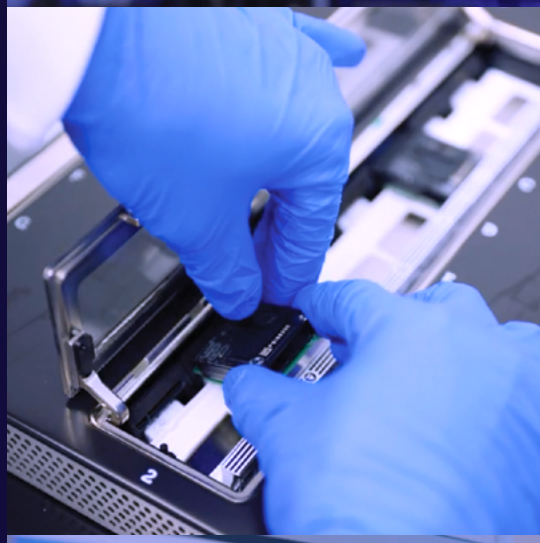
CGEn

Canada's national platform for genome sequencing and analysis

Powering Canada's Genomics Future

DATA FOR DISCOVERY









Annual Report 2025–2026

Land Acknowledgement

CGEn spans the traditional and unceded territories of many nations, including the Musqueam, Squamish, and Tsleil-Waututh Nations, the Wendat Nation and Petun First Nation, the Seneca, and the Mississaugas of the Credit River, and on land which has long served as a site of meeting and exchange amongst Indigenous peoples, including the Haudenosaunee and Anishinabeg nations. These sites are home today to many diverse First Nations, Inuit, and Métis people, and CGEn is grateful to be able to share this land.

It is important for us to take pause, acknowledge and reflect on the impacts of colonialism across Indigenous communities in Canada, particularly in how colonization has influenced and continues to influence genomics and genetic research. We remain eager to hear stories, humble to learn lessons, and ready to continue fostering meaningful and inclusive change.

CEO and Chair's Message

This year, CGEn celebrated a decade of enabling discovery through collaboration, innovation, and excellence in genomic science, releasing our CGEn: 10 Years of Impact report. As Canada's national platform for genome sequencing and analysis, CGEn continues to unite world-class expertise and infrastructure across our nodes in Vancouver, Toronto, and Montréal to deliver high-quality genomic data that powers Canadian research in health, biodiversity, agriculture, and beyond.

In 2025–2026, CGEn served more than 1,000 user laboratories and generated 4.7 petabases of genomic data (a 60% increase from 2024–2025)—driven largely by our support of transformative national genomics initiatives including Genome Canada's Canadian Precision Health Initiative, the Terry Fox Marathon of Hope Cancer Centres Network, and the Canadian BioGenome Project. These programs are building secure, diverse, and accessible genomic resources that will improve health outcomes, strengthen environmental stewardship, and drive economic prosperity for Canadians. CGEn also continued to enable access to the HostSeq databank, and use this dataset as a pilot for large-scale, broadly consented human genomic data in Canada, working with the Pan-Canadian Genome Library to establish HostSeq as its inaugural cohort.

CGEn's support of genomic science is dependent on cutting-edge technologies and continual optimization. This year, we brought additional high-capacity sequencers into production to support Canada's growing demand for genomic data and advanced new sequencing and analysis methods across long-read sequencing, single-cell genomics, spatial transcriptomics and sequence-based proteomics. These activities are critical to ensuring that Canadian researchers have access to efficient and cost-effective services that produce the highest-quality data possible.

By sharing knowledge, harmonizing best practices, and investing in people and infrastructure, CGEn's truly connected network drives discovery and beneficial outcomes for Canada while enabling collaboration with international programs. The dedication of our staff, Board of Directors, Scientific Advisory Board, collaborators, and funders has made this progress possible, and we extend our sincere gratitude for their continued partnership.

As we look ahead, CGEn's Strategic Vision 2030 continues to guide our path forward. We remain committed to acting as a foundation for Canadian research, generating high-quality data at scale, fostering innovation, technology development and talent, and strengthening Canada's genomics ecosystem. With our vision of every biological study powered by genomic data, we are confident that the future will bring even greater opportunities to advance science and create a healthier, more sustainable future for all Canadians.



Gordon C McCauley
Chair, CGEn Board of Directors
Vice-Chair, adMare BioInnovations



Meredith McLaren
CEO, CGEn

Table of Contents



CEO and Chair Message	03
Who We Are	05
What We Do	07
Research Impact	12
Genomics Community Engagement	25
Financial Highlights	29
Acknowledgements	30

Who We Are



CGEn is Canada's national platform for genome sequencing and analysis.

Established in 2015, CGEn employs over 200 staff and is funded primarily by the Canada Foundation for Innovation (CFI) through its Major Science Initiatives Fund (MSIF), leveraging investments from the provincial governments of Ontario, Quebec, and British Columbia, Genome Canada, and others. CGEn operates as an integrated national platform with nodes in Toronto (The Centre for Applied Genomics at The Hospital for Sick Children), Montréal (McGill Genome Centre at McGill University) and Vancouver (Canada's Michael Smith Genome Sciences Centre at the Provincial Health Services Authority), leading large-scale projects and providing advanced genomic services to enable research in the health sciences, agriculture, forestry, fishery, the environment, biodiversity, and other sectors of importance to Canada.

Our Vision

Every biological study powered by genomic data—driving a healthier, more sustainable future for all Canadians.

Our Mission

Strengthen Canada's national capacity for genome sequencing and analysis, enabling impactful regional, national, and international research with large-scale, high-quality data.

Accelerate Canadian genomic science and solidify Canada's global reputation by uniting the country's top genomics expertise.

Anchor strategic collaborations across initiatives, funders, companies, and organizations, positioning Canadian genomics initiatives for the greatest possible impact.

Values

- Excellence
- Connectivity
- Innovation
- Agility
- Diversity
- Reach

CGEn Impact to Date

2017–Present

3 nodes and **220+ staff** serving

550+ organizations **3,000+ laboratories** **1,000s of research projects**

Advancing Canada's most impactful genomics research programs through leadership, collaboration and high-quality data

#CanSeq150 · Canadian Biogenome Project · HostSeq · Marathon of Hope Cancer Centres Network · CARE for RARE · Canadian Precision Health Initiative

20.5 petabases
of data generated

4.5 petabases
publicly accessible for re-use

3,900+ publications
by staff and users

270+ international
co-authorships with CGEn scientific leaders

Driving research, development, application & commercialization across many important sectors

CGEn Vancouver · CGEn Montreal · CGEn Toronto

Technology Development for emerging technologies, enhancing service and developing new tools

Training the next generation of genomics leaders to keep pace with large-scale genomics and its growing applications

Our Partners & Funders

INNOVATION · Provincial Health Services Authority · SickKids · McGill · GenomeCanada · British Columbia · Ontario · Québec

What We Do



Our Priority Areas



Enabling Canadian Genomics Research with High-Quality Data at Scale

Genomic data are central to a growing range of biological research and underpin all CGEn activities. From population-scale and disease-focused studies to applications in biodiversity, agriculture, and beyond, high-quality genomic data enable researchers across academia, industry, and government to address some of Canada's most pressing scientific challenges.

CGEn's experts provide support from study design and technology selection to sample preparation, bioinformatics, and statistical analysis, delivering data at the scale and depth each project requires—from large population studies involving thousands of samples to technically complex reference genomes. Across our distributed platform, CGEn generates genomic data covering a wide range of applications, including short- and long-read whole genome sequencing, transcriptomics, epigenomics, single-cell sequencing, spatial transcriptomics, and proteomics, powered by a comprehensive technology fleet featuring the latest sequencing platforms and associated technologies.

