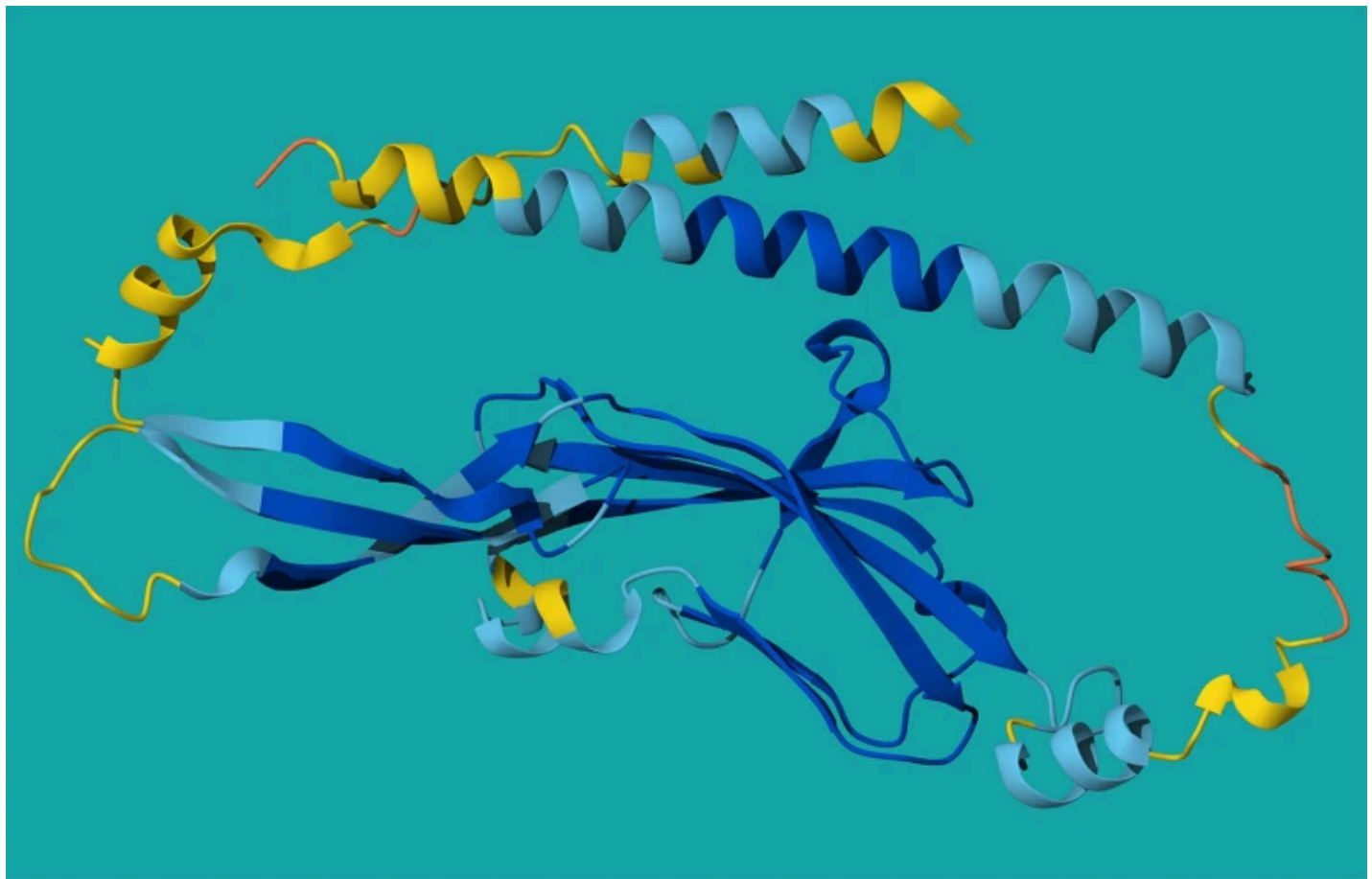# nature

NEWS | 26 November 2025

AlphaFold is five years old — these charts show how it revolutionized science

Since it was unveiled in 2020, Google DeepMind's game-changing AI tool has helped researchers all over the world to predict the 3D structures of hundreds of millions of proteins.

