



Enhance Your Research Capability by Web of Science & Journal Citation Reports



官欣瑩 Renee Guan
Lead Business
Solution Consultant



Promote Information Literacy and Streamline Research Discovery



Each year more researchers enter the field, and the number of published papers increases.

- Over 4 million articles are published annually¹.
- On average, scientists read 264 articles per year².
- The number of predatory journals has increased.



How can you confidently and quickly choose the right papers for your research?

¹ [2021 STM Report](#)

² <http://www.nature.com/news/scientists-may-be-reaching-a-peak-in-reading-habits-1.14658>



**Pinpoint relevant
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Link preprints from several of the largest repositories to the trusted Web of Science ecosystem.

○ **ProQuest Dissertations & Theses Citation Index**

Discover post-graduate works from 4,100+ institutions across 60+ countries

○ **Grants Index**

Inform your proposal and funding strategies with data on 5.2M+ awarded grants from 400+ agencies

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Discover content from locally focused journals throughout Latin America, South Africa, Mainland China, South Korea, and the Arab world.

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Explore the full spectrum of biomedical literature from agriculture to public health to zoology.

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Find content relevant to researchers in many fields including physics, engineering, and food science.

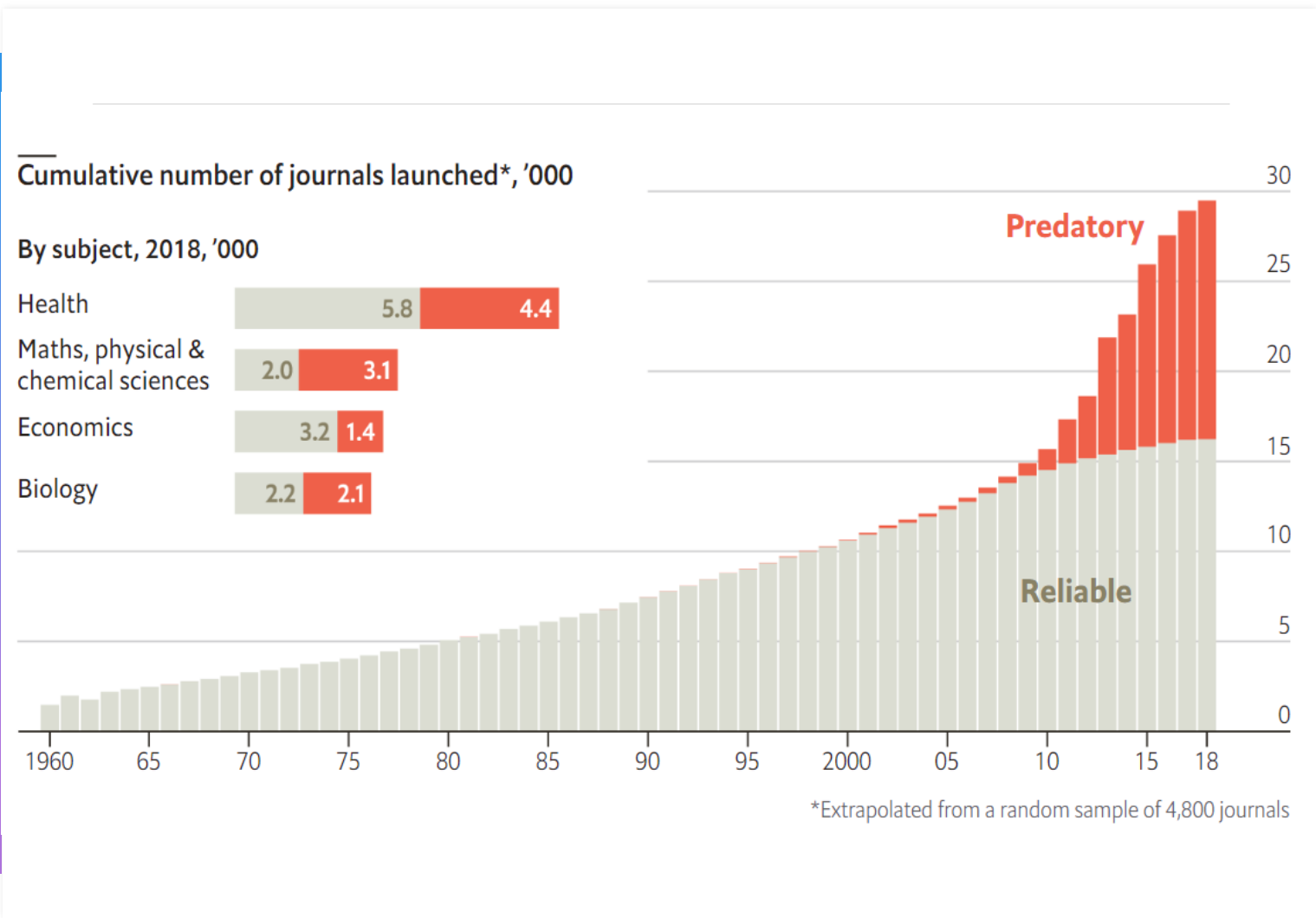


Web of Science Core Collection

Statistics as of October 2021

Increasingly Complex Research Environment

How can librarians support their universities?



Questionable publishing practices are on the rise

These models can undermine public trust in research and research integrity and represent significant waste of research resources

The rigorous journal selection criteria ensure the quality control of academic resources.

- The Web of Science Core Collection strictly follows the consistent selection criteria established over the past 50 years, **curating the most academically influential and high-quality journals worldwide**
- **Cover to cover**, including comprehensive citation details.
- The Web of Science Core Collection curates high-quality academic resources around the world, **saving significant time and effort in reading literature** and selecting top-tier articles.

80/20

80% of significant research findings are published in the top 20% of journals globally.

Web of Science

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Save time with tools that automatically write your bibliography for you, identify reputable, best-fit journals for your manuscripts, and output your CV with the click of a button.



Publisher-neutral expertise

Gain insights into industry trends from the Institute for Scientific Information (ISI) or learn how to peer review from publisher-neutral experts.

What is a citation?



Dr. Eugene Garfield

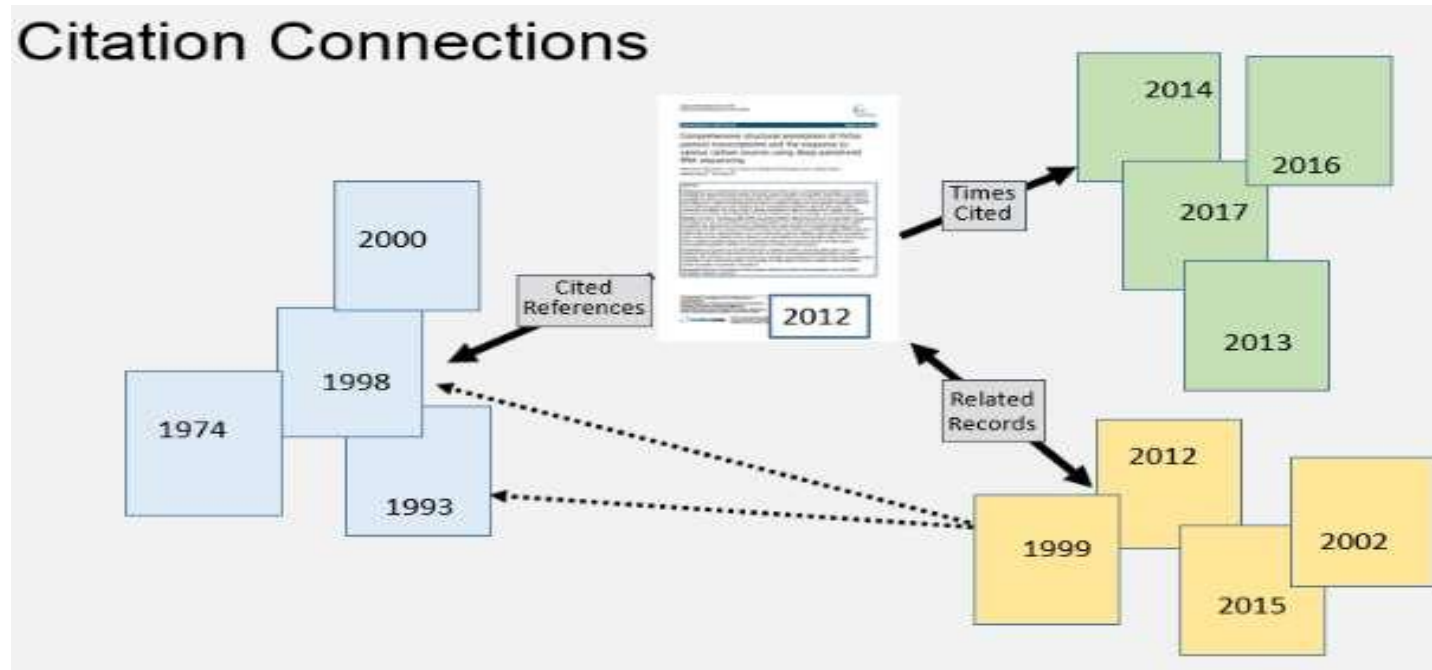
Founders of bibliometrics & scientometrics.

