

2026 CANADA GAIRDNER AWARD WINNERS

Explore the science behind today's biggest
breakthroughs



ABOUT GAIRDNER

The mission of the Gairdner Foundation is to celebrate, inform and inspire scientific excellence around the globe.

Established in 1957, the Gairdner Foundation is dedicated to fulfilling James A. Gairdner's vision to recognize major research contributions to the treatment of disease and alleviation of human suffering. Through the prestigious annual Canada Gairdner Awards, the Foundation celebrates the world's most creative and accomplished researchers whose work is improving the health and wellbeing of people around the world. **The Canada Gairdner Awards are recognized internationally as being among the most prestigious in the world, based on our reputation for rigorous review and early recognition of breakthroughs in science.**

The Gairdner Foundation brings people together to openly discuss science in order to better engage the public, understand the problems we face, and work together to find solutions. Through Gairdner Connects, our national outreach program, we bring science to communities across Canada to inspire future innovators and spark public dialogue about the role of research in addressing the world's most pressing health challenges.

BY THE NUMBERS

5 CANADA GAIRDNER
International Awards
For excellence in biomedical research

2 PETER GILGAN CANADA GAIRDNER
Momentum Awards
For mid-career investigators with exceptional research

1 JOHN DIRKS CANADA GAIRDNER
Global Health Award
For outstanding achievements in global health research

443 AWARDS to scientists from over **40** countries

103
Gairdner awardees have gone on to win the **Nobel Prize**



20 CANADIAN UNIVERSITIES | ENGAGING **6000+** students and researchers annually through outreach programs that give Canadians access to world-renowned scientists



ABOUT THE COLLECTION

This article is part of a larger collection introducing the discoveries of the 2026 Canada Gairdner Award winners, among the world's leading biomedical and global health researchers. From the inner workings of our cells to new approaches to preventing disease and improving treatment, these stories explore research shaping the future of human health.

To explore the other stories in this series, [check out the full collection here](#). By viewing the full collection, you'll discover the science behind this year's award-winning research and explore big questions such as:

- How can viruses help us fight antibiotic-resistant bacteria?
- How can technology help regulate blood pressure after spinal cord injury?
- How can we stop misfolded proteins from causing disease?
- How can scientists identify, measure and study thousands of proteins?
- How can scientists use 3D images to see inside cells?
- How can oral vaccines help prevent cholera?

ABOUT THE CREATORS

Each article was written by Gairdner student intern **Leanne Cherry**, an undergraduate student at McGill University studying Cognitive Science and Communication Studies, and developed in collaboration with the Award winners themselves. Passionate about science communication, Leanne is interested in making research accessible and combating science and health misinformation.

The articles were also reviewed by the students from the **Canadian Association of Girls in Science (CAGIS)**, whose thoughtful feedback helped make these stories clear, accurate and engaging for young readers.

Illustrations were created by **Heather Ng-Cornish**, an illustrator and communicator based in Ontario. Heather brings her science communication experience to her illustrations, creating clear, colourful and accessible visuals that help bring scientific ideas to life. To see more of her work, visit www.heatherngcornish.com

The Gairdner Foundation is committed to sharing the excitement of discovery with people of all ages. We hope this collection sparks your curiosity, encourages you to ask big questions, and inspires you to imagine the discoveries still waiting to be made.



LEANNE
CHERRY



HEATHER
NG-CORNISH



PROTEOMICS:

HOW WE KNOW WHAT WE KNOW ABOUT PROTEINS

CANADA GAIRDNER INTERNATIONAL AWARD WINNERS

Prof. Ruedi Aebersold

Professor Emeritus, Molecular Systems Biology, Institute of Molecular Systems Biology, Department of Biology, ETH Zurich, Switzerland

Prof. Matthias Mann

Director of Department of Proteomics and Signal Transduction, Max Planck Institute of Biochemistry, Martinsried, Germany

Prof. John R. Yates III

John Lytton Young Endowed Chair and Professor, Department of Integrative Structural and Computational Biology, Scripps Research, La Jolla, United States

SUMMARY

Proteomics is the large-scale study of proteins, which aims to identify, quantify, and understand what proteins do across all species. A significant portion of the field's progress over the years can be attributed to the work of Drs. John Yates III, Ruedi Aebersold, and Matthias Mann. These researchers each focused on separate but related proteomics problems: Yates worked on identifying proteins, Aebersold worked on quantifying them, and Mann worked on understanding proteins in the context of medicine. Their techniques are now practiced in proteomics labs around the world and have greatly expanded our knowledge of proteins.