By [Ewen Callaway](#)

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An AlphaFold model of Tmem81, a membrane protein involved in the fusion of egg and sperm.   Credit: Google DeepMind/EMBL–EBI (CC–BY–4.0)

For nearly a decade, Andrea Pauli, a biochemist at the Research Institute of Molecular Pathology in Vienna, has been trying to work out how sperm and egg get together.

In 2018, her laboratory found a protein on the surface of zebrafish (*Danio rerio*) eggs, called Bouncer, that was essential for fertilization. But Pauli's team and others struggled to show how Bouncer recognized sperm cells. Then a revolution happened.

AlphaFold reveals how sperm and egg hook up in intimate

Five years ago, in late November 2020, researchers at London-based Google DeepMind unveiled AlphaFold2. The artificial intelligence tool for predicting protein structures generated stunningly accurate 3D models that, in some cases, were indistinguishable from experimental maps, [dominating a long-running structure-prediction challenge](). The first version of AlphaFold was announced in

2018, but its predictions weren't nearly as good as its successor, which limited its impact.

The 2021 release of AlphaFold2's code and a database that has swelled to hundreds of millions of predicted structures mean that scientists can now get a reliable prediction for almost any protein.

"Having models for anything has had a huge impact," says Janet Thornton, a bioinformatician at the European Bioinformatics Institute in Hinxton, UK, part of the European Molecular Biology Laboratory (EMBL-EBI). "It's like the second coming of structural biology."
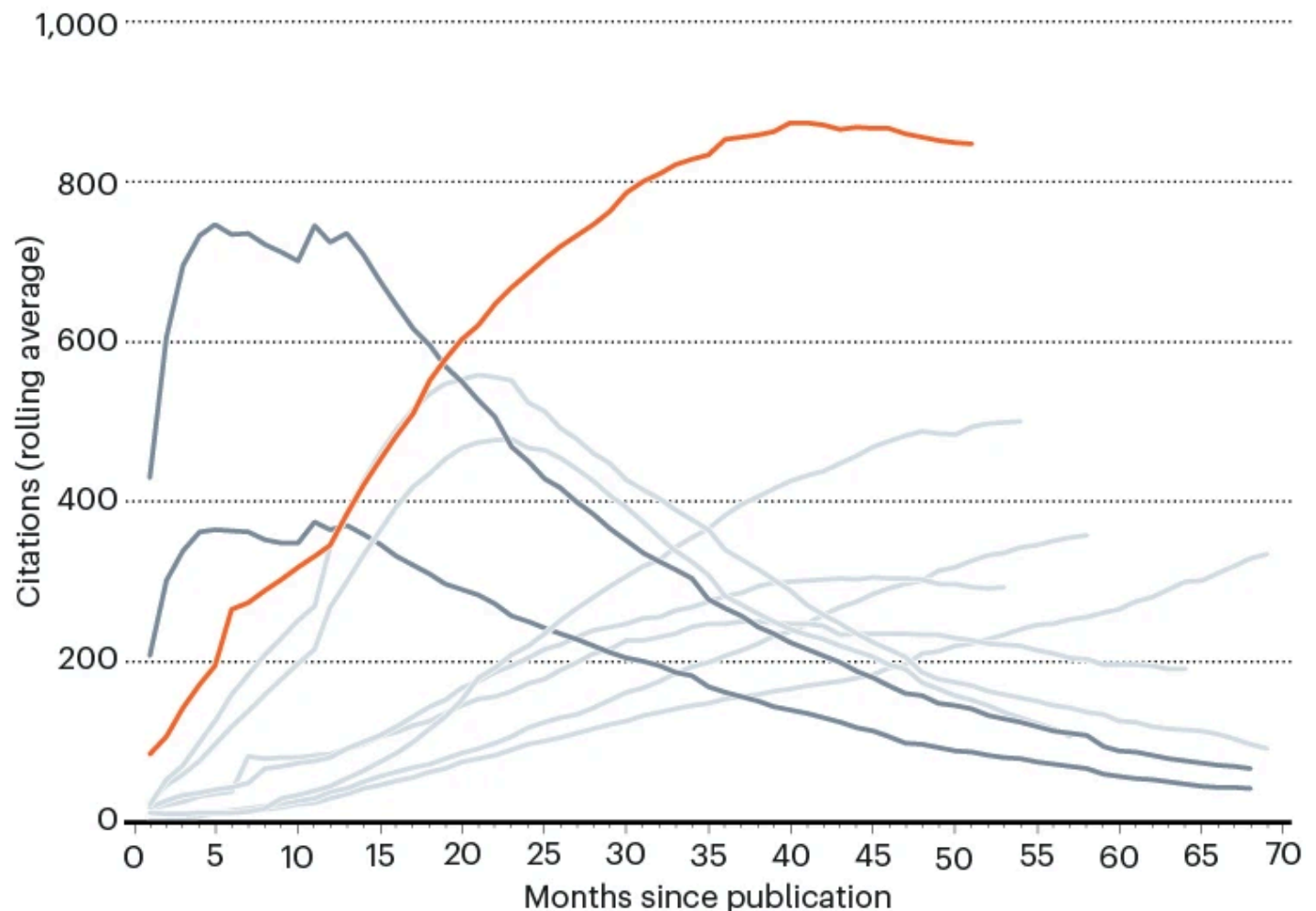
Rapid discovery

