

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



ZOOMING IN ON BIOLOGICAL MOLECULES: A NEW PERSPECTIVE

DR. WOLFGANG BAUMEISTER

CANADA GAIRDNER INTERNATIONAL AWARD WINNER

Director Emeritus and Scientific Member, Max-Planck-Institute of Biochemistry, Martinsried, Germany; Distinguished Professor, ShanghaiTech University, China

SUMMARY

Wolfgang Baumeister developed a technology called cryo-electron tomography which allows researchers to see the 3D structure of the inside of a cell. This method involves flash-freezing cells when they are active and using a beam of electrons like a camera to capture the cell from multiple angles. The result is a detailed 3D image that reveals how molecules interact and come together to form the cell's inner machinery. Traditionally, scientists studied just one part of a cell at a time. Baumeister's technology allows researchers to see how these parts fit together, giving us a much clearer picture of how cells are organized and function.

STUDENT REVIEWERS:



ADRIENNE
Grade 11



DEEPA
Grade 11



RANEEM
Grade 12



VIENNA
Grade 12

Cells are the foundation of life on Earth. Despite their microscopic size, they are incredibly complex living systems which depend on numerous internal components to function. We have been exploring how cells are built since the late 1800s, and this work continues today within the field of structural biology.

A cell's structure can reveal key information about its role in disease or how we could use it to improve our medications. However, structural biologists face a major challenge: most cells are so small that they are invisible to the naked eye. To overcome this, we have had to develop highly innovative imaging techniques.

For Dr. Wolfgang Baumeister, a scientist at the *Max Planck Institute of Biochemistry*, his greatest achievement was developing a groundbreaking new imaging technique called **cryo-electron tomography (cryo-ET)**.

This method allows us to generate clear and accurate 3D models of cells and their components in their natural state. Baumeister's advancements have established cryo-ET as an essential tool in structural biology. His work enables us not only to visualize a cell's individual components, but also to paint a picture of how these components come together and form a living being. Altogether, Baumeister has provided crucial insight into the structure of the most fundamental unit of life.