Our latest sequencing platforms and associated technologies:

- Illumina NovaSeq X Plus
- PacBio Revio
- Oxford Nanopore PromethION
- Ultima UG 100
- NanoString (GeoMx, CosMx) and 10X Genomics (Xenium, Visium) for spatial transcriptomics
- 10X Genomics Chromium for single-cell genomics
- Olink Explore HT, Illumina SomaScan Discovery and SomaSeq Discovery for proteomics
- 34,832 dedicated CPU cores (+13,000 available), 20 GPU servers and over 30 petabytes of primary storage

CGEn nodes also maintain accreditations and certifications, such as Good Laboratory Practice (GLP), International Organization for Standardization (ISO), and clinical certifications/accreditations, enabling collaboration with academic, clinical, and industry partners. For more information on our full list of our nodes' available equipment and services, please visit our website: www.cgen.ca/our-technologies.

Our Users
in 2025–2026



Dr. Ryan Norris and Karen Ong, University of Guelph, measuring a Canada Jay nestling as part of a 60-year demographic study of this species in Algonquin Provincial Park.

This year, CGEn assembled the Canada Jay reference genome to support a greater understanding of the bird's adaptability to climate change (more on pg. 23).

1,093 user laboratories

177 organizations
in all 10 Canadian provinces and 13 countries

67% repeat users from previous year

40% repeat users over the past four years

94%
of respondents to 2025-26 survey report overall satisfaction

Research Areas

Health and Human Studies
85%

Biodiversity and Conservation
10%

Commercial Sectors
5%

28 new organizations

14 from private, non-profit and government sectors

14 from academia/ universities

conducting research in a wide range of sectors, including:

15
Canadian

13
International

marine science

wildlife conservation

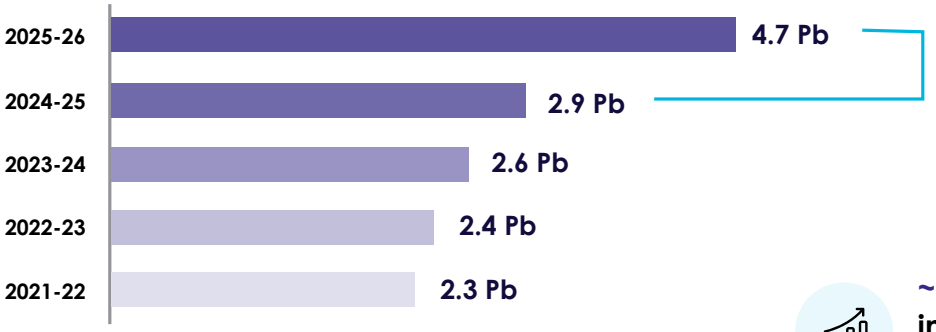
drug development

natural resources management

Data Generated
in 2025–2026



Petabases (Pb) of data produced by CGEn over the past five years



↑ **60% increase**
in 2025–26

This increase in overall data generation is driven primarily by whole genome sequencing (WGS), which continues to underpin large-scale national and international research initiatives.

~40% increase
in long-read genome sequencing in 2025–26

~64% increase
in short-read genome sequencing in 2025–26

22,318
whole genomes sequenced

↑ **69% increase** in 2025–26

17,524
human

4,794
non-human
including 221 species never previously sequenced at CGEn

1.1 Pb of data

(from over 9,000 samples)

deposited into publicly accessible databases

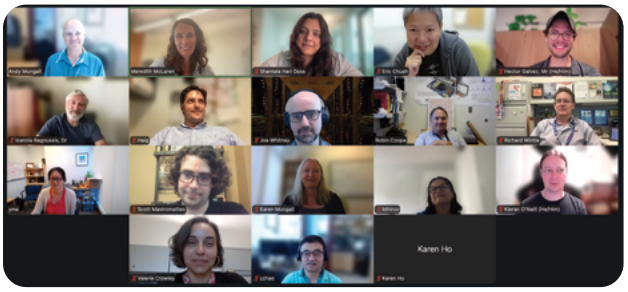
Whole genome sequencing (WGS) reads nearly all of a person's DNA, enabling the detection of genetic variation ranging from single-nucleotide changes to large chromosomal rearrangements, including variants associated with disease.

Short-read genome sequencing produces small DNA fragments, enabling a relatively rapid, accurate and cost-effective understanding of the genome. Long-read genome sequencing produces long stretches of DNA, allowing better resolution of complex regions, structural changes and assembly of more complete high-quality genomes.

Technology Development

Technology development is a critical, core CGEn activity that directly supports service delivery while strengthening CGEn's capacity for future large-scale genomics initiatives. Emerging technology evaluation and the development of new methods and service enhancements result in greater efficiencies, lower costs and higher data yields, making sequencing faster and more affordable for CGEn users. Cross-node exchange on new sequencing platforms, bioinformatics methods, technology development, and large-scale projects is facilitated through monthly meetings of CGEn's Technical Experts Committee (TEC), which informs coordinated decision-making and implementation across CGEn nodes.

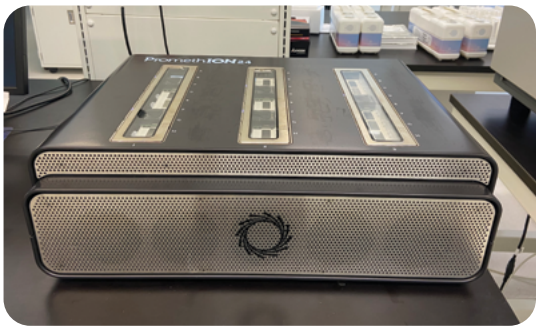
The past year saw improved short- and long-read sequencing workflows, adoption of updated reagents and chemistries, enhanced single-cell and spatial transcriptomics capabilities, expanded Oxford Nanopore Technologies (ONT) pipelines, and implementation of new proteomics platforms such as Olink, Illumina SomaScan Discovery, and Illumina SomaSeq Discovery.



CGEn's Technical Experts Committee (TEC) monthly meeting

2025–2026 Technology Advancement Examples

A major collaborative project involved benchmarking long-read sequencing across all three nodes using ONT high-throughput PromethION instruments. Each node achieved highly comparable outputs, including >40X mean human genome coverage from a single flowcell, despite minor variations in sample preparation. Particularly striking was the very high concordance in DNA methylation detection between the three sites. 'Benchmarking of Oxford Nanopore Whole Genome Sequencing for Germline Variant and CpG Methylation Detection Across Canada's National Platform for Genome Sequencing and Analysis' has been published in *Frontiers in Genetics*. Benchmarking activities using technologies like ONT that are increasingly applied in population genomics research (such as Genome Canada's Canadian Precision Health Initiative) further solidify CGEn's ability to remain in a ready state to generate high-quality, reliable and consistent data for national programs.



Read the full study

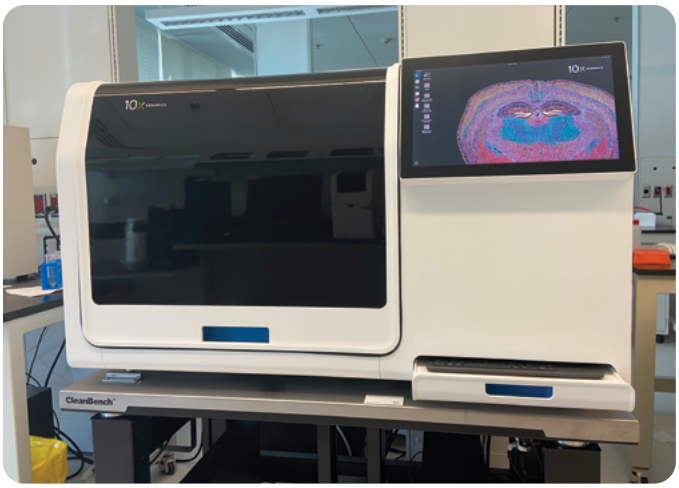
Galvez JH, Mastromatteo S, O'Neill K, et al. Benchmarking of Oxford Nanopore whole genome sequencing for germline variant and CpG methylation detection across Canada's national platform for genome sequencing and analysis. Front. Genet. 2026;17:1863034. Published 2026 Aug 12. doi: 10.3389/fgene.2026.1863034

In DNA sequencing, **40X coverage** means that, on average, every single letter in the targeted region or genome has been read 40 times by the sequencing machine. Sequencing is prone to occasional errors; reading a single letter (nucleotide) 40 times allows associated software to cross-reference the reads and eliminate false positives or other technical artifacts.