...a citation index...tends to bring together material that would never be collated by the usual subject indexing. It is best described as an association-of-ideas index..."

- A **Citation** is a reference to other published materials.
- A **Citation Index** is a database that captures all reference of items, allowing the user to easily establish which later documents cite which earlier documents.
- **What this means to you:**
 - Using the citation index, you can easily find older and newer RELATED papers.

Uncover Hidden Connections

Navigate an interconnected web of multidisciplinary research to locate papers relevant to your work.



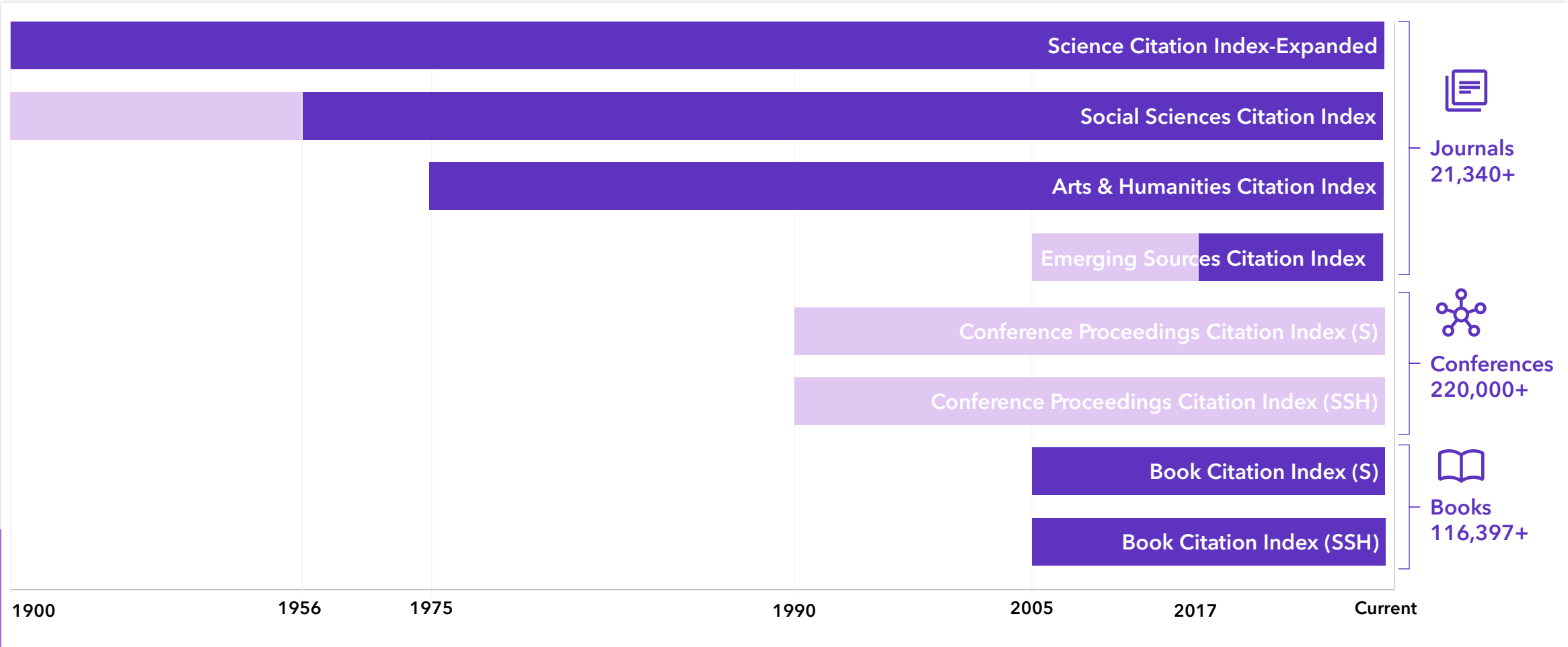
- **Cited References:** the research that a paper cites
- **Time Cited:** more recently published papers that cite the paper
- **Related Records:** papers which share at least one cited reference in common with the paper. If they share citations, they're likely discussing similar topics.

It is particularly useful:

- Where keywords in the topics are not easy to define.
- Where older research needs to be traced.
- When you need to see where a research trend leads.

Web of Science Core Collection data coverage

254 subject categories in WOS CC



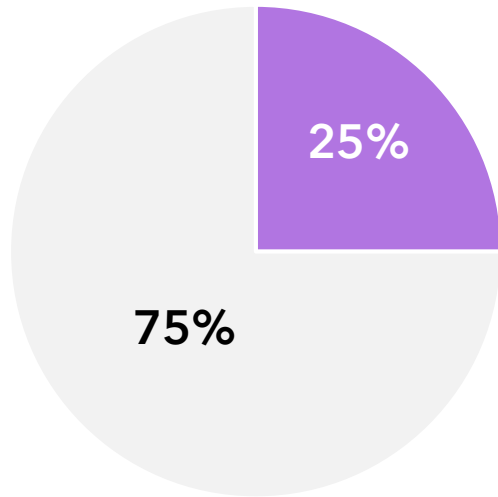


Beyond published literature

Statistics as of October 2021

Broaden your view of a research field

ProQuest Dissertations & Theses Citation Index on the Web of Science



Tap into a trove of graduate research only available in PQDT

One study of psychology dissertations found that only 25%* turn into published journal articles. This integration opens discovery of unpublished work not currently available on the Web of Science platform.

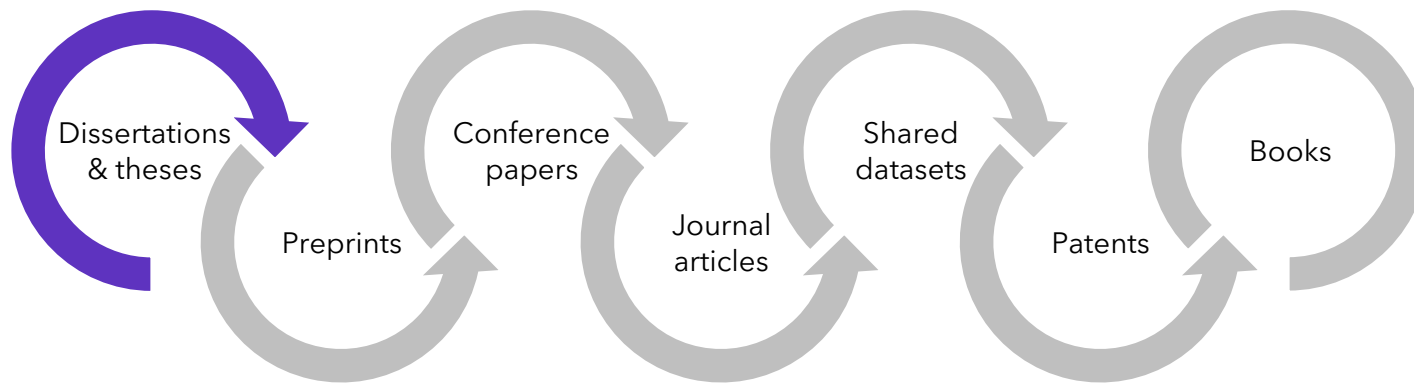


Uncover hidden opportunities to advance your research

- Identify emerging areas of research and the graduate programs that are engaged in this research.
- Understand the evolution of a topic or discipline by making connections between early career, emerging, and established research.
- Explore the details of research methodologies that are not published in the peer-reviewed literature
- Execute more comprehensive literature reviews by including unpublished scholarship and more diverse perspectives.