STUDENT REVIEWERS:



ARSHIA
Grade 10



CYNTHIA
Grade 10



JUNE
Grade 11



VALINI
Grade 11

At any given moment, there are approximately 10 trillion proteins in our bodies. Proteins are crucial for just about every aspect of our functioning, from providing structure to our muscles and organs to transporting messages and nutrients around the body. By uncovering what proteins do and how they function, proteomics researchers come closer to revealing how living systems work overall.

However, understanding how proteins work is no simple task. A single cell can contain approximately 8 billion proteins—roughly equal to the number of humans on Earth. Understanding the purpose, quantity, or state of any given protein can feel like searching for a needle in a haystack. Before researchers could begin to unravel proteins' many mysteries, they needed to have the right tools to do so.

Drs. John Yates III, Ruedi Aebersold, and Matthias Mann have each made immense contributions to proteomics, developing laboratory techniques to analyze, measure, and categorize proteins that inform much of what we know about proteins today. Researchers ask many different questions about proteins, but Yates, Aebersold, and Mann focused on three of the most pressing: How can we analyze and categorize proteins in large numbers? How can we accurately measure the total number of proteins in a sample? And how can we use this data to understand how proteins function in living beings?

BEFORE YATES, AEBERSOLD, AND MANN'S KEY DISCOVERIES

One of the first problems that proteomics researchers solved was that of rapidly uncovering a protein's amino acid sequence—the unique chain of chemical building blocks that make up a protein. Proteins that differ by even a single amino acid can have completely different functions and purposes in an organism, so knowing a protein's amino acid sequence is useful for identifying it and figuring out how it works.

Traditionally, proteins needed to be isolated from each other to be able to sequence their amino acids. In the 1970s and '80s, this was mainly accomplished using a technique called **two-dimensional gel electrophoresis (2DGE)**, which allowed scientists to take a complex mixture of proteins from a cell and separate them according to the **mass** and **electric charge** of each individual protein (**Figure 1**).