For Pauli's team, the software shone a light on a path they might otherwise never have found. The model predicted that a protein, called Tmem81, stabilizes a complex of two other sperm proteins, creating a pocket for Bouncer to bind to[1]. Experiments backed up the tool's predictions. AlphaFold "speeds up discovery", says Pauli. "We use it for every project."

PEAK CITATIONS

The 2021 *Nature* paper describing AlphaFold2 has been cited nearly 40,000 times by other studies. Unlike some other highly cited biomedical studies from 2020–21, including key COVID-19 papers, citations of the AlphaFold2 paper aren't dropping off.

— AlphaFold2[1]   — Early COVID-19 outbreaks[2,3]
— Other highly cited life sciences papers published in 2020 and 2021

*1. Jumper, J. et al. *Nature* **596**, 583–589 (2021).
2. Zhou, P. et al. *Nature* **579**, 270–273 (2020).
3. Wu, F. et al. *Nature* **579**, 265–269 (2020).

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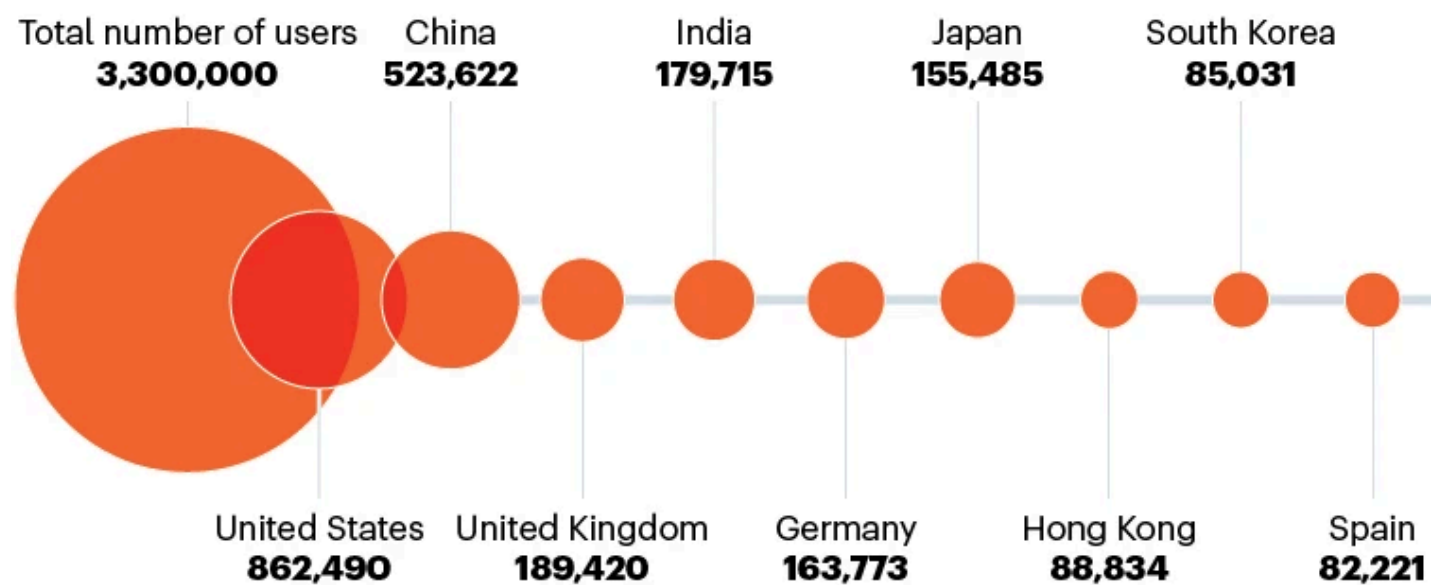Source: OpenAlex/Google DeepMind

