movement. The goal was "to hit pause, to give Black academics a break and to give others an opportunity to reflect on their own complicity in anti-Black racism in academia and their local and global communities", said one of the groups organizing this event. Time-sensitive research on COVID-19 was able to continue.

Many are exhausted by the stream of gut-wrenching news. Cassandra Extavour, an evolutionary and developmental biologist at Harvard University in Cambridge, Massachusetts, said that reports of police brutality and killings alongside the systemic racism in her field test her will to stay in science.

"Every time one of us is rejected, beat down, dismissed, ridiculed or murdered, I question why I am still in academia," she wrote in a series of tweets. "I answer my question by asking myself if today will be the day that another black scientist leaves the field, is pushed out by the toxicity that we have to wade through every day so we can 'be productive' and 'just think about science.' I answer, 'Not today.'"

Critical messaging

Over the past week, scores of universities and scientific societies joined organizations of every stripe in issuing statements about the civil unrest in the United States. Some faced criticism that they had missed the mark. For example, several chemists pointed out that the American Chemical Society (ACS) in Washington DC left out key words, such as "Black", "police brutality" and "racism", in a statement released on 1 June, and took issue with the way that the statement criticized the use of violence during the protests themselves. In doing so, they argued, the society missed the core drivers of the current movement and failed to acknowledge the pain its Black members were experiencing. According to some analyses, Black Americans are killed by police at more than twice the rate of white Americans.

Glenn Ruskin, vice-president for external affairs and communications at the ACS, says that the society followed that "initial response" with a video message from ACS president Luis Echegoyen. "In this message, we condemn racism, stand in solidarity with our Black and Brown members and commit ourselves to using our resources to addressing issues of racism in all its manifestations," Ruskin says.

Many scientists challenged organizations to back up their statements with actions that support or elevate Black scientists, including sharing their figures on diversity and ensuring that they hire staff members from diverse backgrounds. Some spelt out steps that institutions could take.

"Although it's great that universities have made public statements condemning racism, it is important for those statements to include a specific list of anti-racist actions they're planning to take to support their Black students, faculty and staff, such as increasing recruitment and retention efforts, supporting African American Studies programmes and anti-racism education, and providing more funding to support Black faculty and students," says Jioni Lewis, a psychologist who studies discrimination and mental health at the University of Tennessee, Knoxville.

Advice to allies

Lesley Weaver, a cell biologist who is about to take up a post at Indiana University in Bloomington, suggested that scientific institutions and societies should ensure that they include people from minority ethnic groups as editors, reviewers and authors of peer-reviewed papers; that they give students, staff and faculty members regular diversity and inclusion training; and that they make diversity sessions at major conferences main events, rather than side acts that must compete for attention with concurrent sessions. "If academia wants to support Black scientists, they'll train and support them instead of using black bodies for a number quota," Weaver wrote. "If academia wants to support Black scientists, it won't take another senseless death and uprising for it to be clear that Black lives matter."

> **"We appreciate you reaching out, but we'd appreciate it more if you helped us put the fire out."**

Addressing her own field of cell biology, she suggested ending the use in research of HeLa cells, the extraordinary cell line that doctors at Johns Hopkins Hospital in Baltimore, Maryland, took and cultured without permission from Henrietta Lacks, a poor Black woman, in 1951.

Jasmine Abrams, a behavioural scientist at Boston University School of Public Health in Massachusetts and Yale School of Public Health in New Haven, Connecticut, similarly tweeted ways scientists could be allies to Black colleagues: "Drop our names for special opportunities or hires. Post about our work on your social media. Cite us in your papers. Vote in favor of our contract renewals, tenure, and promotion." Abrams continued: "Say something (instead of secretly coming by our office later) in the faculty meeting, hallway, or classroom when a colleague or student says/does something implicitly or explicitly racist." The challenges that Black scientists face — and that white colleagues are now seeing — aren't new, she added. "Keep in mind that the plantation has been on fire for us and that for most, it is a legit daily struggle to do our work. We appreciate you reaching out, but we'd appreciate it more if you helped us put the fire out."

Amid the maelstrom, Bianca Jones Marlin, a neuroscientist at Columbia University, posted a video message addressed to other Black scientists. She spoke out loud something she wished she'd heard at difficult times in her past: "That your presence in science is important, that your purpose in science is seen," she said. "I'm here to hear your stories. Because I get it."