In **single-cell genomics**, comparative evaluation of single-cell methods and technologies informed protocol selection across use cases, including cost-performance trade-offs at varying cell numbers. Implementation of 10x multiome workflows and establishment of enabling processes for Flex-based protocols expanded the range of supported applications. The team has also developed our own "open-well" DLP+ technology which allows for custom multi-omic applications and supports Canadian innovation in robotics for associated functions such as cell-spotting. Ongoing improvements to sample handling, particularly for challenging inputs such as frozen tissues, aim to improve data consistency. Collectively, these activities support more flexible service offerings and provide options for cost management depending on project scale, while maintaining established workflows for data quality.

CGEn is advancing **spatial transcriptomics** by developing innovative methods that combine enabling platforms (10X Genomics Visium and STOmics) with long-read sequencing technologies, allowing for a more complete analysis of gene activity within tissues. By adapting approaches originally developed for single-cell genomics, the team is exploring the ability to identify important gene variants and RNA isoforms that are not captured by conventional methods. In parallel, CGEn has also deployed a high-resolution spatial molecular imaging platform (10X Genomics Xenium) and optimized it for high-throughput tissue microarray applications. This work increased capacity from dozens to nearly 500 tissue samples per experiment, significantly improving cost-efficiency and supporting a growing portfolio of cancer research projects.



Single-cell genomics is a suite of techniques used to analyze the DNA, RNA, or epigenetics of individual cells rather than a bulk tissue sample. By bypassing the "average" signal from millions of cells, it enables researchers to identify unique cellular signatures, track rare cell types, and understand complex diseases like cancer.

Spatial transcriptomics is a cutting-edge molecular profiling technique that maps gene expression within intact tissues. It goes beyond traditional RNA sequencing by revealing not just what genes are active, but where they are located, preserving the native tissue architecture and critical cell-to-cell interactions.

CGEn Research Impact

Advancing genomics in Canada through leadership, collaboration and high-quality data

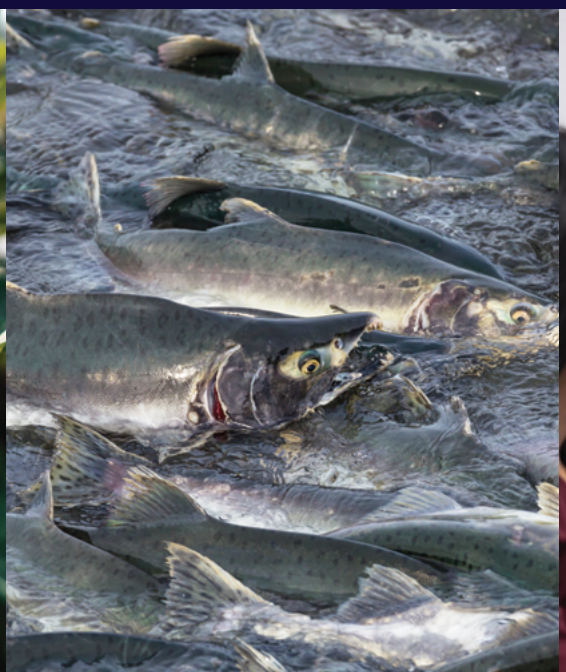
CGEn supports a diverse portfolio of Canadian genomics research, from investigator-led studies to flagship national initiatives such as Genome Canada's Canadian Precision Health Initiative and the Canadian BioGenome Project. Together, these efforts are advancing health care, environmental stewardship, economic growth, and quality of life, while driving continued investment in the secure storage, analysis, and sharing of genomic data.

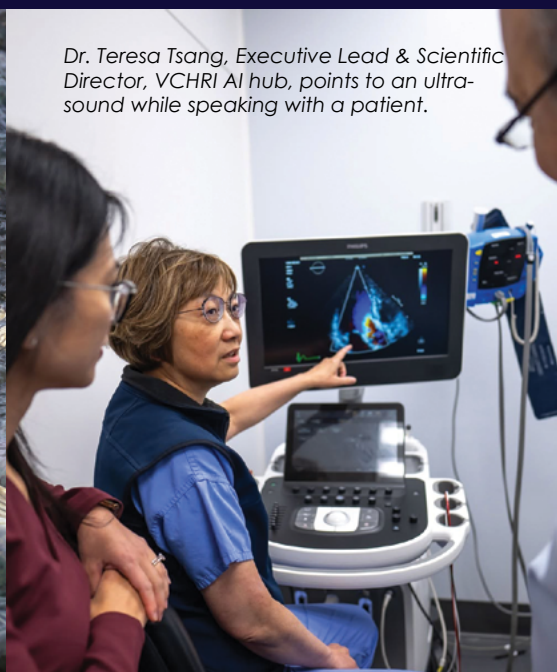
With nodes in Vancouver, Toronto, and Montréal, CGEn combines regional accessibility with the economies of scale of a national, high-throughput infrastructure. By uniting expertise and operating state-of-the-art technologies at scale, CGEn delivers high-quality genomic data efficiently and affordably for projects of all sizes, allowing researchers to focus their resources on discovery.

Guided by the vision of every biological study being powered by genomic data, CGEn is helping build a healthier, more sustainable future for all Canadians.

CGEn is supporting Dr. Tsang's project 'Multi-Omics and Sonography to Advance Integrated Cardiac Care (MOSAIC)' generating whole genome sequences for 8,000 study participants (more on pg.14).







Dr. Teresa Tsang, Executive Lead & Scientific Director, VCHRI AI hub, points to an ultrasound while speaking with a patient.

Major National Research Programs
Powered by CGEn in 2025–2026

Canadian Precision Health Initiative: **Building Canada's largest genomic health dataset**

CGEn is supporting 10 of 12 data-generating projects in Genome Canada's Canadian Precision Health Initiative (CPHI), sequencing more than 80,000 whole genomes toward the goal of creating a 100,000-genome dataset that reflects Canada's diverse population. High-quality genomic data combined with health and demographic information in the CPHI dataset will be housed in the Pan-Canadian Genome Library (PCGL) and made accessible for future research. This AI-ready data will accelerate innovative research applications, improving health outcomes for Canadians. While most data generated through CPHI will contribute to this national resource, data from Indigenous Peoples will be governed through a distinction-based approach that reflects Indigenous data sovereignty.

Leveraging our experience leading the HostSeq initiative (more below), CGEn is working with Genome Canada and the PCGL to establish policies and processes for genomic data generation, analysis, and transfer from CGEn nodes to PCGL.

CPHI data generation at a glance

(as of September 1, 2026)

- Sequencing commenced for eight CPHI projects
- 6,191 whole genome sequences (WGS) generated and stored within CGEn's nodes before deposition into the PCGL



Watch the documentary

Watch *Business Reporter's* mini-documentary "Your genome holds the key to more effective treatment" on YouTube.

> CPHI represents Canada's largest-ever collection of human genomic data. Building a large-scale, diverse, interoperable dataset that researchers can easily access, while keeping personal information private, will help transform a one-size-fits-all health-care approach into a modern, personalized, and equitable precision health system in Canada. CGEn's robust infrastructure and specialized expertise are supporting the generation, integration and utilization of this data so it can be used to its full potential to support advances in patient care.



Dr. Étienne Richer
Director, Precision Health, Genome Canada

SELECTED EXAMPLES OF CPHI PROJECTS

In addition to contributing to CPHI's national genomic health dataset, individual CPHI projects are building their own project-specific datasets to drive important research across many areas of health. Below are a few examples of the CPHI projects that are supported by CGEn.