*Field of psychology. Evans et al. (2018) PLoS ONE 13(2): e0192219.
<https://doi.org/10.1371/journal.pone.0192219>. Range 18%-49% across disciplines.

ProQuest Dissertations & Theses Citation Index



ProQuest Dissertations & Theses Global



Web of Science

- Discovery of 5.7M+ metadata records from ProQuest Dissertations & Theses Global in a standalone database
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Preprint Citation Index

Integrating preprints into the research ecosystem

Preprint

1

Necessity of COVID-19 Vaccination in Persons Who Have Already Had COVID-19
[N. K. Shrestha](#); [P. C. Burke](#); (...); [S. M. Gordon](#)
Apr 01 2022 | medRxiv | Total Versions: 1

Background. The purpose of this study was to evaluate the necessity of COVID-19 vaccination in persons with prior COVID-19. Methods. Employees of Cleveland Clinic working in Ohio on Dec 16, 2020, the day COVID-19 vaccination was started, were included. Anyone who tested positive for COVID-19 at least once before the study start date was considered previously infected ... [Show more](#)

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Preprint

This article is a preprint and has not been formally peer-reviewed. It should not be regarded as conclusive, used to guide clinical or health related decisions, or be reported in news media as established information.

Necessity of COVID-19 Vaccination in Persons Who Have Already Had COVID-19

By: [N. K. Shrestha](#) (N. K. Shrestha) [5], [1]; [P. C. Burke](#) (P. C. Burke) [2]; [A. S. Nowacki](#) (A. S. Nowacki) [3]; [P. Terpeluk](#) (P. Terpeluk) [4]; [S. M. Gordon](#) (S. M. Gordon) [1]
medRxiv
DOI: 10.1101/2021.06.01.21258176
Published: Apr 01 2022
Indexed: 2022-11-23
Document Type: preprint
Version History:

	Publication date	External link
1	2022-04-01	https://www.medrxiv.org/content/10.1101/2021.06.01.21258176v4

Version History

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Grants Index

The screenshot displays the Clarivate Web of Science Grants Index interface. The top navigation bar includes the Clarivate logo, a search bar, and links for Help, English, and Products. The main header shows the search path: Fielded Search > Results for GRANTS:154999... > III: Medium: Collaborative Research: Fairness in Web Database Applications. The interface is divided into a main content area and a right sidebar.

III: Medium: Collaborative Research: Fairness in Web Database Applications

Principal Investigator: Das, Gautam^[1]
Co-Principal Investigator: Nilizadeh, Shirin^[2]
Grant Source: National Science Foundation
Published: 2021
Indexed: 2023-12-08
Program: Info Integration & Informatics
Document Type: Awarded Grant
Grant Description: The Web has affected every corner of human life and society by providing the cyber-infrastructure to remove physical barriers between people. Myriad web database applications, including online recommendation systems, online shopping sites, location-based websites, resource-sharing platforms, social media, and service websites, have made people's lives unimaginably more connected, convenient, and cost-effective. The internal models, algorithms, ranking strategies, user profiling, and data resources shape the behavior of these web database applications. Unfortunately, these can include unfair practices that propagate, or even amplify, historical biases through their services, products, and recommendations. ~br/>This project aims to detect such unfairness and to correct it where possible.~br/>~br/>A central question in detecting and correcting unfairness is how much knowledge can be assumed about these web systems' underlying data and algorithms. It is unrealistic to assume full knowledge, and it is hard even to detect unfairness without such assumptions. This project relies on making limited assumptions, such as the existence of a back-end database. Based on these, the project will detect unwarranted bias, develop responsible design tools one can use to avoid inadvertent unfairness, and implement third-party tools to tailor responses to reduce disparities between different demographic groups.~br/>~br/>This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

Affiliations: Addresses :
1 University of Texas at Arlington
2 University of Texas at Arlington

Grant Details:
Funding Agency: NSF - Directorate for Computer & Information Science & Engineering (CISE); NSF - Division of Information & Intelligent Systems (IIS)
Grant Number: 2107296
Grant Type: Standard Grant
Total Award Amount: \$432,000.00 USD
Grant Start Date: 2021-11-01
Grant End Date: 2024-10-31
Language: English

Associated Publications: 3
Use in Web of Science: 0 Last 180 Days, 0 Since 2013
This record is from: Grants Index
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Understand what's already been funded to differentiate new projects and proposals

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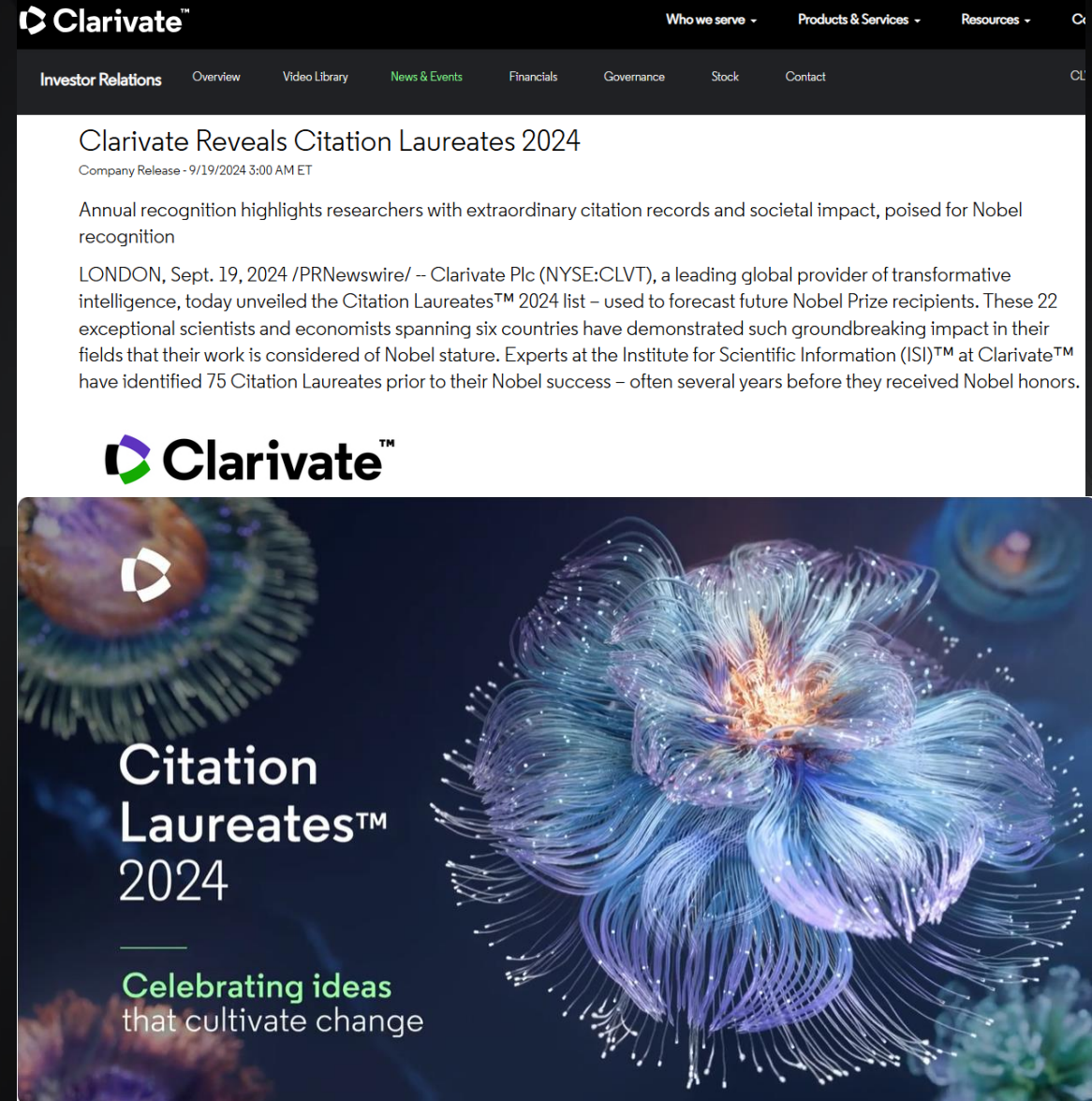
"FOR THE GREATEST
BENEFIT TO HUMANKIND"

ALFRED NOBEL

Citation Laureate

The extensive citation record demonstrates their impact.