Her team's paper about this, published in 2024, is one of nearly 40,000 journal articles to cite the 2021 *Nature* paper describing AlphaFold2[2]. Unlike many other highly cited life-sciences and biomedical papers from the same period, including seminal reports about the COVID-19 pandemic, interest in AlphaFold doesn't seem to be slowing down (see 'Peak citations').

DeepMind's John Jumper – who shared half of the 2024 Nobel Prize in Chemistry with chief executive Demis Hassabis for developing AlphaFold – says he is "deeply proud" of how useful the tool has been for scientists such as Pauli. "When will someone win one of these major awards because they used AlphaFold?" he wonders.

Part of AlphaFold2's rapid impact is down to its accessibility, say researchers. Google DeepMind made the underlying code and other parameters freely available to scientists, and it quickly became possible for them to run the software themselves at scale: this is what Pauli's team did.

GLOBAL APPEAL

The AlphaFold Database of more than 200 million predicted protein structures has been used by more than 3.3 million people worldwide.

Total number of users 3,300,000	China 523,622	India 179,715	Japan 155,485	South Korea 85,031

United States 862,490	United Kingdom 189,420	Germany 163,773	Hong Kong 88,834	Spain 82,221

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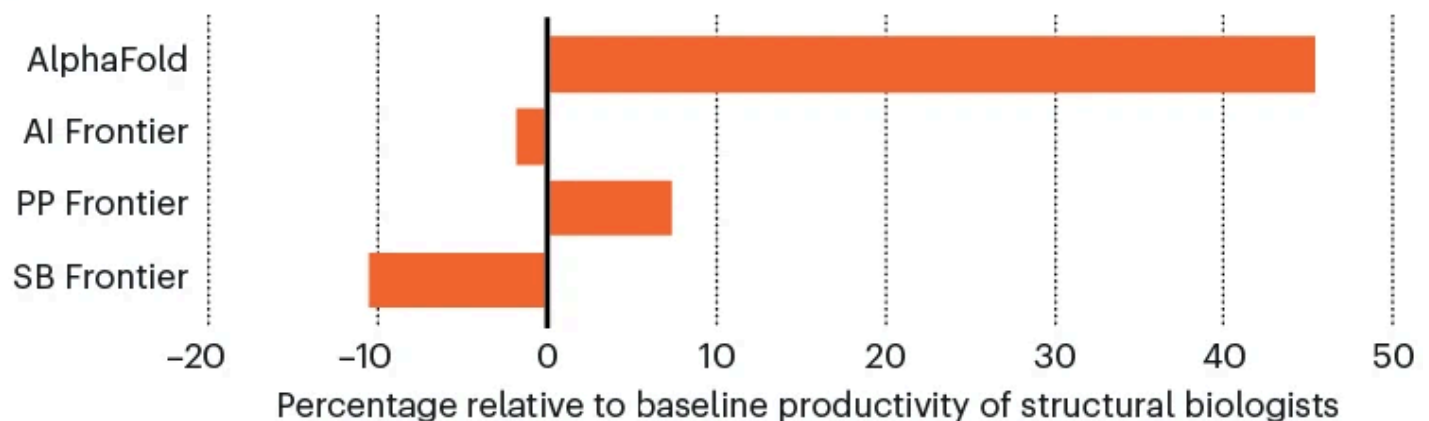Source: AlphaFold Protein Structure Database

Some 3.3 million users in more than 190 countries have accessed the AlphaFold database (AFDB), which is hosted by EMBL-EBI and contains more than 240 million structural predictions, encompassing most known proteins. More than one million AFDB users come from low- and middle-income countries, including China and India (see 'Global appeal').