Precision Child Health – Comprehensive Sequencing for Childhood Life-long Disorders (PCHSeq)

Project lead: Dr. Stephen Scherer, The Hospital for Sick Children (SickKids)

PCHSeq, led by SickKids, will generate 10,300 WGS from diverse participants with childhood-onset disorders and their families, creating a comprehensive dataset to advance diagnosis, discovery, and new therapies. Spanning 18 of 27 SickKids clinical divisions, PCHSeq is expanding access to genome sequencing across pediatric care. The project has enrolled 1,839 participants; 1,584 samples have been collected from existing biobanks and 255 participants have been recruited prospectively, with a focus on improving representation from underserved communities. CGEn-Toronto has generated more than 1,052 WGS to date for this project.

NeuRo Genomics Initiative (NRGI): Cohort Focusing on Neurological Disorders

Project lead: Dr. Ziv Gan-Or, McGill University/The Neuro

NRGI ("energy"), led by The Neuro at McGill University in collaboration with CHUM at Université de Montréal, will generate 8,700 WGS from individuals with neurological conditions, healthy controls, and Indigenous populations to advance the understanding of the genetic drivers of neurological disorders. Combining short- and long-read sequencing with RNA and epigenetic data, the project will create a comprehensive resource to support research into rare and aging-related disorders. CGEn-Montréal has generated more than 2,535 WGS to date for this project.

MOSAIC – Multi-Omics and Sonography to Advance Integrated Cardiac Care

Project lead: Dr. Teresa Tsang, University of British Columbia

MOSAIC aims to improve cardiovascular disease risk prediction and access to care by developing more inclusive, genomics-based approaches. The project will collect genetic, clinical, and lifestyle data from 8,000 diverse participants across British Columbia and Yukon, including WGS generated at CGEn-Vancouver. By combining genomics, point-of-care ultrasound, and AI-driven analysis, MOSAIC will support earlier, more accurate diagnosis and help create a scalable model for equitable cardiovascular care across Canada.

HostSeq: **Fuelling research across many health domains with Canadian data**

In 2020, amid the COVID-19 pandemic, CGEn led the rapid development of a first-of-its-kind Canadian databank, working with partners across the country to sequence the genomes and gather clinical information from more than 10,000 Canadians to understand host genetic contributions to COVID-19 and other health issues. Since then, HostSeq has continued to serve as a foundational national resource for genomic health research and as a pilot for population-scale genomics in Canada.

2025–2026 at a glance

- HostSeq dataset use:
  - 32 active research projects, including 13 focused on non-COVID-19 conditions, such as cardiac disease, scoliosis, autism spectrum disorder, and cancer
  - 140+ researchers and trainees supported
- HostSeq is an inaugural cohort of the Pan-Canadian Genome Library (PCGL), acting as a template for subsequent datasets to be shared with PCGL, such as CPHI
  - Legal framework to enable HostSeq data transfer to PCGL established
  - With PCGL, co-developed genomic data transfer and validation processes, as well as transformation of HostSeq clinical data into the PCGL data schema
- CGEn CEO Dr. Meredith McLaren presented on the use of Global Alliance for Genomics and Health (GA4GH) standards in HostSeq, including in the transfer of HostSeq data to the PCGL, at the GA4GH April Connect 2026 meeting in Montréal
- Genome Aggregation Database (gnomAD) Canada launched with HostSeq as the inaugural dataset. Building on the success of gnomAD, gnomAD-Canada is creating a population-scale reference resource of genetic variation specific to Canada. Managed by the Canadian Genomic Data Commons (CGDC) and PCGL, the platform will include 60,000 Canadian genomes, expanding representation of historically underrepresented populations and improving rare disease diagnosis. The first release, gnomAD-Canada v1.0, includes 10,487 HostSeq genomes and is publicly available to support biomedical research

Implementation of serological and molecular tools to inform COVID-19 patient management (GENCOV)

Project lead: Dr. Jordan Lerner-Ellis, Sinai Health System

The GENCOV study, a project that contributed to HostSeq, investigated how host genetics and immune responses influence COVID-19 severity.

The study 'Findings from comprehensive genome sequencing in the Canadian population: Results from the GENCOV Study' analyzed whole genome sequencing data, generated through HostSeq, from 1,292 participants and provided comprehensive genomic reports with health-related findings. The researchers identified medically actionable variants linked to inherited conditions, including some cancers and cardiovascular diseases, demonstrating the broader value of research-based genomic data in supporting earlier diagnosis, preventive care, and precision medicine.

In a separate study, 'Clinically significant DNA variation from the GENCOV and HostSeq COVID-19 genome sequencing studies', the team estimated the number of pathogenic and likely pathogenic variants in the HostSeq dataset and compared them to those classified in ClinVar (a publicly accessible archive of human genetic variation) to assess the accuracy and completeness of ClinVar variant classifications. The team found that a substantial fraction were either missing from or inconsistently classified in ClinVar, underscoring the need for ongoing expert curation and regular updates of public variant databases to improve the accuracy and completeness of information used for disease diagnosis and research.

Read the full studies

Casalino S, Aujla N, Frangione E, et al. Findings from comprehensive genome sequencing in the Canadian population: Results from the GENCOV Study. *Genet Med Open*. 2026;4:104372. Published 2026 Feb 4. doi:10.1016/j.gimo.2026.104372

Frangione E, Mahajan R, De Los Rios J, et al. Clinically significant DNA variation from the GENCOV and HostSeq COVID-19 genome sequencing studies. *J Med Genet*. 2026;63(5):299-307. Published 2026 Apr 20. doi:10.1136/jmg-2025-111029

> "The identification of pathogenic variants in participants from studies such as HostSeq and GENCOV can provide valuable insights into inherited disease risk, disease penetrance, and variability in clinical presentation, while also informing patient management and screening strategies aimed at reducing the risk of disease development."



Dr. Jordan Lerner-Ellis
Molecular geneticist and Head and Director of the Advanced Molecular Diagnostics Laboratory at Sinai Health System

Marathon of Hope Cancer Centres Network: **Building a national, high-quality data resource to transform how cancer is studied and treated in Canada**

CGEn is a central partner in the Terry Fox Marathon of Hope Cancer Centres Network (MOHCCN), providing **whole genome and transcriptome sequencing (WGTS)** for the BC and Quebec consortia. Over the last five years, CGEn's Montréal and Vancouver nodes contributed to the Network's Gold Cohort dataset, helping surpass the Network's goal of sequencing 15,000 cancer cases by March 2026. Building on our expertise in sequencing, analysis, and clinical translation, CGEn will continue supporting MOHCCN Phase 2, which is expected to add approximately 11,000 cases over the next five years.

2025–2026 at a glance

- 3,400+ cases sequenced at CGEn nodes for the Gold Cohort, bringing CGEn's total contribution over five years to more than 8,300 cases

The Platform for Oncogenomic Reporting and Interpretation (PORI) is an open-source platform developed by CGEn-Vancouver to automate the analysis and interpretation of cancer WGTS data, enabling scalable precision oncology. Successfully deployed across several MOHCCN sites, PORI will play a key role in Phase 2 by supporting the return of genomic results to patients.

> CGEn is contributing to Canada's – and one of the world's – largest and most complete cancer case resources, designed to enable researchers to conduct studies to better understand the molecular drivers of cancer and to accelerate the development of more precise, personalized approaches to diagnosis and treatment. Surpassing our goal of sequencing samples from 15,000 cancer patients is a critical step toward building a truly national, high-quality data resource that can transform how we study and treat cancer in Canada."



Dr. André Veillette
MOHCCN Executive Director

Transcriptome sequencing (often called RNA-Seq) is the process of sequencing all the RNA molecules in a cell or tissue at a specific time. It reveals which genes are turned "on" or "off" and measures their activity levels, providing a dynamic snapshot of cellular function, disease progression, and responses to environmental changes.

SELECTED EXAMPLES OF MOHCCN GOLD COHORT PAN-CANADIAN PROJECTS

In addition to the data generated for MOHCCN regional consortia, CGEn nodes have generated WGTS data for 16 of 19 Pan-Canadian Projects, which unite researchers and clinicians from multiple provinces to accelerate precision medicine for cancer in Canada. Below are two examples.

