California, Davis, who had co-authored both studies with Pruitt, wrote a blogpost about those irregularities (see go.nature.com/39m535t). She had found multiple stretches of data that had been copied and pasted to represent findings for multiple spiders. When Pruitt's explanations failed to account for the anomalies, she requested that the journals retract the papers, reportedly with Pruitt's consent.

"Then, hell broke loose," says Niels Dingemanse, a behavioural ecologist at Ludwig Maximilian University in Munich, Germany, who has helped to uncover the data issues.

More than 20 scientists – co-authors, peers and other interested observers in the field – mobilized to pore through the data in almost 150 papers on which Pruitt is a co-author, looking for evidence of manipulated or fabricated numbers. They found similar signs of copy-and-paste duplications. In at least one instance, researchers identified formulae that had been inserted into a published Excel file, designed to add or subtract from a pasted value and create new data points.

Several have stated that they consider this clear evidence of fraud. Dingemanse says that his mind was made up by the "avalanche of retractions" in progress, as well as the mounting piles of irregular data. "It is hard to believe these data are not fabricated," he says.

The 17 papers that include questionable data have been cited more than 900 times, and it will take scientists a while to sort out which ideas have been supported elsewhere in the literature and which will need to be retested. "My guess is the impact will probably be pretty big," Laskowski says.

Pruitt had written "a lot of really impressive papers" and was regarded by many as a "rising star", says María Rebolleda-Gómez, a microbial ecologist at Yale University in New Haven, Connecticut.

A spokesperson for McMaster University confirmed that the institution was investigating, but would provide no further comment on issues of research integrity. The University of California, Santa Barbara, where Pruitt did most of the work in question, declined to comment on the specific case but said that it "would cooperate with any other institution conducting an investigation".

> **"My guess is that the impact will probably be pretty big."**

Laskowski says that although the wave of retractions deals a blow to behavioural ecology, she is heartened by how quickly the community has acted to set the scientific record straight. Researchers have lessons to learn about making data publicly available – by one estimate, more than 60% of Pruitt's data-containing papers are in journals with no data-sharing requirements – and about checking data that they receive from colleagues. But she and others are optimistic that these lessons will ultimately strengthen the field.

1. Laskowski, K. L., Montiglio, P.-O. & Pruitt, J. N. *Am. Nat.* **187**, 776–785 (2016); retraction **195**, 393 (2020).
2. Laskowski, K. L. & Pruitt J. N. *Proc. R. Soc. B* **281**, 20133166 (2014); retraction **287**, 20200077 (2020).

JOURNAL BANS HIGHLY CITED RESEARCHER FOR CITATION ABUSE

Probe finds that Kuo-Chen Chou repeatedly suggested dozens of citations be added to papers.

By Richard Van Noorden

A US-based biophysicist who is one of the world's most highly cited researchers has been removed from the editorial board of one journal and barred as a reviewer for another, after repeatedly manipulating the peer-review process to amass citations to his own work.

On 29 January, three editors at the *Journal of Theoretical Biology* (*JTB*) announced in an editorial that the journal had investigated and barred an unnamed editor from the board for "scientific misconduct of the highest order" (M. Chaplain *et al. J. Theoret. Biol.* **488**, 110171; 2020).

The journal's publisher, Elsevier, confirmed to *Nature* that the barred editor is Kuo-Chen Chou, who founded and runs an organization that he calls the Gordon Life Science Institute, in Boston, Massachusetts. According to the editorial, Chou asked authors of dozens of papers he was editing to cite a long list of his publications – sometimes more than 50 – and suggested that they change the titles of their papers to mention an algorithm he had developed.

"The magnitude of his self-citation requests are shocking," says Jonathan Wren, an associate editor for *Bioinformatics*, a journal that last year barred Chou from reviewing its papers, although it did not name him at the time. "But what blows my mind is that suspicious citation patterns to him go back decades and authors comply with an apparently amazing frequency."

Chou retired from a career in the pharmaceutical industry in 2003. He then founded the Gordon Life Science Institute, which he calls an institute with "no physical boundaries", of which anyone can become a member. Before 2003, Chou had published 168 papers – mostly in the field of computational biology – which were cited around 2,000 times. But he now has 602 papers with more than 58,000 citations, according to Elsevier's Scopus citations database. He is one of the world's most highly cited researchers.

The *JTB* editorial says that Chou also handled papers written by close colleagues at his own institute – some of whom the journal later couldn't trace, which the editorial says calls into question their veracity. It adds that Chou sometimes reviewed papers under a pseudonym, or chose reviewers from his institution. And in many cases, Chou was added to papers as a co-author during the final stage of review.

"Regrettably, this process was repeated for dozens of papers," the editorial says. It adds that the journal wants to "apologize for missing this blatant misuse of the editorial system".

Chou told *Nature* that mentions of his algorithms in papers were "not from 'reviewer coercion', but from their very high efficacy and widely recognized by many users". But he declined to answer questions about the citation practices for which he was banned, and instead referred *Nature* to his website.

Wren flagged the suspicious citation patterns to the *JTB* after an investigation at his own journal. That probe revealed that in every review, Chou had requested that manuscript authors add citations – an average of 35 of them, 90% to papers he had co-authored. *Bioinformatics* announced that it had barred a referee in January 2019.

Wren, a bioinformatician at the Oklahoma Medical Research Foundation in Oklahoma City, says investigations into Chou's citations are under way at at least three other journals to which he has pointed out suspicious patterns. Wren is currently writing an algorithm to flag unusual citation patterns in papers automatically.