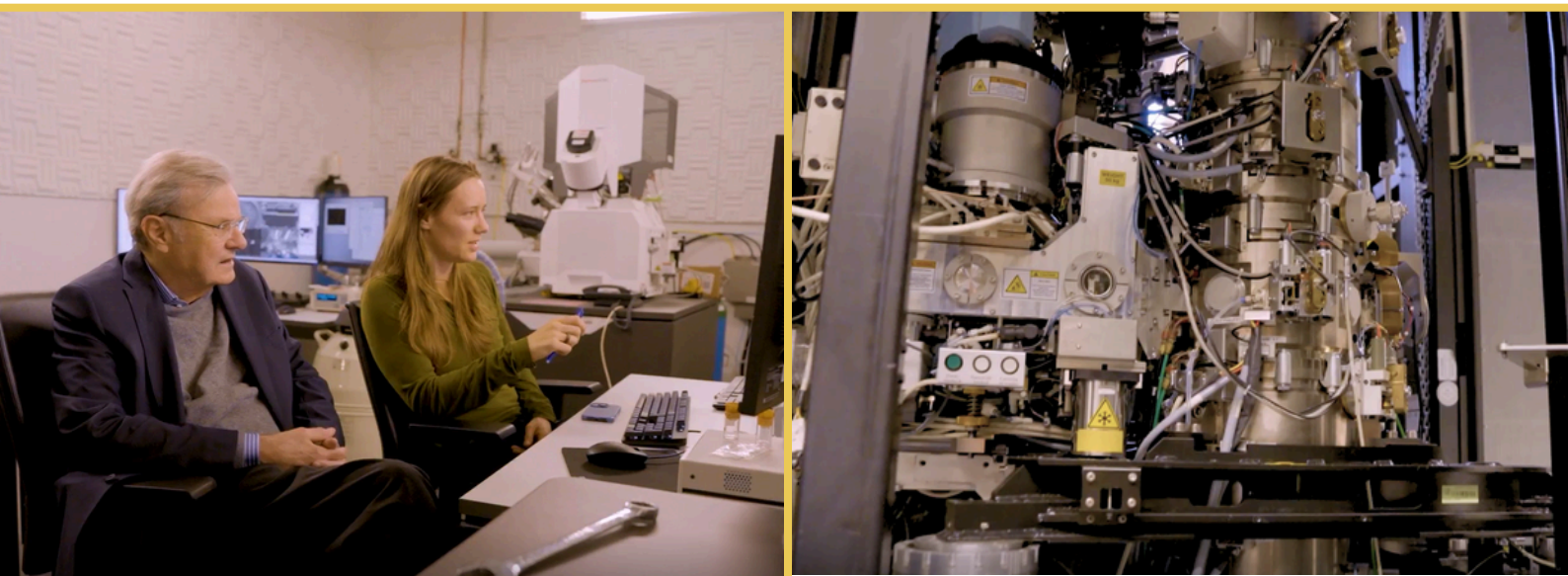
A BRIEF HISTORY OF BIOMOLECULE IMAGING

For most of structural biology's history, we used a technique called **X-ray crystallography** to visualize proteins and other small biological molecules. This technique works by creating millions of copies of a particular protein and arranging them into a crystalline structure—a repeating, symmetric arrangement of molecules which forms a solid crystal. We then direct X-rays at the crystal, and as the rays pass through it, they scatter in different directions depending on the protein's structure. By analyzing these scattering patterns, we can reconstruct a 3D model of the individual protein.

Like any laboratory technique, X-ray crystallography has its limits. Generally speaking, X-rays can only be used to visualize proteins when the proteins are arranged into a larger structure such as a crystal. An individual protein molecule usually cannot scatter the X-rays enough to create a pattern that we can interpret. One of the major problems with X-ray crystallography is that not every biological molecule can readily form a crystal. Determining which proteins can form crystals, along with creating the ideal conditions for the crystallization process, is incredibly difficult.

Moreover, even for proteins that crystallize easily, X-ray crystallography requires that we obtain a highly purified sample, one which contains millions of copies of the protein we want to image. This is to ensure that the resulting protein crystal produces a scattering pattern which accurately reflects the protein's structure. Many purification techniques change the structure or composition of a molecule, and this puts us at risk of losing crucial information during our experiments.

After working with X-ray crystallography for many years, Baumeister became well-acquainted with these challenges. He began to think about new ways of approaching structural biology problems—as did other scientists in the field.



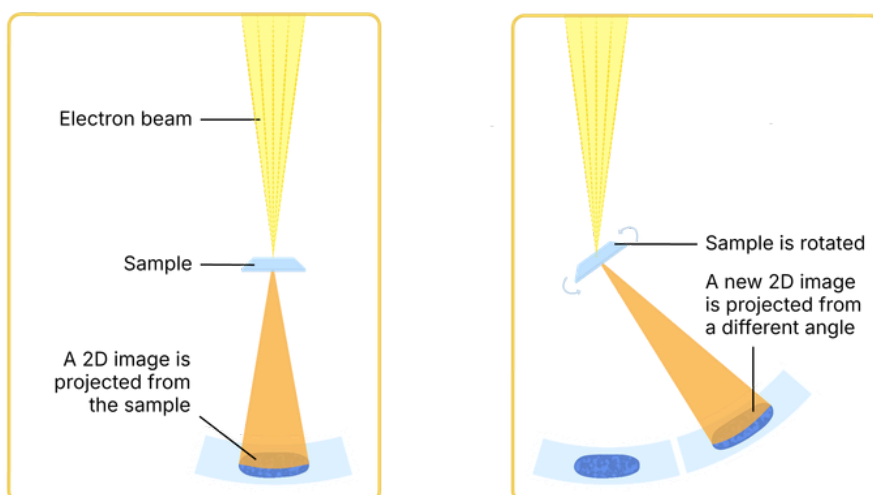
INTRODUCING CRYO-ET

In the 1970s, scientists developed cryo-electron microscopy (cryo-EM), a breakthrough imaging technique that captured flat, two-dimensional views of isolated molecules and earned the 2017 Nobel Prize in Chemistry. Baumeister later built on this technology by developing **cryo-electron tomography (cryo-ET)**, which allowed us to create detailed 3D images of cells in their natural state.