CGEn-Montréal provided WGTS data for 201 participants in the study: 'Longitudinal Molecular Characterization of Lethal Prostate Cancer: A Major Step Towards Precision Oncology'

> "In this project, we aim to elucidate the impact of prostate cancer heterogeneity on disease progression by linking molecular imaging features, cancer gene alterations, and clinical data, using artificial intelligence-assisted analysis."



Dr. Frédéric Pouliot
Project co-lead, Urologist and Clinician-Scientist, Centre de Recherche du CHU de Québec, Université Laval

CGEn-Vancouver provided WGTS data for 91 participants in the study: 'Interrogating the Evolving Clonal Structure of Leukemia from Diagnosis to Relapse'

> "Our goal is to understand why acute myeloid leukemia (AML) becomes resistant to treatment. By sequencing the whole genome and transcriptome of patients' leukemia cells at diagnosis and relapse, and integrating these data with single-cell and epigenomic analyses, we can identify both genetic and non-genetic changes that drive therapy resistance."



Dr. Aly Karsan
Project lead, Distinguished Scientist, Basic and Translational Research, BC Cancer Research Institute

The Canadian BioGenome Project: **Generating high-quality reference genomes to better understand and protect biodiversity across Canada**

As the Canadian branch of the Earth BioGenome Project, the Canadian BioGenome Project (CBP) has a central goal of producing reference genomes for Canadian species and making these data available for research. Reference genomes are the most complete, highest-quality genomes of species, and CGEn nodes are providing collaborative technical support in the generation of CBP's genomes. Since its launch, CBP has collected 5,141 samples representing 832 species. As CBP moves toward completing and exceeding its target of 400 publicly available reference genomes, it is not only building a genomic resource for species conservation in Canada but also shaping a global model for how science, technology, and community partnership can work together to protect biodiversity.

CBP data generation at a glance

(as of September 16, 2026)

- 128 samples sequenced in 2025–2026, bringing the total to 424, which include:
  - 150+ species at risk
  - 140+ Arctic species
  - 70+ invasive or pest species
  - 180+ species of economic importance
  - High-priority species for Indigenous communities
- 280 genomes **assembled**, of which 204 are reference genomes, including improved assemblies for the Canada goose and the polar bear
- 83 genomes **annotated** by European Molecular Biology Laboratory – European Bioinformatics Institute (EMBL-EBI)
- 70 Tb of data released to National Center for Biotechnology Information (NCBI) open database

CBP's genome portfolio spans a broad cross-section of Canadian biodiversity, including fish, plants, birds, and invertebrates such as insects, molluscs, and beetles. CBP species have been selected in collaboration with cultural groups, including those representing Indigenous Peoples, conservation and commercial group partners, or through the CBP's extensive network of 35 taxonomic committees, involving nearly 600 experts.

Assembly uses computational methods to reconstruct a genome from raw WGS reads, either by aligning them to an existing reference genome or through *de novo* assembly when no suitable reference is available. Annotation labels features within the genome, identifying where genes are located and predicting their biological function.

Preceding CBP, CGEn led the **CanSeq150 initiative**, sequencing the genomes of 95 species in honour of Canada's 150th birthday to support conservation and biodiversity research. CanSeq150 promoted the public release of genomic data to enable future research and, to date, has resulted in 93 publications from researchers across the globe, associated with data from 39 CanSeq150 species. Similarly, it is expected that the 400+ high-quality reference genomes generated through CBP will be reused for many high-calibre studies, accelerating biodiversity research and translation across ecosystems and borders.

Recent publication: 'The Genome Sequence of the Hemlock Woolly Adelgid, Adelges tsugae Annand 1924'

This study presents the first chromosome-scale genome assembly for the hemlock woolly adelgid, *Adelges tsugae*, one of the most destructive and invasive forest pests affecting eastern North American hemlock forests. An international research team assembled a high-quality 216.6 Mb genome consisting of 10 chromosomes, identified approximately 11,800 protein-coding genes, and produced the largest adelgid mitochondrial genome sequenced to date. These genomic resources provide an important foundation for studying the insect's biology, evolution, host adaptation, and invasiveness, and may help inform future management and conservation strategies for threatened hemlock ecosystems.



Read the full study

Brunet BMT, Dial DT, Burke GR, et al. The Genome Sequence of the Hemlock Woolly Adelgid, Adelges tsugae Annand 1924. *Genome Biol Evol.* 2025;17(10):evaf170. doi:10.1093/gbe/evaf170

"Genetic diversity is a fundamental component of biodiversity, reflecting the natural variation in DNA within and between individuals and populations of a species. This diversity shapes resilience and adaptation, helping species respond to challenges such as climate change, emerging diseases, and habitat loss. Initiatives like the Canadian BioGenome Project and the Earth BioGenome Project are critical because they help us understand and preserve this diversity. By generating genomic resources for species across Canada and around the world, these efforts provide the foundation for conservation, scientific discovery, and informed environmental stewardship."



Dr. Federica Di Palma
Chief Health Genomic Officer and VP Research, Laboratory Services and BCCDC, Provincial Health Service Authority (PHSA) and member of the Earth BioGenome Project Executive Council

Other Examples of **CGEn-Enabled Research Impact** in 2025–2026

Health

Improving care for diabetes and other diseases with genomics and AI

BioPortal is a research platform at the Jewish General Hospital and Lady Davis Institute in Montréal, in partnership with the McGill Canada Excellence Research Chair (CERC) at McGill University, focused on improving diabetes care. It includes ~6,000 participants with Type 1 (386), Type 2 (5,071), and gestational diabetes (409), plus controls (134), with plans to expand to 12,500 participants to support research into both common and rare diseases. The cohort links: rich clinical data; retinal imaging; **high-throughput sequencing-based proteomics data, generated at CGEn-Montréal using Olink technology, for 3,086 participants**; genotyping data from Illumina's high-throughput Infinium Global Screening Array with Multi-Disease content; and bioimpedance measurements, together enabling biomarker discovery and improved understanding of disease risk, progression, prognosis, and treatment response.

Dr. Brent Richards' team at McGill University is applying AI to these data to refine genetic risk prediction, improve diagnosis, and identify new therapeutic opportunities. Participants may also be re-contacted for clinical trials, supporting translation into patient care and access to emerging therapies. BioPortal also serves industry needs by providing high-quality real-world clinical data and access to well-characterized sub-populations for clinical trial recruitment.



International team identifies new genes responsible for congenital diarrhea and intestinal disorders



A study published in The New England Journal of Medicine by an international team led by researchers at SickKids conducted whole genome and exome sequencing on 129 infants with suspected CODE (congenital diarrhea and enteropathies), providing a diagnosis for 48% of cases. **CGEn-Toronto provided whole exome sequencing (WES) for some of the patients who were part of the Pediatric Congenital Diarrhea and Enteropathies (PediCODE) Consortium**. The study findings uncovered three new genes associated with CODE (GRWD1, MYO1A and MON1A) and provided answers to 62 families.

> "This is a striking improvement from the 20% diagnosis rate in our clinic at SickKids. Not long ago, diagnostic rates were as low as 3%. Undiagnosed infantile diarrhea can be fatal, but even when it isn't, early diagnosis of rare conditions can help provide much-needed answers for families. As a result of this study, we can now provide a diagnosis to more families and move closer to precision treatments tailored to their child's specific genetic variant."



Dr. Aleixo Muise
Staff Gastroenterologist, Co-Director of the Inflammatory Bowel Disease (IBD) Centre, and Senior Scientist in the Cell & Systems Biology program at SickKids

Read the full study

Gaibee Z, Warner N, Bugda Gwilt K, et al. The Genetic Architecture of Congenital Diarrhea and Enteropathy. *N Engl J Med*. 2025;392(13):1297-1309. doi:10.1056/NEJMoa2405333

High-throughput sequencing-based proteomics enables the simultaneous measurement, characterization, and quantification of thousands of proteins from complex biological samples (like blood plasma, serum, or tissue) in a rapid, automated fashion.
Whole exome sequencing focuses specifically on the "exome," the protein-coding regions of the genome where most known disease-causing mutations occur.