Protein-structure revolution

The field in which AlphaFold seems to have made its biggest impact is structural biology. Researchers who used AlphaFold submitted around 50% more protein structures to a repository of experimental models, called the Protein Data Bank (PDB), than did a non-AlphaFold-using 'baseline' of structural-biology researchers, finds a Google DeepMind-funded study of AlphaFold's impacts released this week. AlphaFold2 use was also associated with higher rates of PDB submissions than those of researchers using other 'frontier' methods in AI, structural biology and protein structure prediction (see 'Protein pile-up').

PROTEIN PILE-UP

AlphaFold users deposit around 50% more experimental structures into the Protein Databank than structural biologists who don't use the tool. AlphaFold users also deposited more structures than scientists using other 'frontier' methods in AI, protein prediction (PP) and structural biology (SB).

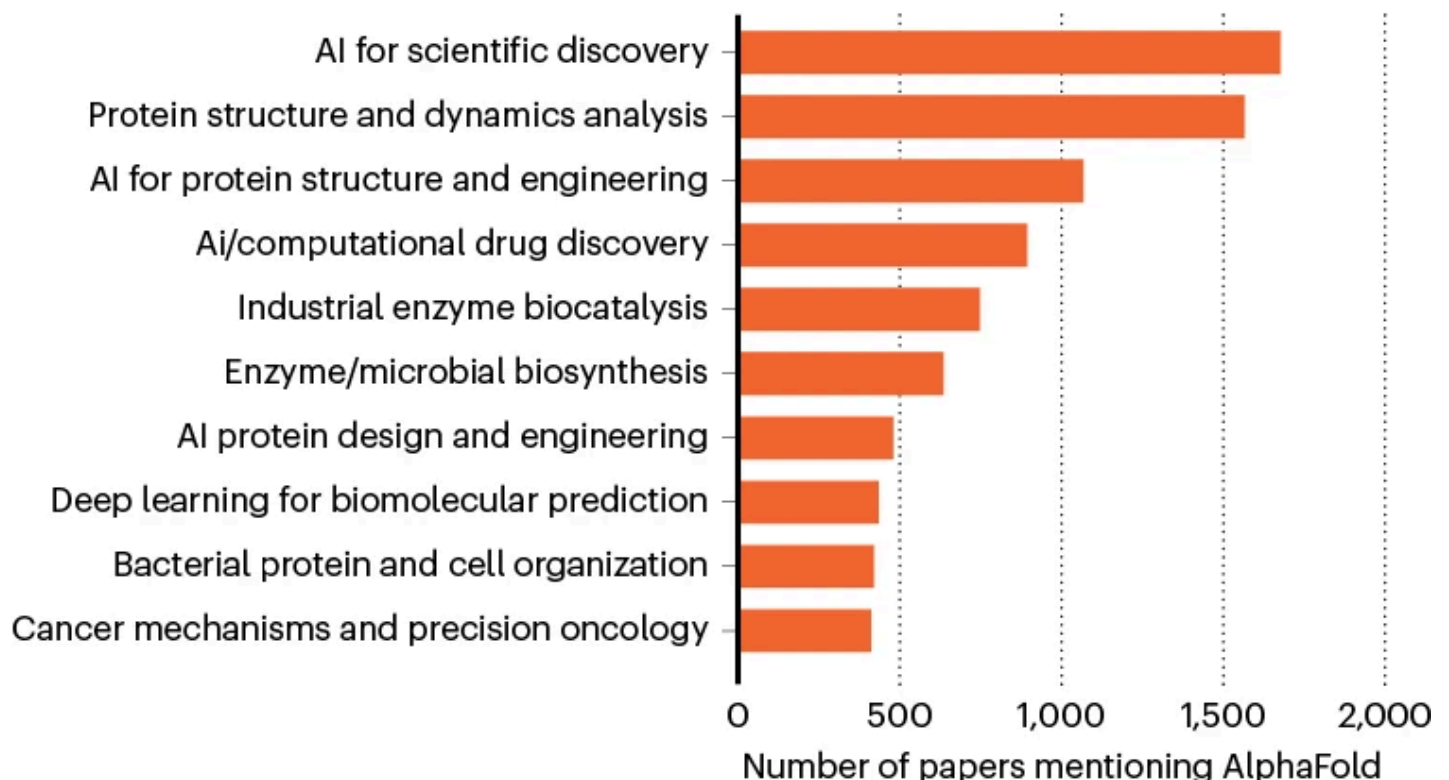Percentage relative to baseline productivity of structural biologists