- Since 2002, analysts from the Institute for Scientific Information (ISI) have selected the most influential researchers worldwide from the fields of Physiology or Medicine, Physics, Chemistry, and Economics based on citation data from the Web of Science™ Core Collection.
- Since 1970, of the approximately 61 million papers indexed in the Web of Science™ Core Collection, only 0.01% have been cited more than 2,000 times. Citation Laureates are typically selected from among the authors of these highly-cited papers.





How many Nobel Prize winners has
Clarivate accurately predicted since 2002?

83



How many 2024 Nobel Prize winners has
Clarivate accurately predicted?

8

Citation Laureate

英國倫敦，2024年9月19日——全球領先的專業資訊服務提供商科睿唯安（Clarivate，紐約證券交易所代碼：CLVT）今天公佈了被譽為「諾貝爾獎風向球」的2024年度引文桂冠獎名單。來自6個國家的22位傑出科學家和經濟學

The Nobel Prize in Chemistry 2024

David Baker

“for computational protein design”



David Baker, III, Niklas Elmehed © Nobel Prize Outreach

Demis Hassabis

“for protein structure prediction”



Demis Hassabis, III, Niklas Elmehed © Nobel Prize Outreach

John Jumper

“for protein structure prediction”



John Jumper, III, Niklas Elmehed © Nobel Prize Outreach

化學領域

David Baker

美國華盛頓大學醫學院生物化學教授、霍華德·休士頓研究所研究員兼蛋白質設計研究所所長

John M. Jumper

谷歌DeepMind主管

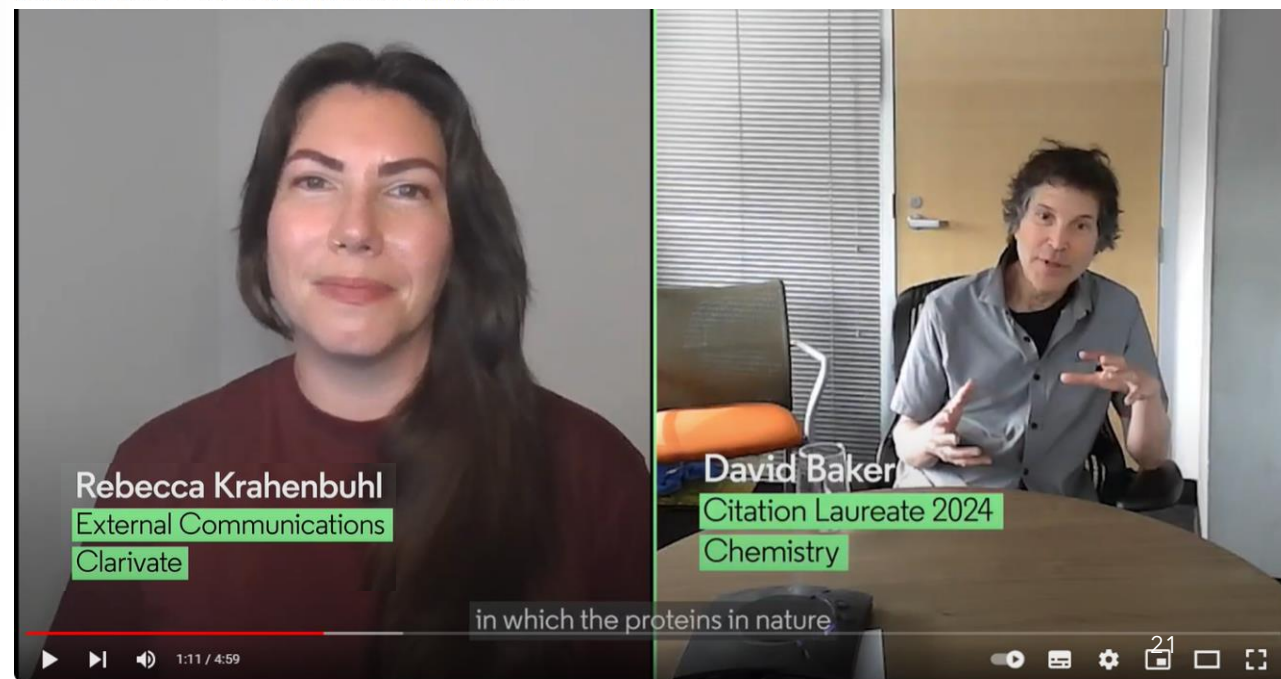
Demis Hassabis

谷歌DeepMind創始人兼首席執行官

獲獎原因：對蛋白質3D結構和功能的預測與設計作出貢獻



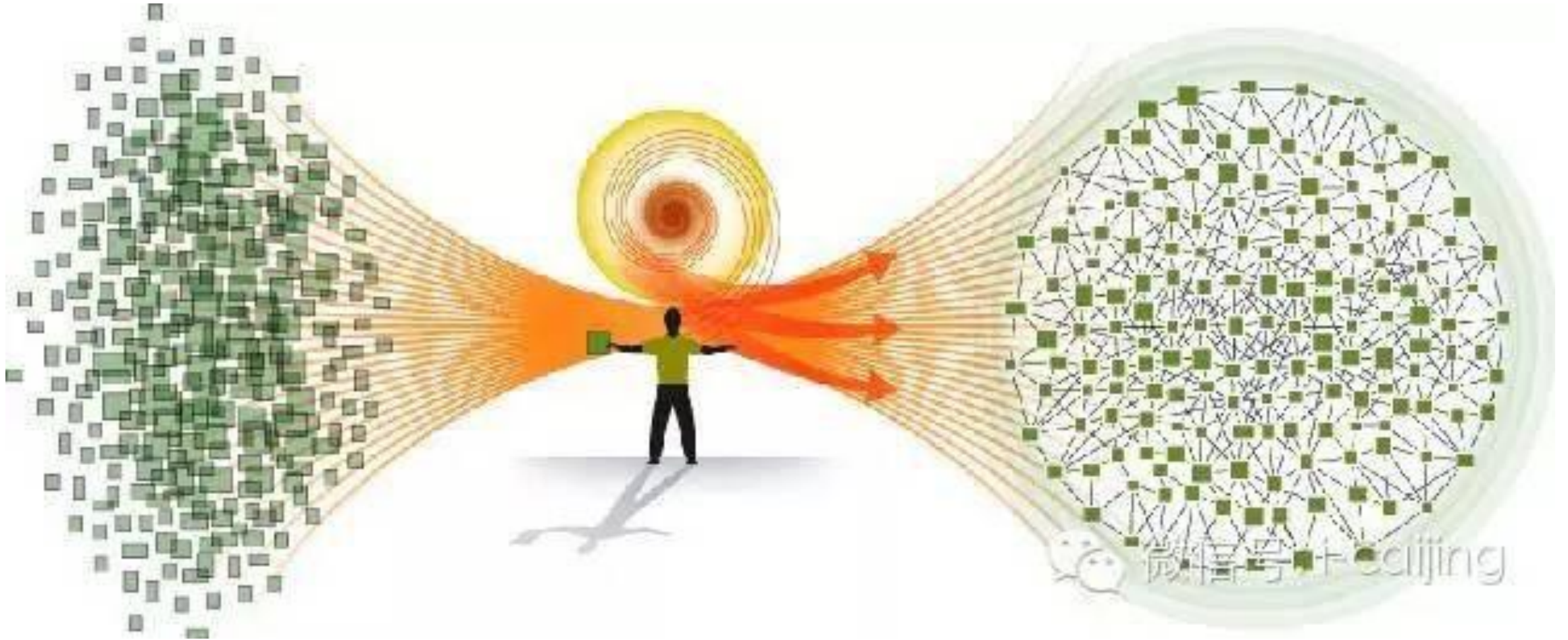
2024 引文桂冠獎：化學領域得主(John M. Jumper)訪談



2024 引文桂冠獎：化學領域得主(David Baker)訪談

Citations: Giving life to scientific literature

Accurate and Comprehensive Research Data Network



Searching "Protein Structure" in Web of Science

43,441 articles???!!!! How to read these papers?