Strengthening Canadian and global pathogen surveillance through environmental sample sequencing

CGEn-Montréal's Dr. Ioannis Ragoussis led the Coronavirus Variants Rapid Response Network (CoVaRR-Net) Pillar 5: Viral Genomics and Sequencing, which tracked SARS-CoV-2 variants across Canada through large-scale sequencing of clinical and environmental samples. **CGEn-Montréal sequenced more than 116,000 clinical and 4,200 wastewater and environmental samples for this program.** The team also developed sensitive methods to detect low-frequency variants, applying them to animal studies and helping establish international standards for wastewater surveillance through the European ELIXIR working group, extending CoVaRR-Net's impact globally. In addition, through an international study co-authored by Dr. Jesse Shapiro (McGill University), a team in Bangladesh found that identifying cholera-specific bacteriophages in wastewater can provide a low-cost early warning system for cholera outbreaks. Building on all of this work, Ragoussis now leads new collaborations with the Public Health Agency of Canada and provincial health authorities to develop genomic assays for pathogens, antimicrobial resistance, and invasive species in environmental samples, while ongoing projects continue to advance RNA virus detection in clinical and wastewater surveillance.



Read the full studies

Psomopoulos F, O'Cathail C, Anastasiadou N, et al. Toward a unified approach: Considerations for bioinformatic and sequencing activities & data in wastewater surveillance of biologic public health threats. *Open Res Eur*. 2026;5:267. Published 2026 Jul 6. doi:10.12688/openreseurope.20934.3

Akhtar M, Amin MA, Hussain SN, et al. Clinical and environmental wastewater-based bacteriophage surveillance for high-impact diarrheal diseases, including cholera, in Bangladesh. *mBio*. 2026;17(1):e0265425. doi:10.1128/mbio.02654-25

Hodzic-Santor B, Hinz A, Kassen R, et al. Sequencing and variant calling of SARS-CoV-2 from floor swabs: a potential tool for identifying emergent lineages. *Microb Genom*. 2025;11(12):001575. doi:10.1099/mgen.0.001575

Bayega A, Reiling SJ, Liu JL, et al. A Benchmark of methods for SARS-CoV-2 whole genome sequencing and development of a more sensitive method. *Front Genet*. 2025;16:1516791. Published 2025 Aug 15. doi:10.3389/fgene.2025.1516791

Scientists identify the first non-coding gene that controls cell size, a hallmark of cancer and other diseases

The genetic basis behind cell size has largely been a mystery. New research led out of SickKids, enabled by **high-throughput RNA sequencing (RNA-seq) at CGEn-Toronto,** has, for the first time, identified a gene that can directly control cell size. Cell size is both an indicator and regulator of cellular health, and changes are often hallmarks of disease, such as cancer.

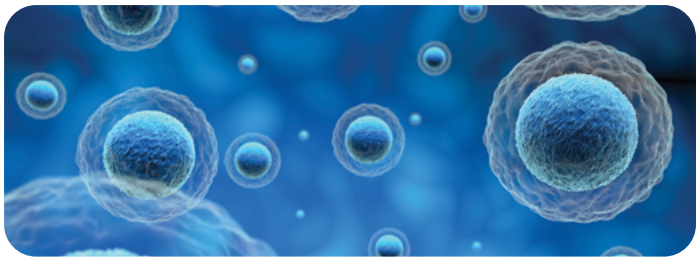
In a study published in Nature Communications in December 2025, the team found that a gene for a long non-coding RNA (lncRNA) called CISTR-ACT helps control cell growth in two different ways. First, its location in the genome helps organize physical interactions between chromosomes, allowing it to influence other genes involved in controlling cell size. Second, the CISTR-ACT lncRNA works with a protein called FOSL2 to regulate genes involved in cell shape and development. Unlike genes that encode proteins, CISTR-ACT belongs to the non-coding genome—the largely unexplored part that makes up about 98% of our DNA.

> "Our study shows that long non-coding RNAs and the non-coding regions of the genome can drive important biological processes, including cell size regulation. By carefully examining a wide range of cell types and phenotypes, we identified the first causal long non-coding RNA that directly influences cell size."



Dr. Philipp Maass

Senior Scientist in the Genetics & Genome Biology program, and Canada Research Chair in Non-Coding Disease Mechanisms



Read the full study

Kiriakopulos K, Soleimanpour K, McMurray BJ et al. LncRNA CISTR-ACT regulates cell size in human and mouse by guiding FOSL2. *Nat Commun* 2025;17(1):872. Published 2025 Dec 16. doi:10.1038/s41467-025-67591-x

Using AI and omics for sustainable agriculture

insporos is an agricultural technology start-up based at the University of British Columbia's HATCH Venture Builder accelerator in Vancouver that is developing an AI-powered platform capable of predicting germination, vigour, and disease presence at the individual seed level. By replacing destructive batch testing with continuous, scalable analysis, the platform has the potential to improve crop health, conserve resources for growers, and advance sustainable agriculture in Canada.

A key component of insporos' commercialization strategy is benchmarking its proprietary technology against established molecular-based pathogen testing methods delivered by CGEn-Vancouver. With funding from Genome British Columbia's Genomics Innovation Fund (GIF), **CGEn-Vancouver has supported insporos with protocol development and tailored genomics services, including optimization of RNA isolation from tomato seeds and RNA sequencing for viral species identification.** This collaboration provides gold-standard molecular-based testing that enables insporos to evaluate the accuracy, sensitivity, and overall performance of its platform against current industry benchmarks.



Assembling a reference genome to assist in Canada Jay conservation

As part of the technology development portfolio, CGEn-Toronto scientists assembled the reference genome of the Canada Jay, testing new technical approaches while supporting a better understanding of the bird's adaptability to climate change. The sample was captured by Dan Strickland, a field researcher who has studied the jays for decades and pioneered research into the bird's unique winter survival strategies, such as storing food underground during the winter months. Studies co-led by Strickland and Dr. Ryan Norris (University of Guelph) strongly suggest that warmer winter temperatures are causing increased degradation of those perishable food stores and thus explain the lower production of young Canada Jays needed to replace the inevitable losses of older jays.



Genomic information may help conservationists like Norris and Strickland to track population health, identify distinct conservation units, and assess the jay's ability to adapt to climate change. **CGEn-Toronto has generated both the Canada Jay and Blue Jay genomes, which will be useful for comparative genomic analyses.**

Globe and Mail science reporter Ivan Semeniuk published an article describing this work: 'Genetic sequence promises new window into beloved 'camp robber' Canada jay' on World Wildlife Day (March 3, 2026). Read the press release on our website: www.cgen.ca/news.

Harnessing genomics for more resilient sunflower crops

Dr. Marco Todesco, an Assistant Professor and plant geneticist at the University of British Columbia (UBC), is using genomic sequencing at CGEn-Vancouver to understand how plants adapt to their environments and to harness their diversity to develop more sustainable and resilient crops. Working with the Rieseberg Lab at UBC, Todesco studied 1,500 wild sunflowers from across North America, identifying genes and genomic regions associated with environmental adaptation and traits such as flowering time and floral pigmentation. His research showed that a single gene controls UV patterns in sunflowers, influencing both pollinator attraction and water loss in dry environments. Now, he is using **long-read sequencing at CGEn-Vancouver to sequence the complete genome of dozens of wild and cultivated sunflowers** to understand the role that chromosome organization plays in adaptation and crop improvement.



Developing biomarker tools to assess food deprivation in juvenile Chinook salmon

In British Columbia, juvenile Chinook salmon (Oncorhynchus tshawytscha) may experience prolonged food deprivation during their early marine migration and first winter at sea, increasing vulnerability and reducing survival. A team led by Dr. William Bugg at the University of British Columbia used **RNA sequencing at CGEn-Vancouver to identify gene expression biomarkers associated with food deprivation and energetic stress**.

Published in Conservation Physiology, the study team used this information to develop a panel of gill-based biomarkers that can assess the nutritional status of wild juvenile salmon. The team is working with the Pacific Biological Station (PBS) to deploy this panel using high-throughput quantitative PCR (qPCR) and machine learning approaches. The resulting assay can detect nutritional stress after only a few weeks of food deprivation using small, non-lethal gill samples, helping researchers better understand how environmental stressors influence long-term survival in wild salmon in the Strait of Georgia.