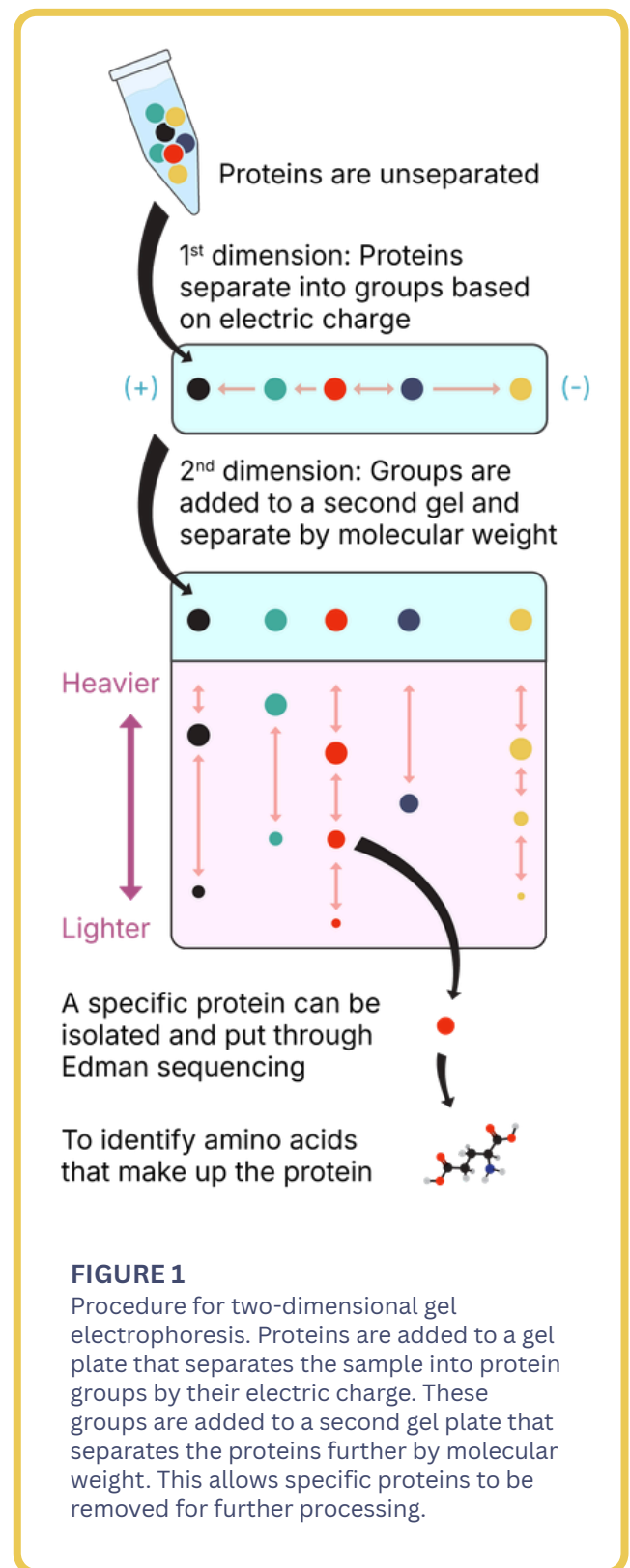


FIGURE 1

Procedure for two-dimensional gel electrophoresis. Proteins are added to a gel plate that separates the sample into protein groups by their electric charge. These groups are added to a second gel plate that separates the proteins further by molecular weight. This allows specific proteins to be removed for further processing.

MASS

A fundamental property that determines how much matter is present in an object.

ELECTRIC CHARGE

A fundamental property that determines how matter will behave in an electric field. Matter's charge is influenced by the ratio of positively and negatively charged particles it carries. Opposite charges attract whereas like charges repel.

The result of running 2DGE on this large collection of proteins would be an array on a gel comprised of thousands of different spots, each one containing one or several proteins of a particular mass and electric charge.

From there, scientists could remove the spot from the gel and use a technique called **Edman degradation sequencing** to uncover its amino acid sequence. Edman sequencing was the first major advance for protein sequencing as it automated a process of sequentially removing amino acids from the front of a protein. By removing amino acids one at a time you could learn the sequence of the protein. When used on an intact protein, Edman sequencing could reveal the first 25-30 amino acids of the protein's sequence.

These techniques were not perfect. While 2DGE was good at separating proteins with stark differences in mass and charge, there are many kinds of proteins with similar mass and charge that have different identities. These frequently ended up in the same spot on a 2DGE gel, making it difficult to figure out an individual protein's amino acids using Edman sequencing. Even when you were able to get a relatively pure protein spot from 2DGE, Edman sequencing was painstakingly slow and labour intensive. Furthermore, about half of all human proteins have a modification on their first amino acid that prevents Edman sequencing from being carried out.

A major advance in protein sequencing was the use of a technique called **tandem mass spectrometry** (aka **MS/MS**). A mass spectrometer—the instrument used for MS/MS—measures the mass and electric charge of molecules, allowing scientists to identify them. When MS/MS was first used for protein sequencing, researchers would often begin by separating proteins with 2DGE. They would then choose a particular spot from the 2DGE plate, and break its proteins down into smaller pieces called **peptides**. These would be analyzed by MS/MS.

MS/MS blasts the peptides with a gas that breaks the peptides into fragments of different masses and electric charge. These fragments form a distinct pattern, effectively becoming a peptide's fingerprint (**Figure 2**). The pattern can be interpreted to identify the peptide, and by analyzing all the peptides created by digestion of the protein, the sequence of the intact protein can be reassembled like a jigsaw puzzle.

Peptides and proteins are both fundamentally the same thing: a chain of amino acids. They differ mainly in term of size and structure. Peptides are smaller (2-50 amino acids), whereas proteins are larger (50+ amino acids) and fold into more complicated structures.