Additional reporting by Giuliana Viglione

REVOLUTIONARY MICROSCOPY TECHNIQUE SEES INDIVIDUAL ATOMS

Cryo-electron microscopy feat will allow the workings of proteins to be probed in unprecedented detail.

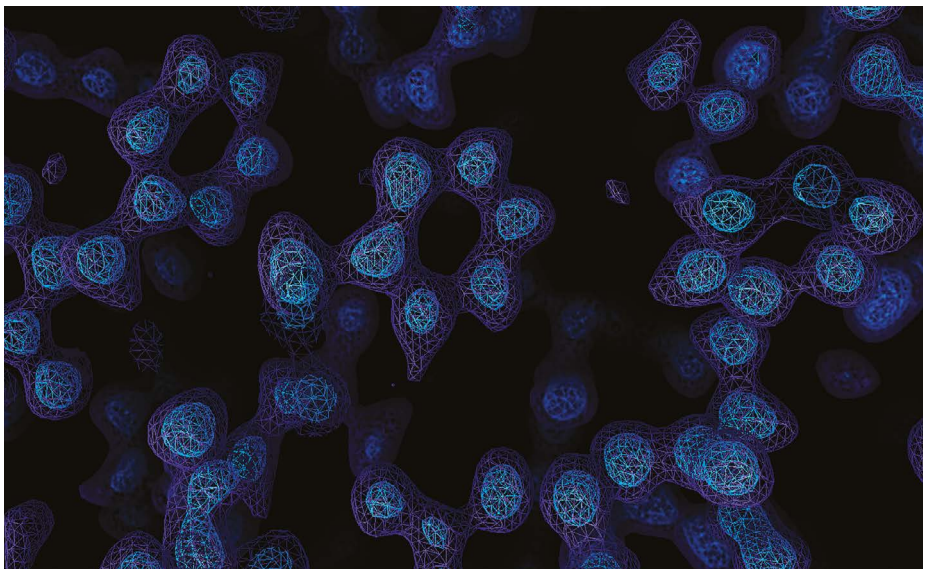
By Ewen Callaway

A game-changing technique for imaging molecules, known as cryo-electron microscopy, has produced its sharpest pictures yet — and, for the first time, discerned individual atoms in a protein.

By achieving atomic resolution using cryo-electron microscopy (cryo-EM), researchers will be able to understand, in unprecedented detail, the workings of proteins that cannot easily be examined by other imaging techniques, such as X-ray crystallography.

The breakthrough, reported by two laboratories late last month, cements cryo-EM's position as the dominant tool for mapping the 3D shapes of proteins, say scientists. Ultimately, these structures will help researchers to understand how proteins work in health and disease, and lead to better drugs with fewer side effects.

"There's really nothing to break any more. This was the last resolution barrier," says Holger Stark, a biochemist and electron microscopist at the Max Planck Institute for Biophysical Chemistry in Göttingen, Germany, who led one of the studies



PAUL EMSLEY/MRC LABORATORY OF MOLECULAR BIOLOGY

A cryo-electron-microscopy map of the protein apoferritin.

(K. M. Yip *et al*. Preprint at bioRxiv http://doi.org/dx3w; 2020). The other was led by Sjors Scheres and Radu Aricescu, structural biologists at the Medical Research Council Laboratory of Molecular Biology (MRC-LMB) in Cambridge, UK (T. Nakane *et al*. Preprint at bioRxiv http://doi.org/dx3x; 2020). Both were posted on the bioRxiv preprint server on 22 May.

"True 'atomic resolution' is a real milestone," adds John Rubinstein, a structural biologist at the University of Toronto in Canada. Getting atomic-resolution structures of many proteins remains a daunting task because of other challenges, such as a protein's flexibility. "These preprints show where one can get to if those other limitations can be addressed," he adds.

Breaking boundaries

Cryo-EM is a decades-old technique that determines the shape of flash-frozen samples by firing electrons at them and recording the resulting images. Advances in technology for detecting the ricocheting electrons and in image-analysis software catalysed a 'resolution revolution' that started around 2013. This led to protein structures that were sharper than ever before — and nearly as good as those obtained from X-ray crystallography, an older technique that infers structures from diffraction patterns made by protein crystals when they are bombarded with X-rays.