In collaboration with CGEn-Vancouver, the team is also transitioning the high-throughput qPCR-based approach used at PBS to a capture-based sequencing platform, expanding accessibility while providing more comprehensive insights into the factors affecting salmon survival in the early marine environment.

Read the full study

Bugg WS, Akbarzadeh A, Ming T, et al. Identification of food deprivation in salmonids using gill biomarkers. *Conserv Physiol*. 2025;13(1):coaf088. Published 2025 Dec 19. doi:10.1093/conphys/coaf088



Genome sequencing to understand the evolution of the ancient "Toronto Subway Deer"

An 11,315-year-old deer fossil was discovered by a Toronto Transit Commission (TTC) employee during subway construction between Islington and Kipling stations in 1976. Roughly caribou-sized, its unusual antlers did not match any known species, leading the Royal Ontario Museum (ROM) to describe it as a new, now extinct genus and species in 1982. It remains housed at the ROM as specimen ROMM75974, nicknamed the "Toronto Subway Deer."

More recently, a team led by Dr. Aaron Shafer at Trent University extracted ancient DNA from the specimen and used **WGS at CGEn-Toronto to resolve its evolutionary relationships**. Genomic and mitochondrial analyses of related cervids (deer) showed it is closely related to—but highly diverged from—Odocoileus species such as white-tailed and mule deer, splitting from other deer lineages roughly 2–3 million years ago. The findings suggest it likely went extinct due to climate-driven habitat change at the end of the last Ice Age, as open landscapes shifted to denser woodlands. This study garnered considerable attention from local and international media outlets, including the New York Times, Globe and Mail, Toronto Life, and CTV News.



Courtesy of ROM (Royal Ontario Museum), Toronto, Canada. ©ROM

Read the full study

Kessler C, Haddrath O, Lim BK, Shafer A. Ancient DNA of the Toronto Subway Deer adds to the extinction list of ice age megafauna. *Biol Lett*. 2025;21 (10):20250497. doi:10.1098/rsbl.2025.0497

Genomics Community Engagement

Strengthening Canada’s position as a global genomics leader

Beyond service provision, CGEn and its nodes actively collaborate with Canadian and international partners as experts in data generation, analysis, sharing, storage, and related ethical and privacy issues, helping strengthen Canada's position as a global genomics leader. Over the past year, these collaborations have expanded, enhancing Canada's research competitiveness and accelerating scientific innovation. From supporting vaccine development in low- and middle-income countries to advancing genomic data sovereignty in Canada, the examples below highlight how CGEn supported collaboration and genomics innovation in Canada and beyond throughout 2025–2026.



The Human RNome Project Consortium meeting in Toronto



Life Sciences BC’s Annual Access to Innovation conference in Vancouver

Advancing AI-driven drug discovery

Ligand-AI is one of the largest global open-science drug discovery initiatives and a new international public-private partnership led by Canadian institutions, including SickKids, University Health Network, and the Structural Genomics Consortium. As a participating member in LIGAND-AI, CGEn-Toronto is leading the genomics-based component of the consortium, supporting the experimental design, sequencing and primary data analysis of DNA-encoded libraries to generate open protein-compound interaction datasets that enable AI-driven drug discovery. The initiative is among the first to launch under Canada's new association with Horizon Europe.

Collaborative research and training in genomics

CGEn is a partner in two **NSERC Collaborative Research and Training Experience (CREATE) in Genomics** programs: CANSSI Genomic Data Science (led by Dr. Lisa Strug, Associate Director CGEn-Toronto) and Genomics for Engineering, Environmental Monitoring and Agriculture (GEEMA) (led by Dr. Ioannis Ragoussis, Assistant Director CGEn-Montréal). These programs train and mentor the next generation of genomics researchers and are a part of Canada's Genomics Strategy. CGEn nodes will host annual workshops to provide CREATE trainees with hands-on insights into sequencing infrastructure, analysis, technology development, and major initiatives such as HostSeq, PCGL, and CPHI starting in late 2026.

RNA vaccine development in low- and middle-income countries

The **PATH RNA Cooperative** is a global initiative funded by the Gates Foundation that advances RNA vaccine development and technology transfer in low- and middle-income countries. CGEn-Montréal is contributing expertise in data science, bioinformatics, and sequencing to support training, therapeutic design, and quality control methods with partners in Senegal, South Africa, and other regions. The network is expanding in 2026–27 to include additional industry partners in countries including Malaysia and Brazil.

Mapping the entire set of RNA to advance fundamental biology and beyond

The **Human RNome Project** is an international consortium creating the first comprehensive, modification-resolved map of human RNA to advance biology, therapeutics, agriculture, and biotechnology. In 2026, Canadian researchers joined the consortium with CGEn-Montréal currently contributing to consortium-wide data generation activities, and all CGEn nodes expected to support future data analysis. CGEn is supporting Canadian participation in this global initiative, which unveiled its first draft Human RNome at its annual meeting hosted by SickKids in July 2026.

Supporting Canadian data sharing, sovereignty and security

The **Canadian Genome-Phenome Archive (CGA)** is a national platform that provides secure, permanent archiving and controlled access to personally identifiable genetic and phenotypic data generated by Canadian biomedical projects, hosted at CGEn-Vancouver as part of the Pan-Canadian Genome Library (PCGL). In April 2025, the CGA joined the Federated European Genome-Phenome Archive, marking the first major expansion of the federation outside Europe.

Dr. Steven Jones, CGEn-Vancouver Scientific Director, presented Canada's journey toward establishing a Canadian Genome-Phenome Archive node at the European ELIXIR All Hands 2025 meeting. The presentation highlighted the institutional, legal, technical, and policy considerations for secure genomic data sharing, positioning CGEn as an active contributor to global efforts in federated genomic data infrastructure.

Snapshot: CGEn nodes participate in national and international conferences

The McGill-RIKEN partnership, led by CGEn-Montréal, McGill, and the RIKEN Centre for Integrated Medical Sciences in Japan, advances interdisciplinary research at the intersection of genomics, immunology, computational methods, and related policy, social, legal, and ethical issues. CGEn-Montréal helped organize two international meetings in 2025, bringing together more than 200 participants to foster collaboration and identify opportunities for future research partnerships.



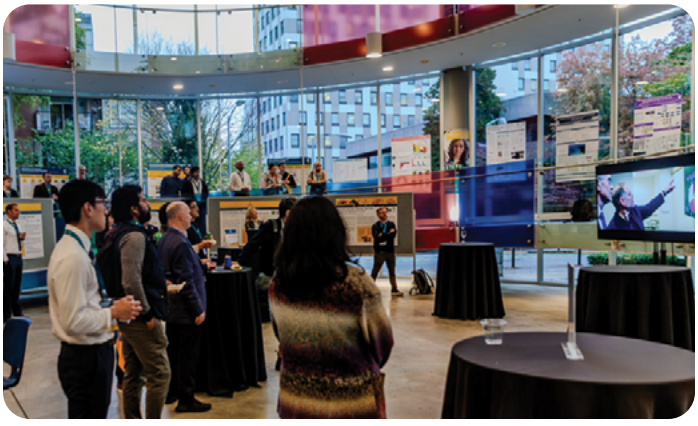
Dr. Yussanne Ma, CGEn-Vancouver Director of Operations, contributed to a panel on "Canada's Genomic Future: Ethics, Data Sovereignty & Defence" at Life Sciences BC's 11th Annual Access to Innovation, highlighting how ethical governance frameworks support translation of genomics research into real-world health and economic benefits.



CGEn-Toronto Assistant Director Dr. Richard Wintle participated in a meeting hosted by the Ontario Brain Institute with The Honourable Nolan Quinn, Minister of Colleges, Universities, Research Excellence and Security, where he highlighted CGEn-enabled research, including a seven-year collaboration among researchers in Ontario, Quebec, and Alberta. Using data generated at CGEn-Toronto, the study found that more than one in ten children with cerebral palsy carried a genetic variant associated with their condition. The study's open dataset is available through the Ontario Brain Institute's Brain-CODE platform and the European Genome-phenome Archive, supporting future research.