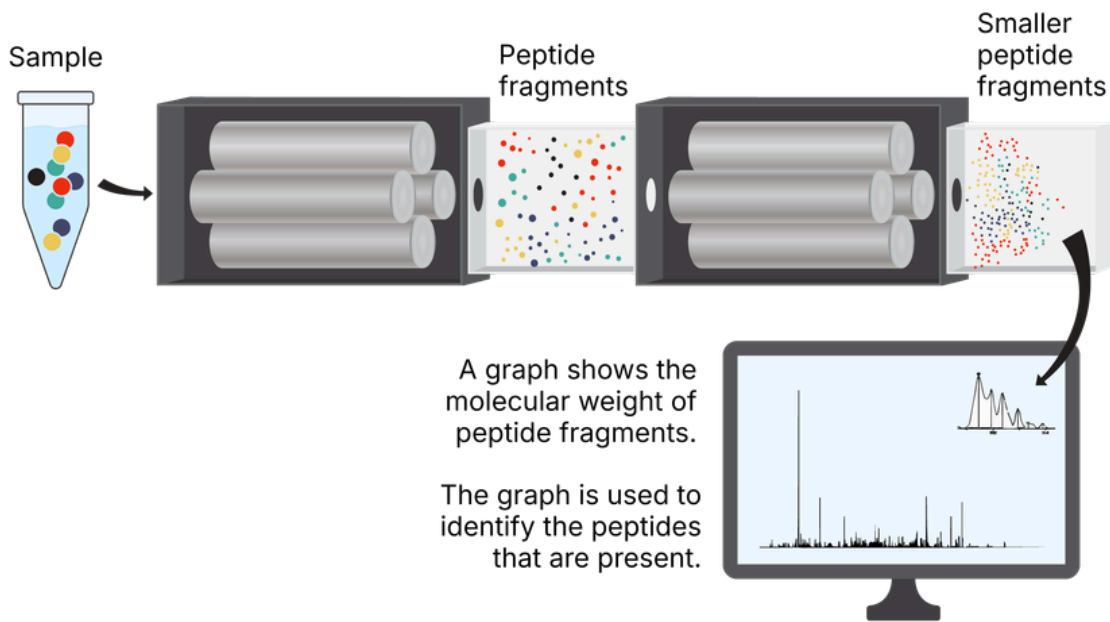


FIGURE 2

A tandem mass spectrometer. “Tandem” means “two” mass analyzers. The sample moves through the first mass analyzer to produce fragments. The fragments pass through a second mass analyzer to produce even smaller fragments. The mass of these fragments is read by a computer, which provides information on the peptides that are present in the sample.

JOHN YATES: IDENTIFYING PROTEINS AT SCALE

Yates has made many important contributions to the field of proteomics, but the most groundbreaking of these has to do with his use of MS/MS.

MS/MS sequencing experiments produce many peptide fragmentation patterns, and researchers were initially stuck manually interpreting these patterns to identify each peptide derived from their protein of interest. This process was time-consuming and difficult. To make this more efficient, Yates drew data from a massive scientific endeavour that began in the early 1990s: the **genome** sequencing projects.

At this time, researchers around the world were attempting to sequence the genomes of various model organisms, including humans. Yates recognized that these emerging genomic databases could provide the missing key to uncovering peptides’ amino acid sequences.



John R. Yates III

GENOME

The complete set of an organism’s genetic information (DNA). It acts as the master blueprint, containing all the instructions needed to build and maintain that organism, including the templates for every protein it can produce.

Using genome data, we can generate an image of how a peptide might fragment in a theoretical MS/MS experiment. Because the image is generated directly from the genome data, we would also know the amino acid sequence associated with this theoretical fragmentation pattern. Yates created **SEQUEST**, a computer algorithm that matched *real* MS/MS peptide data against this *theoretical* peptide fragmentation pattern created from genome sequence data.