Web of Science™ Search Advanced search Research Assistant Renee Guan

Search > Results for "protein structure" (Topic)

43,441 results from Web of Science Core Collection for:

"protein structure" (Topic) [Copy query link](#)

+ Add Keywords Quick add keywords: < + protein structure + protein structure prediction + membrane protein structure + protein structure determination + prote >

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<input type="checkbox"/> Highly Cited Papers	248
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<input type="checkbox"/> Review Article	4,267
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<input type="checkbox"/> Open publisher-invited reviews	144

☐ 0/43,441 [Add To Marked List](#) [Export](#) Citations: highest first < 1 of 869 >

☐ 1 **MUSCLE: multiple sequence alignment with high accuracy and high throughput** **35,815**
Edgar, RC Citations
Mar 2004 | **NUCLEIC ACIDS RESEARCH** 32 (5) , pp.1792-1797 **44**
References
We describe MUSCLE, a new computer program for creating multiple alignments of protein sequences. Elements of the algorithm include fast distance estimation using kmer counting, progressive alignment using a new profile function we call the log-expectation score, and refinement using tree-dependent restricted partitioning. The speed and accuracy ... [Show more](#)
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☐ 2 **UCSF chimera - A visualization system for exploratory research and analysis** **33,584**
Pettersen, EF; Goddard, TD; (...); Ferrin, TE Citations

A Simple Tip for Selecting High-Impact Papers: Citations: highest first

Citations are the most direct and formal indicator of a paper's impact

Web of Science™

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1

Highly accurate protein structure prediction with AlphaFold

17,927 Citations

84 References

Jumper, J; Evans, R; (...); Hassabis, D

Aug 26 2021 | NATURE 596 (7873) , pp.583+

Proteins are essential to life, and understanding their structure can facilitate a mechanistic understanding of their function. Through an enormous experimental effort(1-4), the structures of around 100,000 unique proteins have been determined(5), but this represents a small fraction of the billions of known protein sequences(6,7). Structural coverage is l ... Show more

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By [Jumper, J](#) (Jumper, John) ^[1]; [Evans, R](#) (Evans, Richard) ^[1]; [Pritzel, A](#) (Pritzel, Alexander) ^[1]; [Green, T](#) (Green, Tim) ^[1]; [Figurnov, M](#) (Figurnov, Michael) ^[1]; [Bates, R](#) (Tunyasuvunakool, Kathryn) ^[1]; [Bates, R](#) (Bates, Anna) ^[1]; [Bridgland, A](#) (Bridgland, Alex) ^[1]; [Ballard, A](#) (Ballard, Andrew J.) ^[1]; [Cowie, A](#) (Cowie, Andrew) ^[1]; [Nikolov, S](#) (Nikolov, Stanislav) ^[1]; [Jai, S](#) (Jai, Shyam) ^[1]; [Petersen, S](#) (Petersen, Stig) ^[1]; [Reiman, D](#) (Reiman, Michal) ^[1]; [Steinegger, M](#) (Steinegger, Michael) ^[1]; [Berghammer, T](#) (Berghammer, Tamas) ^[1]; [Bodenstein, B](#) (Bodenstein, Benjamin) ^[1]; [Senior, A](#) (Senior, Andrew) ^[1]; [Hassabis, D](#) (Hassabis, Demis) ^[1] ...Less



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Source: **NATURE** 
Volume: 596 Issue: 7873 Page: 583-+
DOI: 10.1038/s41586-021-03819-2

Published: **AUG 26 2021**

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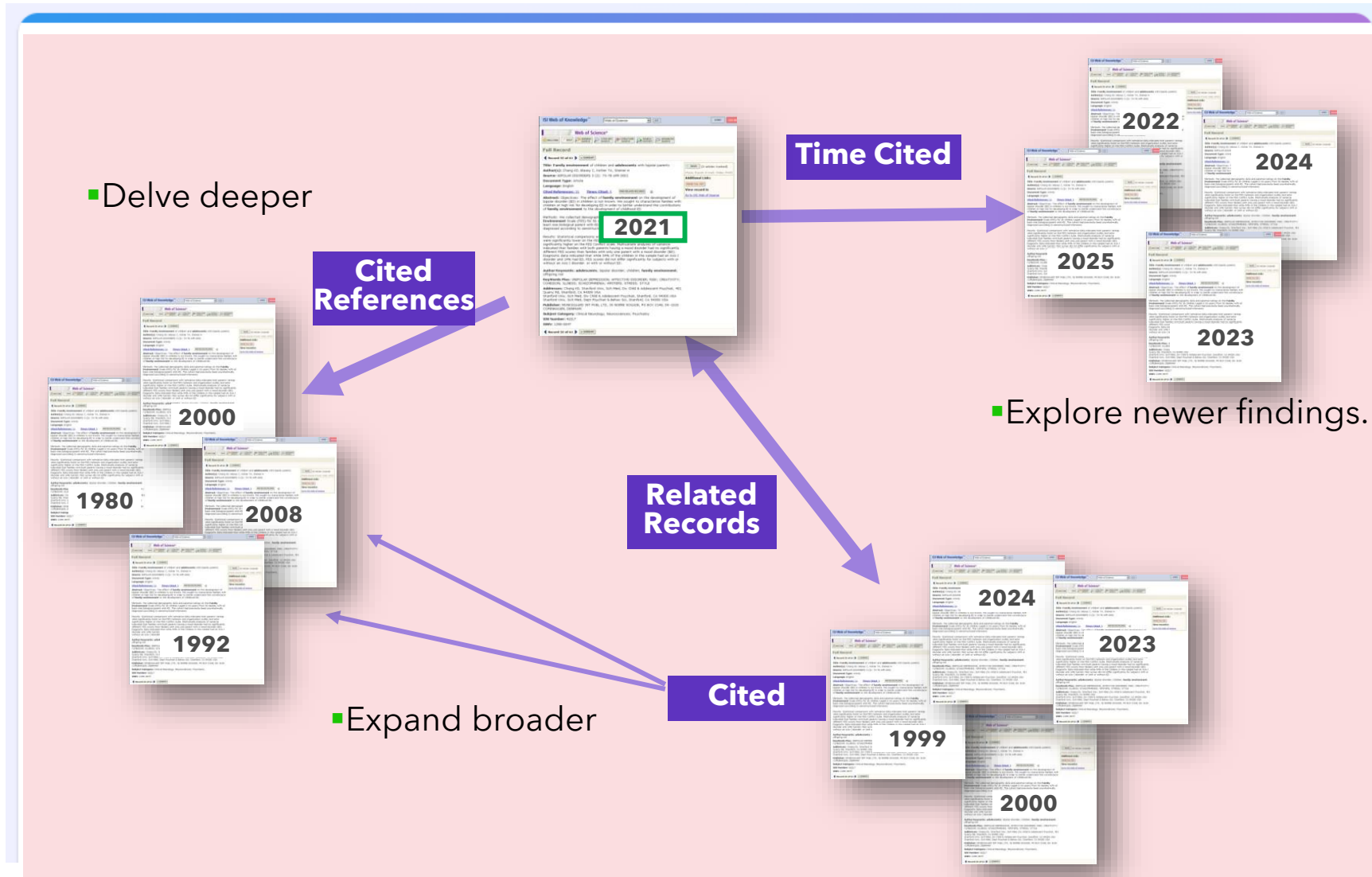
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Utilize citation networks to trace the development of a topic

Mining More Research Gems via Citation Networks



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14 Improved protein structure prediction using potentials from deep learning



Senior, AW; Evans, R; (...); Hassabis, D

Jan 30 2020 | NATURE ▾ 577 (7792), pp. 705-714



DeepMind claims that **AlphaFold 2** can identify protein structures within days, a task that previously often took the academic community years to accomplish

1,736

引用文獻

55

參考文獻

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23 Improved protein structure prediction using predicted interresidue orientations



Yang, JY; Anishchenko, I; (...); Baker, D



Jan 21 2020 | PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA ▾ 117



David Baker used a deep residual network and Rosetta software to quickly generate accurate structural models.

849

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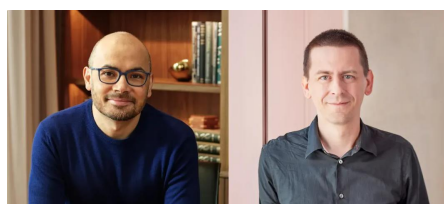
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51 Protein structure prediction using multiple deep neural networks in the 13th Critical Assessment of Protein Structure Prediction (CASP13)



Senior, AW; Evans, R; (...); Hassabis, D



FUNCTION AND BIOINFORMATICS ▾ 87 (12), pp.1141-1148

AlphaFold 1 accurately predicted the toughest structures without using templates from similar sequences.

