Why Choose the PromethION 2 Solo?

- **Comprehensive Data:** Simultaneous sequencing of native DNA and RNA for sequence and epigenetic insights.
- **Unmatched Read Lengths:** Resolve complex regions with reads over 4 Mb in length.
- **Real-Time Analysis:** Generate data in real-time to accelerate discoveries.
- **Versatility:** Ideal for structural variant detection, isoform characterization, cancer research, and single-cell transcriptomics.

We are excited to offer this transformative technology and look forward to supporting groundbreaking research in genomics, transcriptomics, and epigenetics.

GMP Engineering & Cell Manufacturing Facility (GEM)

The [GMP Engineering and Cell Manufacturing Facility \(GEM\)](#) at Roswell Park has reached an exciting milestone with the completion of construction and a successful grand opening event. As we look ahead, our focus is on taking critical next steps to begin manufacturing. This includes hiring additional skilled staff, strategically moving and installing equipment within the facility, and performing rigorous commissioning and validation processes. Additionally, we are preparing for the tech transfer of clinical programs as we gear up to support groundbreaking therapies advancing into the clinic. These efforts will position the GEM facility as a leader in cell and gene therapy manufacturing.



Scientific Editing & Research Communications Core (SERCC) Resource

SERCC provides professional-level scientific editing services to faculty and postdoctoral fellows with the goal of helping them succeed in their pursuit of funding and publication of high-impact research. Grant proposals and manuscripts are edited over a turn-around time of 7–10 business days, and requests for editing support can be submitted through the form on [SERCC's website](#). Please review the website prior to submission.

The SERCC team is pleased to announce that several of our educational factsheets from 2021–2023 were compiled into an open-access e-book and published by Milne Open Textbooks, State University of New York at Geneseo. The e-book, titled "[Avoiding Common Pitfalls in Medical Writing: An Editor's Advice](#)," can now be downloaded for free. We continue to produce educational factsheets on a quarterly basis, and topic suggestions are always welcome!



Avoiding Common Pitfalls in Medical Writing

An Editor's Advice

Deanna Erin Connors