SEQUEST made it so that researchers didn't have to sequence a protein's entire amino acid sequence to identify it. Rather, they could observe a few of its peptide fragments and the algorithm would match the fragments to a known protein in the genome sequence database. Overall, this made it much easier for researchers to identify all the proteins in a sample.

Even with SEQUEST though, MS/MS had yet to reach its full potential. Many proteomics researchers were still using 2DGE as a precursor to mass spectrometry analysis, which still had the problem of containing multiple proteins in each sample. Moreover, analyzing individual spots one at a time was slow. This made it particularly hard to identify large numbers of proteins from the gel and to find the less abundant proteins of a sample. For example, if you had 1000 copies of protein A and only 10 copies of protein B but both proteins had the same mass and charge, mass spectrometry analysis may only pick up the fragments of protein A, meaning you might miss B entirely. To get over these hurdles, Yates introduced a new approach that removed the use of gel electrophoresis to separate proteins.

In the Yates approach, an entire mixture of proteins are broken down to produce a complicated mixture of peptides. The peptides are then separated by a technique called liquid chromatography, which is faster and more sensitive than 2DGE. It also allows peptides to be introduced directly into the mass spectrometer, almost as though they are on a conveyer belt. As each peptide enters the mass spectrometer it identifies its mass and then performs MS/MS on the peptide. Yates and others also developed software tools to automate the process of MS/MS to make it more efficient.

Yates's technique is known as **shotgun proteomics**, and it has been indispensable in allowing scientists to identify and categorize large numbers of proteins from complicated biological samples. Shotgun proteomics significantly expanded the ability to perform large studies of proteins, cells, and tissues, and ultimately helped to establish proteomics as a field.





Ruedi Aebersold

SUBATOMIC COMPONENTS

The building blocks of atoms themselves, such as protons, neutrons, and electrons. The number and ratio of subatomic components in an atom determines its chemical and physical properties as well as its overall identity.

PHYSICAL PROPERTY VS. CHEMICAL PROPERTY

A **physical property** is a quality of a substance that we can observe without changing its identity, such as its colour or its state at room temperature. For example, hydrogen is a colourless gas.

A **chemical property** is a quality of a substance that we can observe in a chemical reaction, which typically alters its identity. For example, hydrogen reacts quickly and aggressively with oxygen gas and produces water.

RUEDI AEBERSOLD: ACCURATELY COUNTING PROTEINS

After you have figured out *which* proteins are in your sample, you still have to figure out *how many* of them there are. Quantifying proteins is especially important for studying the role they play in diseases. For example, a cancerous cell may produce the exact same kind of proteins as a healthy cell, but it may produce 10 times more of a growth protein that makes it toxic.

While MS/MS does tell us how abundant a particular peptide is, the measurement device catches some fragments much more easily than others. This can make it challenging to accurately count all the peptides in a sample. To overcome this, Aebersold made use of a concept from chemistry: **isotopes**. An atom becomes an isotope when there is a change to its number of neutrons—one of its key **subatomic components**. While isotopes act the same way as standard atoms in a chemical reaction, they have slightly different **physical properties** which we can track in mass spectrometry data.

In 1999, Aebersold introduced a technique called Isotope-Coded Affinity Tagging (ICAT), creating chemical tags that could be attached directly to peptides. Aebersold tagged the peptides from a healthy cell with a “light” isotope tag using a standard carbon atom, and he tagged the peptides from a diseased cell with a “heavy” isotope tag using a carbon atom with an extra neutron. He then mixed the samples together and ran them through a shotgun proteomics procedure. The light and heavy peptides are shown to have the same charge, but because of the extra neutron, the peptide from the diseased cell has a slightly higher mass. As a result, the heavier peptide shows up shifted slightly to the right of the light peptide on the mass spectrometry graph.

For the first time, scientists could compare relative quantities of the same proteins in different cells—all thanks to Aebersold’s introduction of the isotope tag.

Aebersold also helped overcome some of the limits of shotgun proteomics. He realized that, while it was great for scanning a lot of peptide fragments blindly, sometimes scientists needed a more focused tool. To address this, his lab pioneered **targeted proteomics**. Rather than analyzing millions of peptides fragments, a researcher could program the measurement device of a mass spectrometer to look for a specific set of disease-linked proteins with razor-sharp precision. This breakthrough was so impactful that the journal *Nature Methods* named targeted proteomics its “Method of the Year” in 2012.