189

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0/17,910

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1

Enzymatic degradation of mycotoxin patulin by a short-chain dehydrogenase/reductase from *Bacillus subtilis* and its application in apple juice

Niu, JF; Ma, B; (...); Zhu, P

Mar 2025 | FOOD MICROBIOLOGY 126

Enriched Cited References

Patulin (PAT), a notorious mycotoxin widely found in fruits and their derived products, poses serious health risks to humans and animals due to its high toxicity. Biodegradation based on microbial enzymes has shown broad application prospects in controlling PAT contamination due to its environmental friendliness, high efficiency, strong specificity, ... Show more

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Toward understanding the role of genomic repeat elements in neurodegenerative diseases

An, ZY; Jiang, AD and Chen, JQ

Mar 2025 | NEURAL REGENERATION RESEARCH 20 (3) , pp.646-659

Neurodegenerative diseases cause great medical and economic burdens for both patients and society; however, the complex molecular mechanisms thereof are not yet well understood. With the development of high-coverage sequencing technology,

169 References

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☐ 0/239,974

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Relevance

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1 Artificial intelligence for template-free protein structure prediction: a comprehensive review

Mufassirin, MMM; Newton, MAH and Sattar, A

Aug 2023 | ARTIFICIAL INTELLIGENCE REVIEW 56 (8) , pp.7665-7732

Protein structure prediction (PSP) is a grand challenge in bioinformatics, drug discovery, and related fields. PSP is computationally challenging because of an astronomically large conformational space to be searched and an unknown very complex energy function to be minimised. To obtain a given protein's structure, template-based PSP a ... [Show more](#)

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2 OpenProteinSet: Training data for structural biology at scale

Ahdritz, G; Bouatta, N; (...); AlQuraishi, M

37th Conference on Neural Information Processing Systems (NeurIPS)

2023 | ADVANCES IN NEURAL INFORMATION PROCESSING SYSTEMS 36 (NEURIPS 2023)

Multiple sequence alignments (MSAs) of proteins encode rich biological information and have been workhorses in bioinformatic methods for tasks like protein design and protein structure prediction for decades. Recent breakthroughs like AlphaFold2 that use transformers to attend directly over large quantities of raw MSAs have reaffirmed their importance. Ge ... [Show more](#)

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Summary

Strategies for Defining Research Directions

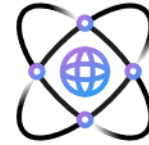
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and **Interdisciplinary**
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Selecting Topics from
Unresolved issues
within the Field

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first**

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papers**

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Review article

**Refine results
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Categories 、 Citation Topics)**

Web of Science: Analyze Your Research Topics

How to accurately grasp the development direction of a topic?

Which funding bodies support this topic area?

What are the potential interdisciplinary directions for this topic?

How to seek domestic/international collaboration in this field?

Who are the main researchers in this topic?

How is this field perceived in the domestic context?

...

Analyze Results

Looking for collaborators? Journals? Funding?

Web of Science Categories

Publication Years

Final Publication Year

Document Types

Researcher Profiles

Authors

Web of Science Categories

Citation Topics Meso

Citation Topics Micro

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1,379 publications selected from Web of Science Core Collection

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In the past ____ years, research on _____ has shown a global trend towards _____, with a significant number of papers coming from _____ (country/region).
Research institutions that have published many papers on the related topics include _____. **Affiliations**

**Web of Science Category
or Citation Topics**

Global researchers mainly focus on related issues from fields such as _____, while we also note that research from fields like _____ may offer different perspectives and insights.

Publication Titles

The research findings on the related topics are primarily published in journals such as _____. In this area of study, scholars like _____ have contributed to a large number of papers.

Authors/Research Profiles

The most influential papers are from scholars at _____ (institution) in _____ (country/region).

**Citation:
High first**

In the past six months, the _____ direction has garnered more attention from researchers.

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We recommend choosing the _____ review literature as a quick entry point for understanding this topic.

The latest research progress indicates that this research direction is currently developing _____.

Document type: Review

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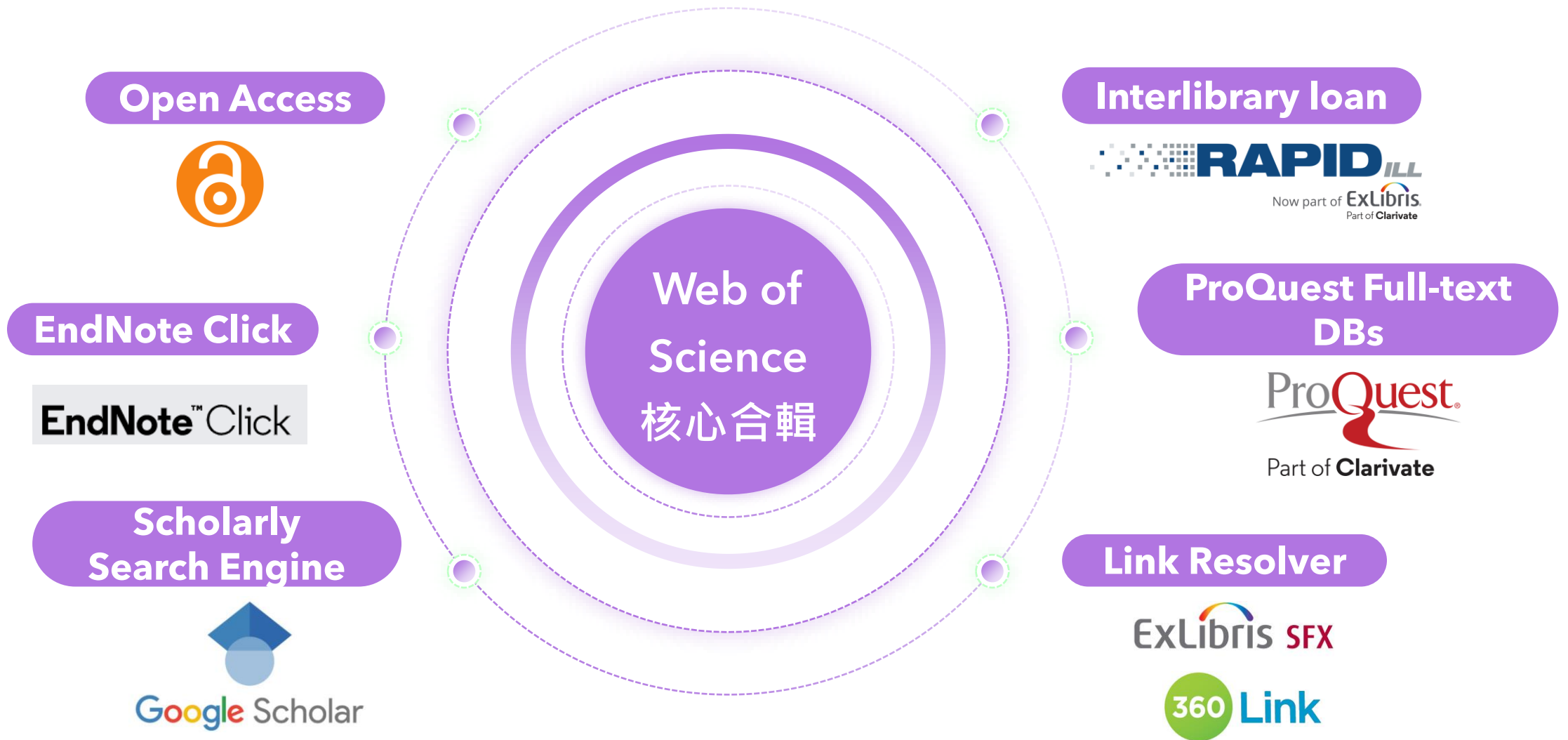
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Highly accurate protein structure prediction with AlphaFold

高被引論文

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作者 Jumper, J (Jumper, John) [1]; Evans, R (Evans, Richard) [1]; Pritzel, A (Pritzel, Alexander) [1]; Green, T (Green, Tim) [1]; Figurnov, M (Figurnov, Michael) [1]; Ronneberger, O (Ronneberger, Olaf) [1]; Tunyasuvunakool, K (Tunyasuvunakool, Kathryn) [1]; Bates, R (Bates, Russ) [1]; Zidek, A (Zidek, Augustin) [1]; Potapenko, A (Potapenko, Anna) [1]; ...更多