The "Sequence to Innovate" competition was launched in Vancouver to enable impactful sequencing projects that push the boundaries of technology development and genomics research. Researchers were invited to submit projects for awards of up to $15,000 in sequencing services. Five finalists were invited to present rapid talks at CGEn-Vancouver's annual Collaborator Forum, where participants voted for two winning projects. Through these and other efforts, 25 new collaborations were formed with Canadian and international users who had not previously used CGEn-Vancouver's sequencing services.



Looking ahead by looking back
CGEn's 10 Years of Impact

In 2025–2026, CGEn engaged with users, partners and the wider community to conduct a broad scan of the landscape, reflecting on CGEn's impact since its establishment in 2015, and informing future planning. As a result, CGEn published a comprehensive report, *CGEn: 10 Years of Impact*, and *Strategic Vision 2030*, a guiding document that anchors our focus on four priority areas: High Quality Data At-Scale, Technology Development, Training & Skill Development, and Genomics Ecosystem Engagement. Visit our website to learn more: www.cgen.ca/publications.



What's next for CGEn?

By enabling major national research programs, expanding our reach across academia, industry, and government, and advancing collaborative technology development, CGEn continues to strengthen Canada's leadership in genomics and enable transformative research that improves health, sustainability, and economic prosperity.

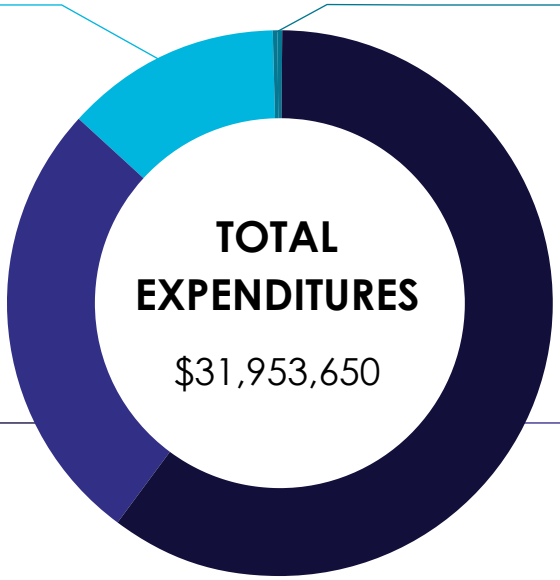
Over the next year, CGEn will focus on maximizing the impact of HostSeq data and continuing to position it as a model for large-scale genomic data storage, linkage, and sharing, including through its deposition in the Pan-Canadian Genome Library (PCGL). CGEn will also continue to support the delivery of Genome Canada's Canadian Precision Health Initiative (CPHI), generating high-quality genomic data at scale as sequencing for new CPHI projects is initiated and overall sample submissions increase. Working with Genome Canada and partners, CGEn will also enable secure and validated CPHI data deposition into the PCGL on behalf of CPHI projects. Alongside these activities, we will initialize new activities for MOHCCN Phase 2, enable our 1,000+ laboratory user base with advanced genomics services, as well as continue technology evaluation and technology development activities, specifically within the areas of long-read data analysis, single-cell genomics, spatial transcriptomics and the integration of AI approaches to improve genomic science.

By synthesizing past learnings, implementing the most cutting-edge technologies, consolidating expertise across CGEn's scientific leadership, operational teams, and our wider national and international network, CGEn will remain in a ready state to respond to Canadian challenges and opportunities where genomics can play central or supporting roles. Given the current global context, the connectivity, agility and sovereignty afforded by CGEn's national platform are key national capacities, critical to ensuring Canada and Canadians receive maximum benefit from advances in genomic science.

Financial Highlights

CGEn's cutting-edge facilities and consolidation of world-class scientific expertise are made possible by the support of our partners and funders. Our cornerstone funding comes from the Canada Foundation for Innovation (CFI) Major Science Initiatives Fund (MSIF 2023-29), which, along with host institutions and other leveraged funding, supports the operation and maintenance of national facilities critical to Canadian research. Additionally, CGEn receives peer-reviewed, competitive funding from CFI's Innovation Fund and from Genome Canada's Technology Development program for MSIF facilities.

These funds enable CGEn to continue to assess and implement strategic infrastructure upgrades and perform leading-edge genomic science, while leveraging provincial funding, private-sector in-kind contributions, philanthropic and other funding sources. CGEn's revenue and expenditures balance over multi-year funding cycles.



12.8%

Maintenance

$4,094,737

(extended warranties, parts, upgrades, services, supplies/consumables)

0.5%

Professional Development, Non-Salary Administrative and Outreach Expenses

$162,696

26.4%

Infrastructure

$8,444,606

60.2%

Salaries and Benefits

$19,251,611



Acknowledgements

CGEn's scientific leadership and staff, Board of Directors, Scientific Advisory Board, and many collaborators continue to guide and strengthen our impact. We extend our sincere thanks to the many individuals, partners, and funders whose leadership, expertise, and commitment make our work possible.

Board of Directors

Gordon McCauley (Chair)
Vice-Chair, adMare BioInnovations

Dominique Bérubé
Vice-President, Research and Innovation, and Professor, Faculty of Engineering at McGill University

Sir Mark Caulfield
Chief Executive of Barts Life Sciences, Director of the NIHR Biomedical Research Centre at Barts, William Harvey Research Institute, Queen Mary University of London

Philippe Gros
Professor, Department of Biochemistry, McGill University

David Malkin
Professor of Paediatrics and Medical Biophysics at University of Toronto, Co-lead, SickKids Precision Child Health

Sharon Peacock
Master of Churchill College, Professor of Microbiology and Public Health at the University of Cambridge

Vardit Ravitsky
President and CEO, The Hastings Center

Sharon Wu
Managing Director, Vice-President Research & Innovation Portfolio, University of British Columbia

Scientific Advisory Board

Edward M Rubin (Chair)
Director and Founder, Science Corps

Mark Blaxter
Head, Tree of Life Programme, Wellcome Sanger Institute

Ivo G Gut
Director, Centro Nacional de Análisis Genómico (CNAG)

Elaine R Mardis
Co-Executive Director of the Steve and Cindy Rasmussen Institute for Genomic Medicine at Nationwide Children's Hospital and Professor of Pediatrics at The Ohio State University College of Medicine

Gabor Marth
Professor of Human Genetics, University of Utah

Richard M Myers
Chief Scientific Officer, President Emeritus and Faculty Investigator, HudsonAlpha Institute for Biotechnology

Beth Shapiro
Professor, Ecology & Evolutionary Biology Department Genomics Institute, University of California Santa Cruz and Howard Hughes Medical Institute Professor

Alexandra-Chloé Villani
Director, Massachusetts General Hospital (MGH) Single Cell Genomics Research, and Program Institute Member, Broad Institute of MIT and Harvard

Executive Committee

Meredith McLaren
Chief Executive Officer, CGEn

Steven Jones
Scientific Director CGEn-Vancouver, University of British Columbia

Mark Lathrop
Scientific Director CGEn-Montréal, McGill University

Stephen Scherer
Scientific Director CGEn-Toronto, SickKids and University of Toronto

Federica Di Palma
Chief Health Genomic Officer and VP Research, Laboratory Services and BCCDC, Provincial Health Service Authority (PHSA)

Ioannis Ragoussis
Assistant Director, CGEn-Montréal, McGill University

Richard Wintle
Assistant Director, CGEn-Toronto, SickKids

Institutional Partners and Funders

SickKids · Provincial Health Services Authority · The University of British Columbia · McGill · Innovation Canada Foundation for Innovation · Genome Canada · Innovation, Science and Economic Development Canada · Québec · Ontario · British Columbia



CGEn is a Major Science Initiative of the Canada Foundation for Innovation

communications@cgen.ca

www.linkedin.com/company/cgen

www.cgen.ca