Aebersold's final masterpiece was a targeted strategy called **DIA-SWATH MS**, building on a technique called Data-Independent Acquisition (DIA), which had been proposed by Yates a few years earlier. DIA-SWATH MS allowed scientists to turn a tiny clinical sample like a drop of blood into a permanent digital time capsule representing every measurable protein in the sample. Decades from now, if a scientist discovers a new protein linked to a disease, they don't need a new blood sample—they can just open Aebersold's digital file and check if that protein was there all along.



Matthias Mann

Nano-ESI made proteomics accessible to virtually all biologists and biochemists, because now they only needed a tiny speck of biological material to run an experiment.

MATTHIAS MANN: DETECTING PROTEINS IN THE SMALLEST BIO-SAMPLES

With Yates solving how to identify proteins, and Aebersold solving how to count them, the final puzzle piece belonged to Mann. Mann was responsible for making the measurement sensitive enough to work on real biological material. While earlier methods needed large, highly purified samples, Mann's tools brought proteomics down to the scale of a speck of tissue, a drop of blood, and eventually a single cell. These developments allowed proteomics to be used where it counts most: in human biology and medicine.

Mann completed his PhD under John Fenn, the Nobel Prize-winning scientist who invented Electrospray Ionization (ESI). This method is used to turn liquid biomolecules into an airborne gas so the mass spectrometer can analyze them. Mann adapted his mentor's Nobel Prize-winning technique by shrinking it down and developing **nano-electrospray ionization (nano-ESI)**, which allowed the mass spectrometer to analyze microscopic droplets of liquid.

Before Mann, you needed massive, highly purified biological samples to get a reading. With nano-ESI, the machine became so sensitive that it could sequence proteins in femtomole amounts—a scale far below what previous proteomics techniques could reach.

Like Yates and Aebersold, Mann also pioneered a kind of software for proteomics. His was called the “**peptide sequence tag**” approach, which was one of the first computational methods to instantly identify peptides and their chemical modifications directly from tandem mass spectra by matching them against genome databases. Later, his lab created **MaxQuant**, which remains one of the most widely-used software tools for analyzing raw mass spectrometry data today.

Mann then revolutionized quantitative proteomics with a method called **SILAC**. Rather than attaching tags to peptides after harvesting them (like Aebersold’s method), Mann fed the isotope labels directly to living cells in a petri dish, so that the cells built the labels into their own proteins as they grew. This made comparing and quantifying proteins in living cells far simpler. It also enabled a landmark: using SILAC, Mann’s group completed the first analysis of a complete proteome, identifying and quantifying every protein in living yeast cells. This was the first time the full protein complement of any organism had been measured.



Mann’s methods are on the way to being used heavily in biomedicine and medical practice. If a patient is sick, doctors will take a microscopic slice of tissue or a tiny finger-prick of blood, run it through Mann’s high-speed workflows, and screen their entire proteome in real-time to design personalized medical treatments.

Mann’s lab has also pushed proteomics into intact tissue. In 2022, it introduced Deep Visual Proteomics (DVP), which could extract single cells from a tissue slice and read their full protein content without losing spatial context. DVP has several medicinal applications, whether it is zooming in on cancer cells within otherwise healthy tissue or finding a new use for an existing drug. DVP helped launch spatial proteomics as a field, and Nature Methods named it Method of the Year for 2024—a decade after Aebersold’s targeted proteomics received the same honour.

BUILDING THE FUTURE OF PROTEOMICS

Science rarely moves forward because of a single breakthrough; it progresses when independent findings come together and push us towards new discoveries. John Yates III gave the mass spectrometer the ability to identify proteins, automating how we read a protein's structural fingerprint and organizing peptide fragments with liquid chromatography. Ruedi Aebersold gave the machine the ability to quantify proteins, using isotope chemistry to precisely count fluctuating protein levels and shifting the world of proteomics into an open-access digital era. And Matthias Mann gave the machine the sensitivity to work on real biological material, shrinking the required sample down to microscopic droplets, providing the software tools necessary to map out entire living proteomes, and more recently letting clinicians read a single cell's proteome straight from tissue or blood.