檢視 Web of Science ResearcherID 和 ORCID (Clarivate 提供)

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文獻類型 Article

摘要 Proteins are essential to life, and understanding their structure can facilitate a mechanistic understanding of their function. Through an enormous experimental effort (1-4), the structures of around 100,000 unique proteins have been determined (5), but this represents a small fraction of the billions of known protein sequences (6,7). Structural coverage is bottlenecked by the months to years of painstaking effort required to determine a single protein structure. Accurate computational approaches are needed to address this gap and to enable large-scale structural bioinformatics. Predicting the three-dimensional structure that a protein will adopt based solely on its amino acid sequence—the structure prediction component of the ‘protein folding problem’—has been an important open research problem for more than 50 years (9). Despite recent progress (10-14), existing methods fall far short of atomic accuracy, especially when no homologous structure is available. Here we provide the first computational method that can regularly predict protein structures with atomic accuracy even in cases in which no similar structure is known. We validated an entirely redesigned version of our neural network-based model, AlphaFold, in the challenging 14th Critical Assessment of protein Structure Prediction (CASP14) (8), demonstrating accuracy competitive with experimental structures in a majority of cases and greatly outperforming other methods. Underpinning the latest version of AlphaFold is a novel machine learning approach that incorporates physical and biological knowledge about protein structure, leveraging multi-sequence alignments, into the design of the deep learning algorithm.

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Jumper, John; Evans, Richard; Pritzel, Alexander; Green, Tim; Figurnov, Michael; et al. > Nature: London Vol. 596, Iss. 7873, (Aug 26, 2021): 583-2,589A-589C. DOI:10.1038/s41586-021-03819-2

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Abstract

Proteins are essential to life, and understanding their structure can facilitate a mechanistic understanding of their function. Through an enormous experimental effort (1-4), the structures of around 100,000 unique proteins have been determined (5), but this represents a small fraction of the billions of known protein sequences (6,7). Structural coverage is bottlenecked by the months to years of painstaking effort required to determine a single protein structure. Accurate computational approaches are needed to address this gap and to enable large-scale structural bioinformatics. Predicting the three-dimensional structure that a protein will adopt based solely on its amino acid sequence—the structure prediction component of the ‘protein folding problem’—has been an important open research problem for more than 50 years (9). Despite recent progress (10-14), existing methods fall far short of atomic accuracy, especially when no homologous structure is available. Here we provide the first computational method that can regularly predict protein structures with atomic accuracy even in cases in which no similar structure is known. We validated an entirely redesigned version of our neural network-based model, AlphaFold, in the challenging 14th Critical Assessment of protein Structure Prediction (CASP14) (8), demonstrating accuracy competitive with experimental structures in a majority of cases and greatly outperforming other methods. Underpinning the latest version of AlphaFold is a novel machine learning approach that incorporates physical and biological knowledge about protein structure, leveraging multi-sequence alignments, into the design of the deep learning algorithm.

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Proteins are essential to life, and understanding their structure can facilitate a mechanistic understanding of their function. Through an enormous experimental effort (1-4), the structures of around 100,000 unique proteins have been determined (5), but this represents a small fraction of the billions of known protein sequences (6,7). Structural coverage is bottlenecked by the months to years of painstaking effort required to determine a single protein structure. Accurate computational approaches are needed to address this gap and to enable large-scale structural bioinformatics. Predicting the three-dimensional structure that a protein will adopt based solely on its amino acid sequence—the structure prediction component of the ‘protein folding problem’—has been an important open research problem for more than 50 years (9). Despite recent progress (10-14), existing methods fall far short of atomic accuracy, especially when no homologous structure is available. Here we provide the first computational method that can regularly predict protein structures with atomic accuracy even in cases in which no similar structure is known. We validated an entirely redesigned version of our neural network-based model, AlphaFold, in the challenging 14th Critical Assessment of protein Structure Prediction (CASP14) (8), demonstrating accuracy competitive with experimental structures in a majority of cases and greatly outperforming other methods. Underpinning the latest version of AlphaFold is a novel machine learning approach that incorporates physical and biological knowledge about protein structure, leveraging multi-sequence alignments, into the design of the deep learning algorithm.

Research Assistant

Here is the key takeaway for this document.

By developing an accurate protein structure prediction algorithm coupled with existing large and well curated structure and sequence databases, we hope to accelerate the advancement of structural bioinformatics that can keep pace with the genomics revolution. Additional topics discussed in the text are: the role of AlphaFold in structural bioinformatics, the challenges of experimental structure determination, and the significance of evolutionary history in protein structure prediction. These topics are significant for researchers as they highlight the importance of computational methods in overcoming experimental limitations and advancing our understanding of protein structures.

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Proteins are essential to life, and understanding their structure can facilitate a mechanistic understanding of their function. Through an enormous experimental effort (1-4), the structures of around 100,000 unique proteins have been determined (5), but this represents a small fraction of the billions of known protein sequences (6,7). Structural coverage is bottlenecked by the months to years of painstaking effort required to determine a single protein structure. Accurate computational approaches are needed to address this gap and to enable large-scale structural bioinformatics. Predicting the three-dimensional structure that a protein will adopt based solely on its amino acid sequence—the structure prediction component of the ‘protein folding problem’—has been an important open research problem for more than 50 years (9). Despite recent progress (10-14), existing methods fall far short of atomic accuracy, especially when no homologous structure is available. Here we provide the first computational method that can regularly predict protein structures with atomic accuracy even in cases in which no similar structure is known. We validated an entirely redesigned version of our neural network-based model, AlphaFold, in the challenging 14th Critical Assessment of protein Structure Prediction (CASP14) (8), demonstrating accuracy competitive with experimental structures in a majority of cases and greatly outperforming other methods. Underpinning the latest version of AlphaFold is a novel machine learning approach that incorporates physical and biological knowledge about protein structure, leveraging multi-sequence alignments, into the design of the deep learning algorithm.


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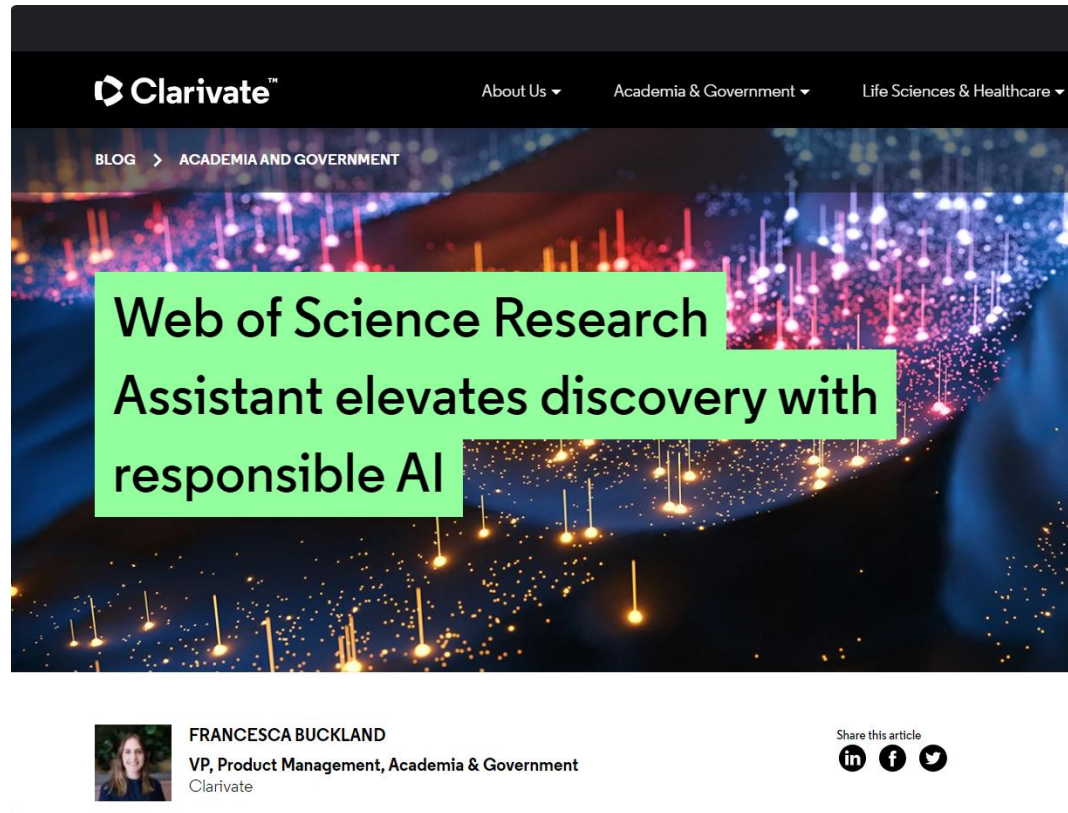
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线粒体在癌症中扮演着重要角色。它们是细胞能量生产和细胞代谢的主要细胞器。研究表明，癌细胞可以从免疫细胞中劫持线粒体，这揭示了癌症谜团中一个关键部分，即对正常细胞的依赖。功能性线粒体有助于癌细胞在恶性肿瘤微环境中生存，避免免疫监视，促进进展和治疗抵抗[1]。线粒体在癌症干细胞的代谢中起着关键作用，这些细胞是导致癌症复发和转移的肿瘤组分[1]。通过线粒体，癌细胞可以避免免疫监视，增强其恶性转化能力[4]。针对线粒体的药物在癌症治疗中显示出显著优势[4]。因此，针对线粒体可能提供新的癌症治疗机会[2]。总的来说，线粒体在癌症中扮演着重要角色，研究线粒体可能为未来提供有效且低毒性的癌症治疗方案提供理论支持[4]。