The case comes amid efforts by Elsevier to crack down on the practice of 'coercive citation'. Last year, the Amsterdam-based publisher said it was investigating hundreds of researchers whom it suspected of manipulating peer review to boost their citations. Chou's case is the first to be revealed since that announcement. "While thankfully rare, such practices are an abuse of the peer-review system and undermine the hard work and commitment that editors and reviewers devote to ensuring the integrity of the scholarly record," a spokesperson says. "Elsevier has developed analytical tools to help detect such practices and is committed to implementing technology to flag citation manipulation before publication."

From 2014 to 2018, Chou was named as a highly cited researcher in a list produced by Clarivate Analytics, an information-services firm in Philadelphia, Pennsylvania, that owns the citation database Web of Science. But his name does not appear on the 2019 list; last year, Clarivate decided to remove scientists whose papers showed "unusually high levels of self-citation".

Elsevier hasn't yet decided what to do about papers that Chou handled that liberally cite his work, the spokesperson says.

THE PROTEIN-IMAGING TECHNIQUE TAKING OVER STRUCTURAL BIOLOGY

The number of structures being determined by cryo-electron microscopy is growing explosively.

By Ewen Callaway

A revolutionary technique for determining the 3D shape of proteins is booming. Last week, a database that collects protein and other molecular structures obtained using cryo-electron microscopy, or cryo-EM, acquired its 10,000th entry.

Submissions to the Electron Microscopy Data Bank (EMDB) – a popular repository for structures solved using electron microscopy – have increased exponentially in recent years, largely because of the explosive growth in the number of cryo-electron microscopes in laboratories worldwide (see 'Structure sleuths'). The EMDB curates structures solved with other microscopy methods, but the vast majority use cryo-EM.

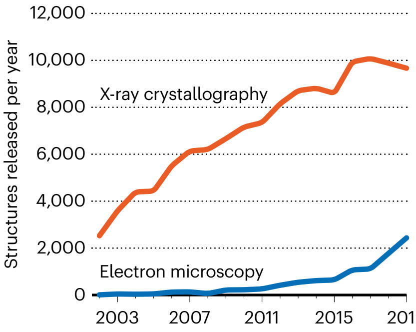
The technique involves flash-freezing solutions of proteins or other biomolecules, and then bombarding them with electrons to produce microscope images of individual molecules. These are used to reconstruct the 3D shape, or structure, of the molecule. Such structures are useful for uncovering how proteins work, how they malfunction in disease and how to target them with drugs.

For decades, structural biologists preferred to use X-ray crystallography, a technique that involves crystallizing proteins, pummelling them with X-rays and reconstructing their shape from the resulting tell-tale patterns of diffracted light. X-ray crystallography produces high-quality structures, but it's not easy to use with all proteins – some can take months or years to crystallize, and others never crystallize at all. Cryo-EM doesn't require protein crystals, but the technique languished because it tended to produce low-resolution structures – some scientists called it blobology.

Breakthroughs in hardware and software in 2012–13 produced more sensitive electron microscopes and more sophisticated software for transforming the images they captured into sharper molecular structures. That paved the way for the current growth of cryo-EM, says Sjors Scheres, a structural biologist and specialist in the technique at the MRC Laboratory of Molecular Biology (LMB) in Cambridge, UK.

STRUCTURE SLEUTHS

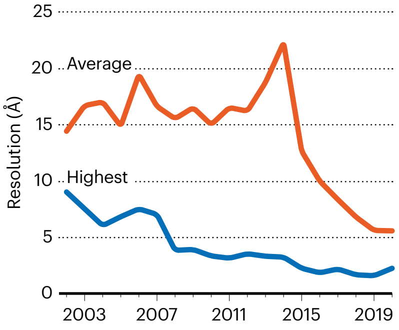
Most structures of proteins and other biological molecules are still solved with X-ray crystallography. But a revolutionary technique called cryo-electron microscopy (cryo-EM) is catching up.



The electron microscopy line shows structures submitted to the Electron Microscopy Data Bank. Nearly all use cryo-EM.

Fine detail

Cryo-EM can now resolve features that are less than 2 ångströms across.



SOURCE: EMDB

Richard Henderson, an LMB structural biologist who shared the 2017 Nobel Prize in Chemistry for his work developing the technique, says that even after these advances, growth was slow at first, because only a small number of labs had access to the equipment. But when they started using cryo-EM to produce detailed maps of molecules such as the ribosome – cells' protein-making machines – other scientists, as well as their institutions and funders, quickly took notice. "All the people who had invested in other things and made the wrong decisions, it took them a year to catch up," says Henderson.

He estimates that, by 2024, more protein structures will be determined by cryo-EM than by X-ray crystallography. Cryo-EM has already supplanted X-ray crystallography for one category of proteins that scientists are especially interested in – those embedded in cell membranes. Many such membrane-bound proteins are implicated in disease and serve as targets for drugs.

Advanced imaging

The structures of molecules determined by cryo-EM are also getting more detailed, thanks to continuing improvements in hardware and software, says Scheres.

Initially, the sharpest cryo-EM structures were of highly stable proteins that were used to test the limits of the technology. But Scheres has noticed that researchers are increasingly obtaining very high-resolution structures of medically important molecules, such as cell-membrane proteins, even though they tend to flop around.

"We're now coming to the point where the easy samples have been done and people are looking at more complex problems," says Ardan Patwardhan, a structural biologist at the European Molecular Biology Laboratory–European Bioinformatics Institute in Hinxton, UK, who leads the team that runs the EMDB.

Henderson expects the boom in cryo-EM structures to slow at some point. One factor that could sap growth, he says, is the high cost of the most powerful microscopes, which can exceed £5 million (US$7 million). They also cost thousands of pounds each day to run, and require specialized labs that minimize vibrations. Henderson is campaigning to convince firms to develop cheaper, but still useful, microscopes that could spread the technique even further. "At the moment, you cannot go wrong by putting more investment into cryo-EM," he says.