Rather than using X-rays, cryo-ET directs a beam of electrons at a biological sample, such as a cell or one of its many components. Because electrons interact strongly with matter, they can image a molecule's structure with incredible precision. However, this intense interaction also makes the beam likely to cause **radiation damage** to the sample.

To keep the cells hydrated and to minimize the damage, we plunge the sample into a liquid cooled to about -180°C . When water freezes, its molecules typically rearrange into a rigid, crystalline structure. This is how liquid water becomes solid blocks of ice. However, the method used in cryo-ET freezes our sample via a different process called vitrification, which solidifies our sample's molecules in place without allowing rigid ice crystals to form. By preventing the molecules from rearranging into ice crystals, the sample is essentially frozen in time, meaning we can observe it while it is close to its natural state. The vitrification process also protects the sample from the energy of the electron beam.

When the electrons pass through the biological sample, they leave a shadow that reflects the sample's internal and external structure (**Figure 1**). We rotate the sample several times so that we can send electrons through it from many different angles. Each shadow that the high-energy beam leaves behind shows us the sample's molecular structure from a slightly different perspective, just as though we were photographing an object from multiple positions (**Figure 2**). From there we can compile the images and compute a 3D model of our sample (**Figure 3**).



RADIATION DAMAGE

The process by which beams of particles or waves alter the atomic structure of a target. In structural biology, these beams break the chemical bonds holding a molecule together, which can distort or destroy the sample before an image can be captured.

FIGURE 1

An electron beam passes through the sample which projects a two-dimensional image of a cell.

FIGURE 2

The sample is rotated, allowing the electron beam to project an image of the cell from a different angle.

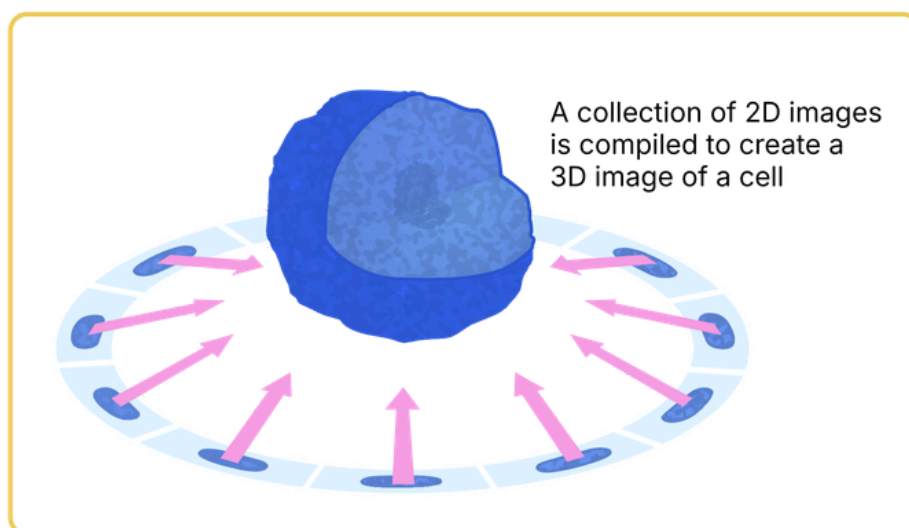


FIGURE 3
Many two-dimensional images are taken of the cell. This collection is used to create a three-dimensional representation of the cell.

ADVANTAGES OF CRYO-ET

Baumeister's technique provided several important advantages over earlier methods of imaging cells. Like X-ray crystallography, the original cryo-EM methodology also suffered from needing incredibly pure samples of a biological molecule, as it needed many copies of the same molecule frozen in different orientations to render a 3D model.

Cryo-ET is a different story. Because we rotate the sample to capture it from different angles, this technique only requires a single copy of the sample to visualize its 3D structure. As a result, we are not limited to molecules that need to form a crystalline structure to be seen or undergo a harsh purification process. We can therefore use cryo-ET to uncover the structure of whole, individual cells—along with all of their internal components—while they are still in their native state.

Previously, we approached structural biology problems by isolating individual components of a cell and trying to capture what they looked like. With cryo-ET, we can observe a cell in its near-natural environment, allowing us to produce a much more accurate model of its structure and gain insight into how it functions.