Subsequent hardware and software advances led to more improvements in the resolution of cryo-EM structures. But scientists have had to rely largely on X-ray crystallography for obtaining atomic-resolution structures. However, researchers can spend months to years getting a protein to crystallize, and many medically important proteins won't form usable crystals; cryo-EM, by contrast, requires only that the protein be in a purified solution.

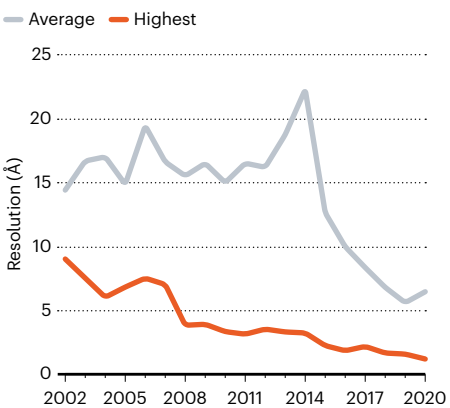
Atomic-resolution maps are precise enough to unambiguously discern the position of individual atoms in a protein, at a resolution of around 1.2 ångströms (1.2×10^{-10} metres). These structures are especially useful for understanding how enzymes work and using those insights to identify drugs that can block their activity (see 'Imaging atoms').

To push cryo-EM to atomic resolution, the two teams worked on an iron-storing protein called apoferritin. Because of its rock-like stability, the protein has become a test bed for cryo-EM: a structure of the protein with a resolution of 1.54 ångströms was the previous record.

The teams then used technological improvements to take sharper pictures of apoferritin. Stark's team got a 1.25-ångström structure of the protein, with help from an instrument that ensures that the electrons travel at similar speeds before hitting a sample, enhancing the resolution of the resulting images. Scheres, Aricescu and their group used a different technology to fire electrons travelling at similar speeds; they also benefited from a technology that reduces the noise generated after some electrons career off the protein sample, as well as a more sensitive electron-detecting camera. Their 1.2-ångström structure was so complete, says Scheres, that they could pick out individual hydrogen atoms, both in the protein and in surrounding water molecules.

IMAGING ATOMS

The imaging technique known as cryo-electron microscopy can now resolve features at the atomic level — about 1.2 ångströms across.



SOURCE: ELECTRON MICROSCOPY DATA BANK

See clearly

Scheres and Aricescu also tested their improvements on a simplified form of a protein called the $GABA_A$ receptor. The protein sits in the membrane of neurons and is a target for general anaesthetics, anxiety medications and many other drugs. Last year, Aricescu's team used cryo-EM to map the protein to 2.5 ångströms. But with the new kit, the researchers attained a 1.7-ångström resolution, with even better resolution in some key parts of the protein. "It was like peeling off a blur over your eyes," Aricescu says. "At this resolution, every half ångström opens up a whole universe."

The structure revealed never-before-seen details in the protein — including the water molecules in the pocket where a chemical called histamine sits. "That is a gold mine for structure-based drug design," says Aricescu, because it shows how a drug could displace the water molecules, potentially resulting in medications with fewer side effects.

An atomic-resolution map of $GABA_A$, which isn't as stable as apoferritin, would be a challenge, says Scheres. "I don't think it's impossible, but it would be very impractical," because of the vast amount of data that would need to be collected. But other improvements, particularly in how samples are prepared, could offer some hope. Protein solutions are frozen on tiny grids made of gold, and alterations to these grids could hold proteins even more still.

"Everyone is very excited and amazed by the truly astounding level of performance demonstrated by the MRC-LMB and Max Planck groups," says Radostin Danev, a cryo-EM specialist at the University of Tokyo. But he agrees that sample preparation is the field's major challenge for wobblier proteins.

The breakthroughs are likely to cement cryo-EM's position as the go-to tool for most structural studies, says Scheres. But Stark thinks X-ray crystallography will retain some appeal. If a protein can be crystallized — and that's a big if — it's relatively efficient to generate structures of it bound to thousands of potential drugs in a short amount of time. But it can still take hours to days to generate enough data for extremely high-resolution cryo-EM structures.

"There are still pros and cons for each of the techniques," says Stark. "People have published lots of papers and reviews that say these latest advances in cryo-EM will be the death signal for X-ray. I doubt that."