Together, these three pioneers transformed proteomics from a pipe dream into a cornerstone of modern biology, changing how we understand life, health, and disease forever.

Article written by Leanne Cherry

Illustrated by Heather Ng-Cornish

This article has been reviewed by Drs. Ruedi Aebersold, Matthias Mann & John Yates and colleagues for accuracy and accessibility.

MEET THE SCIENTISTS:



Ruedi Aebersold is a Swiss-Canadian scientist and a pioneer in the field of proteomics. He held faculty positions at the University of British Columbia and the University of Washington before co-founding the Institute for Systems Biology in Seattle. In 2004, he joined ETH Zürich, where he established the Institute of Molecular Systems Biology. His research group developed widely used technologies, software and statistical tools for studying the proteome, helping make proteomic research more accurate, reproducible and accessible. His work has received numerous international honours, including the Marcel Benoist Swiss Science Prize and the 2024 Heineken Prize for Biochemistry and Biophysics.



Matthias Mann is a pioneer in mass spectrometry-based proteomics. He studied physics and mathematics at Göttingen University and completed his Ph.D. at Yale University, where his work contributed to the development of electrospray ionization for large biomolecules. Throughout his career, he has developed foundational technologies and computational methods for identifying and measuring proteins, including approaches now widely used in proteomics research. Since 2005, he has led the Department of Proteomics and Signal Transduction at the Max Planck Institute of Biochemistry in Munich. His many international honours include the Leibniz Prize, Louis-Jeantet Prize for Medicine and 2024 Heineken Prize for Biochemistry and Biophysics.



John R. Yates III is a pioneer in mass spectrometry-based proteomics and a professor at Scripps Research. He earned his Ph.D. in Chemistry at the University of Virginia, where he studied protein sequencing using tandem mass spectrometry, before completing postdoctoral training at Caltech. Yates is the lead inventor of SEQUEST, software that helps identify proteins by matching mass spectrometry data with sequences in protein databases, and a principal developer of shotgun proteomics for analyzing complex protein mixtures. His laboratory continues to develop proteomic technologies for investigating proteins and biological systems. His work has been recognized with numerous international awards in analytical chemistry and proteomics.

We wish to thank Profs. Aebersold, Mann, and Yates and their collaborators for their input in this article.



YOUTH ACCESSIBILITY REVIEW

This article was reviewed by high school students through the Canadian Association for Girls in Science (CAGIS)—Canada’s largest and longest-running STEM (science, technology, trades, engineering, and math) club for girls and gender-diverse youth aged 7-17. This award-winning club, founded in 1992, supports interest in STEM with virtual programming and local clubs that visit labs, workshops, and field sites to meet mentors and do fun, hands-on activities. Their thoughtful feedback on clarity, accessibility, and reader engagement helped shape the final version of this article and ensure it is engaging and accessible for youth readers.



Arshia Nair • Grade 10

“I am interested in the science of neurodegenerative diseases, which fuels my desire to pursue a career in healthcare.”



Cynthia Rayson • Grade 10

“I hope to study biomedical engineering and develop new dental technologies to enhance patient care.”



Valini Parasram • Grade 11

“In the future I hope to study chemistry and its nuclear applications.”



June Liu • Grade 11

“I aspire to pursue a career in healthcare or biomedicine with a focus on applied research and potentially business, re-imagining the way we approach real world issues with practical and innovative solutions.”

GAIRDNER CONNECTS

Gairdner Connects brings award-winning scientists to communities across Canada to engage, inspire, and spark dialogue. In doing so, it fosters meaningful connections between Gairdner Award winners and the next generation of researchers. **Through interactive events, classroom visits, community discussions, and digital resources, we inspire future innovators and spark dialogue about the role of science in addressing global health challenges.**

This article, developed in partnership with the **Canadian Association for Girls in Science (CAGIS)**, is part of the Gairdner Foundation's student outreach program to bring science to communities across Canada.

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