DEVELOPING CRYO-ET

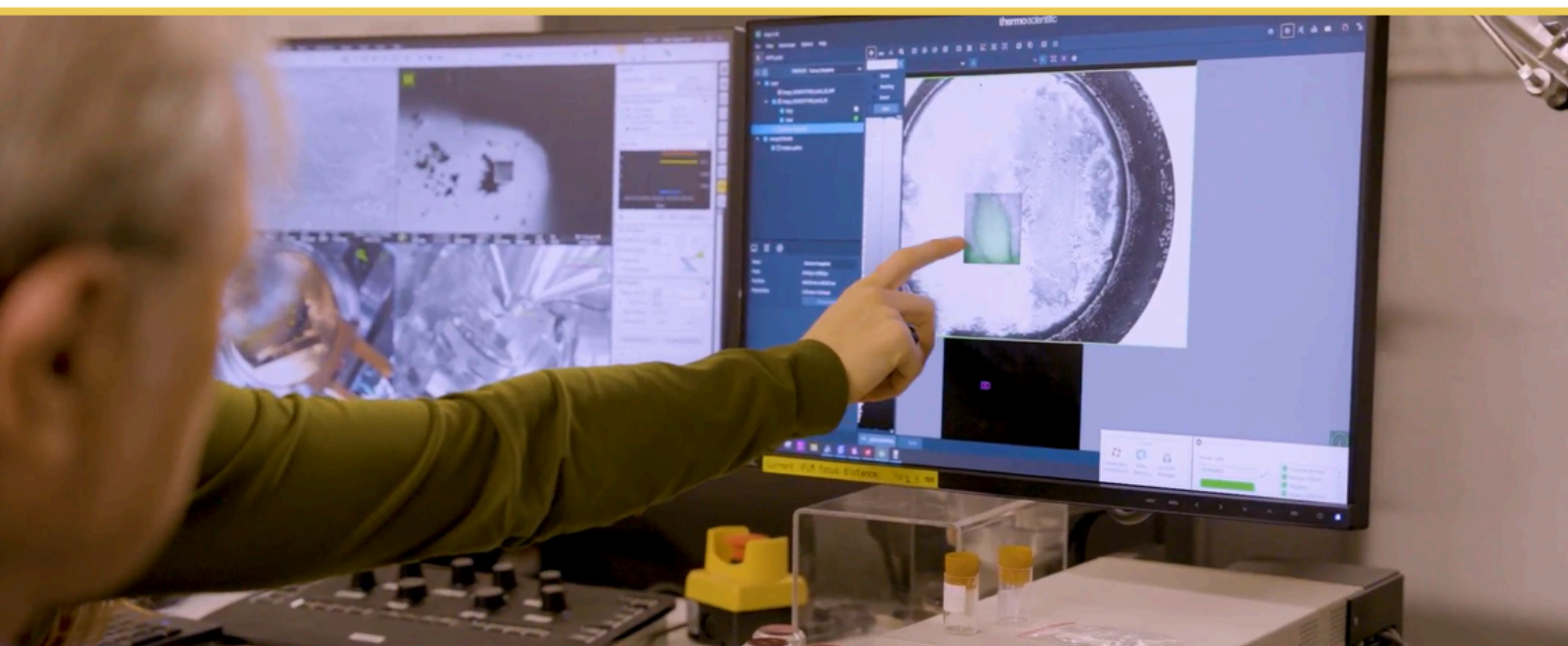
While cryo-ET is incredibly powerful today, it would never have gotten to where it is now without Baumeister's career-long devotion to its advancement. He had to overcome hurdle after hurdle, not only to refine the technology, but to prove that it could be used to solve structural biology problems in the first place.

Electron microscopy—the technique that first enabled us to image tiny structures using a beam of electrons—was initially designed to be operated and adjusted manually. With the help of a computer, we would position the sample, focus the electron beam, and shoot the sample to capture a 2D image. However, cryo-ET, which also uses an electron beam, requires the sample to be shot from around 100 different angles. At one point, this meant we had to manually reposition and recentre the biological sample before every image. This process was not only time-consuming, but also increased the risk of introducing errors and causing radiation damage.

Knowing the limitations of manual cryo-ET, Baumeister developed software and hardware that helped to automate this process. He also developed technology to help keep the electron dose within tolerable limits, thereby minimizing radiation damage.