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Source: *AI in science: Emerging evidence of impact from AlphaFold2*

Jumper says he is especially gratified that AlphaFold2 — which was trained using PDB data — has proved so useful for deducing protein structures. The predicted structures can help researchers to make sense of raw data generated by X-ray crystallography and cryo-electron microscopy. "I love that it helps the people that gave us the data," Jumper adds.

Another field riding the AlphaFold wave is computational biology. "You go to meetings and almost every talk mentions AlphaFold," says Thornton. Among the papers directly citing the 2021 description of AlphaFold2, computation-heavy fields including AI-aided drug discovery and protein design are well represented (see 'Broad applications').

BROAD APPLICATIONS

Papers citing AlphaFold cover a diverse range of topics. The most common involve research in machine learning and computation-heavy life-sciences applications such as AI for protein design and drug discovery, according to an analysis of citation data.
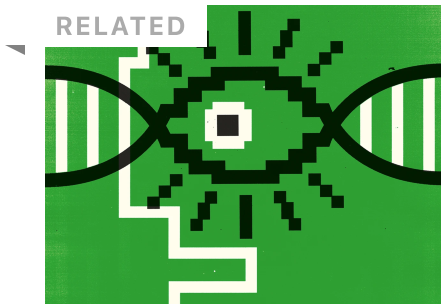

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Source: OpenAlex / Google DeepMind

In the weeks and months after AlphaFold2 was announced, there was an "existential crisis" among academic researchers who worked on protein-structure prediction, says Mohammed AlQuraishi, a computational biologist at Columbia University in New York City, and the sense that main goal was now a solved problem. Instead, AlphaFold has opened fresh avenues of research — AI protein design is one of the most promising — and brought renewed interest and funding. "It's a good time to be a computational biologist," says AlQuraishi.

Indirect impacts

Numbers of scientists directly citing AlphaFold2 or using the AFDB tell only part of the story of the tool's reach. A broader analysis of research connected to AlphaFold2 — including looking at papers downstream of key AlphaFold studies — identified more than half a million studies that used AlphaFold directly or indirectly, encompassing work by nearly two million scientists.

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The analysis, funded by Google DeepMind but conducted independently by researchers at the non-profit Innovation Growth Lab in London, found a complex picture when it attempted to measure the benefits of using AlphaFold. Labs that used the software published only around 5% more papers than those that didn't, and for individual researchers this difference was just 2%.

"You might expect AlphaFold has helped some labs become 'paper factories'. We don't see that," says George Richardson, who did the study with fellow data scientist David Ampudia Vicente. The picture was also mixed when the researchers attempted to measure clinical and commercial applications of AlphaFold, possibly because five years might be too short a window to quantify impacts such as patents, Richardson adds.

Jumper, too, expects that it will take time to translate biological insights from AlphaFold into practical applications, such as drug development. An updated version of the model, AlphaFold3, which is more relevant to drug discovery because it can predict how potential therapeutics interact with proteins, was only released in 2024, and much is happening behind the scenes. Still, insights from before the update are already helping researchers to unravel the biology of disease, says Jumper. "I'm certain that there are people that will go home from the hospital because of AlphaFold2."

doi: https://doi.org/10.1038/d41586-025-03886-9

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1. Deneke, V. E. *et al. Cell* **187**, 7066–7078 (2024).

2. Jumper, J. *et al. Nature* **596**, 583–589 (2021).

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