Even after making the technique easier to use, Baumeister still had to demonstrate just how useful cryo-ET could be. The vitrification technique used in cryo-ET today was first used for the Nobel-Prize-winning cryo-EM. On his quest to demonstrate cryo-ET's utility, Baumeister used cryo-EM's solidification technique to image *Dictyostelium*—a tiny, single-celled organism. *Dictyostelium* cells are incredibly thin, making them ideal for cryo-ET trials because electrons can pass through them without much trouble. Baumeister's work with this organism proved definitively that cryo-ET could visualize the internal structure of cells, all the way down to the scale of five nanometres—which is over ten thousand times smaller than a human hair.

Baumeister's work also greatly increased the range of cells we could examine using cryo-ET. As mentioned, cryo-ET is best suited for thinner samples. However, many of the cells that we are interested in, such as human cells, are too thick to be put through a cryo-ET procedure in their native state. To overcome this hurdle, Baumeister adapted an existing technology called **focused ion beams (FIBs)** to help make cells thinner. Essentially, FIBs allow us to make razor-thin slices of a biological sample directly out of tissues and organisms. We can then use cryo-ET on each of the tissue slices to render a 3D model of the tissue's structure. Baumeister's innovative use of FIBs gave us the opportunity to image practically any biological sample we could think of; the possibilities became endless.



The algorithm provides so much clarity that it can identify individual structures found within the cell which carry-out essential cellular functions.

Additionally, Baumeister and his team created a computer algorithm that helps clarify the images taken during a cryo-ET procedure. Because cells are so complex and densely organized, cryo-ET images can look very busy when they are first taken. Moreover, while the electron beam is essential for capturing images, it can also introduce noise and irregularities into our images, making image processing even more difficult. Baumeister thus created a **denoising algorithm for cryo-ET**, which was the first of its kind to both remove the unnecessary information added by the electron beams and preserve structural information of the cell.

BAUMEISTER'S OWN DISCOVERIES USING CRYO-ET

Beyond all of the work that he did to improve cryo-ET as a technology, Baumeister made many important structural biology discoveries through his own use of the technique. The bulk of his research focused on the **proteasome**—the structure within cells responsible for breaking down damaged or faulty proteins.

Over the course of his career, Baumeister has revealed much of the proteasome's structure, beginning with a few particles and eventually rendering the whole thing. Proteasome malfunction is thought to play a role in many diseases such as Alzheimer's and Parkinson's, and understanding how the proteasome is built can help us figure out how to help it when it stops working. Since his work on the proteasome, he has gone on to image several other important molecular machines within cells.

Baumeister's dedication and contributions to the field of structural biology cannot be overstated. Thanks to his career's worth of effort to pioneer, refine, and apply cryo-ET, Baumeister has given us a glimpse into the structure of life itself.

Article written by Leanne Cherry

Illustrated by Heather Ng-Cornish

This article has been reviewed by Dr. Wolfgang Baumeister and colleagues for accuracy and accessibility.



MEET THE SCIENTIST: Dr. Wolfgang Baumeister

Wolfgang Baumeister is a German biophysicist and a pioneer in structural biology. He studied biology, chemistry and physics and earned his Ph.D. in Biophysics from the University of Düsseldorf. In 1982, he joined the Max Planck Institute of Biochemistry, where he later became Director of the Department of Structural Biology. Baumeister and his team have developed and advanced electron microscopy techniques that allow scientists to study the molecular structures inside cells in remarkable detail. His work has transformed how researchers investigate the organization and function of cells. His many international honours include the Louis-Jeantet Prize for Medicine and the 2025 Shaw Prize in Life Science and Medicine.



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.



Adrienne Ma • Grade 11

"I hope to pursue a career in optometry to combine my love for helping others and my fascination for the human eye."



Raneem Salah • Grade 12

"I'm excited to study human biology and find ways to impact society using that knowledge!"



Deepa Kalia • Grade 11

"I hope to combine my love of technology with my passion for business and explore how technology can be used to create innovative solutions and opportunities."



Vienna Cipparrone • Grade 12

"I am intending on studying neuroscience and psychology, and I want to explore how psychological disorders affect brain structure and function."

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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