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Klein, K; He, KW; (...); Welsh, JW
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Zeng, Z; Fang, C; (...); Zhang, K
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See patterns in publishing on this topic

 See top authors on this topic
Most cited and connected authors

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Armeth, A; Shin, YJ; (...); Saito, O
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- 3 Biodiversity and Anthropogenic Climate Change: A Review of Knowledge for the Handling of the Risk
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Nedopil, C; Larsen, M; (...); Narain, D
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Journal

SCIENCE OF THE TOTAL ENVIRONMENT
Volume655Page1197-1206
10.1016/j.scitotenv.2018.11.319

Abstract

We assess whether a Payments for Ecosystem Services (PES) programme met its objectives of reducing soil erosion and yielding water in an environmental protected area, the Guariroba River Basin, Midwestern Brazil. We measured rainfall and water discharge throughout 2012 and 2016. During the same period, soil and water conservation practices were performed in the basin, such as: building level terraces and riparian vegetation recovery. We separated streamflow into baseflow and direct runoff, then we evaluated the baseflow index that indicated that groundwater significantly contributes to total flow. Therefore, to investigate the effects on streamflow, we performed a trend analysis in the baseflow time series using the Mann-Kendall test. In addition, we analysed the efficiency of soil erosion regulation practices over time, considering the total payment and the trends found in the baseflow. Whereas precipitation records present a decreasing trend (1 mm month⁻¹), baseflow tends to increase by 0.018 m(3) s⁻¹ in the same period. Our findings show that soil conservation practices performed in the basin increase baseflow and also provide a better resilience to endure extreme events such as drought based on an increase in forest areas and soil conservation practices such as level terrace. (C) 2018 Elsevier B.V. All rights reserved.

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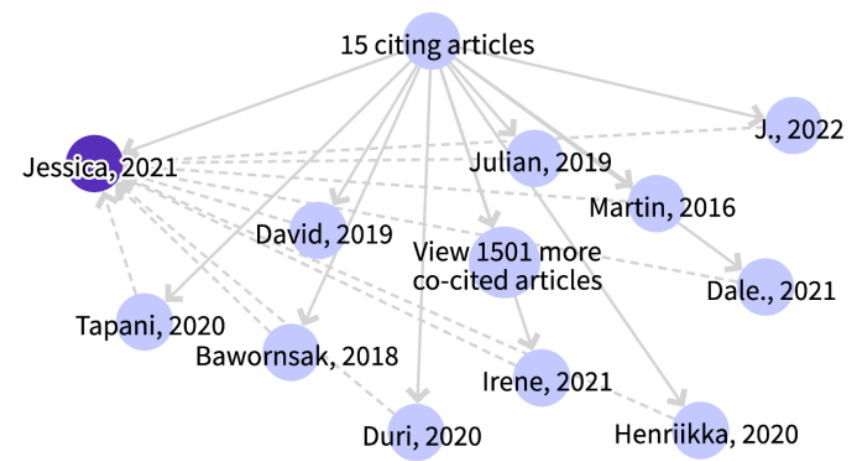


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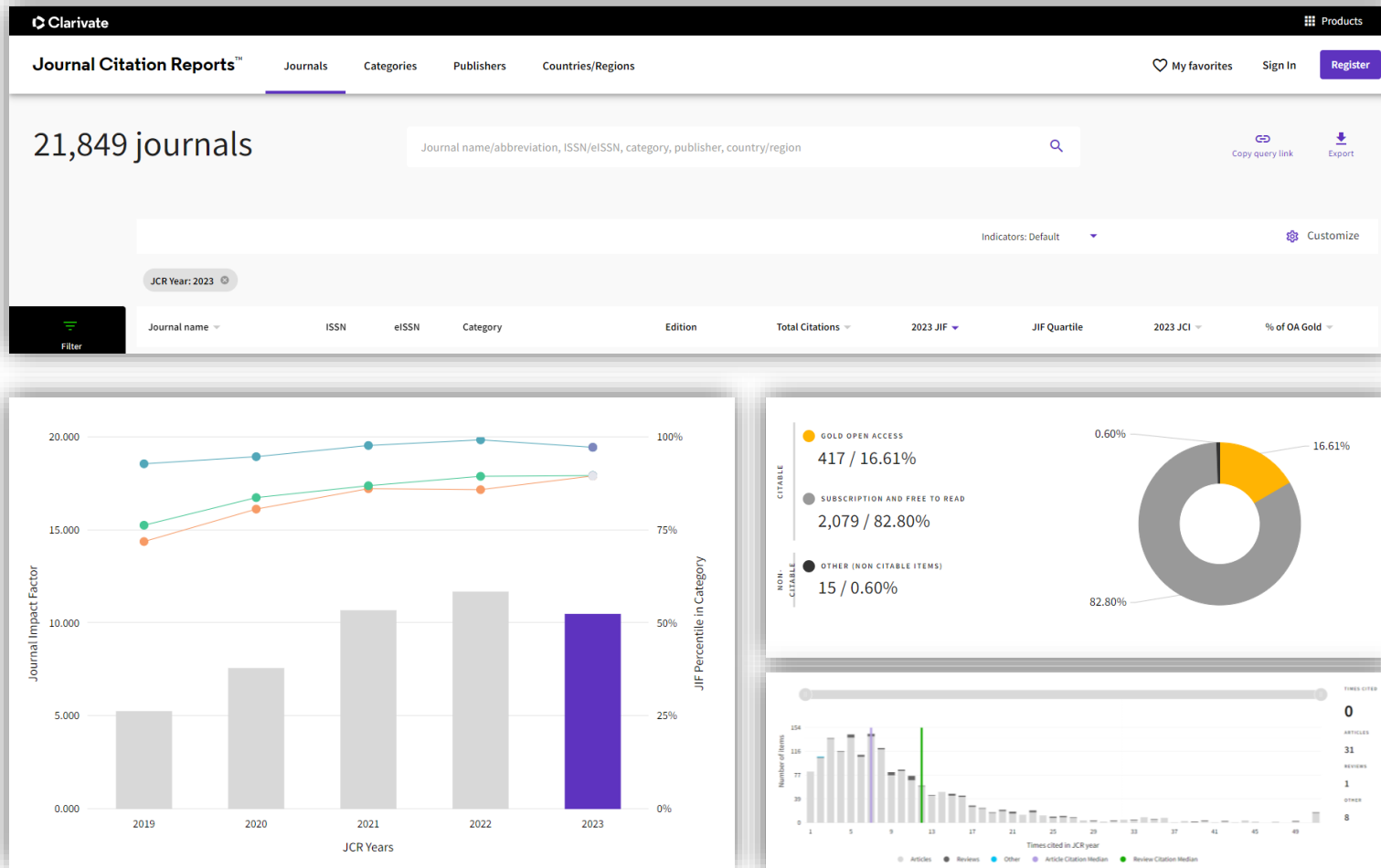


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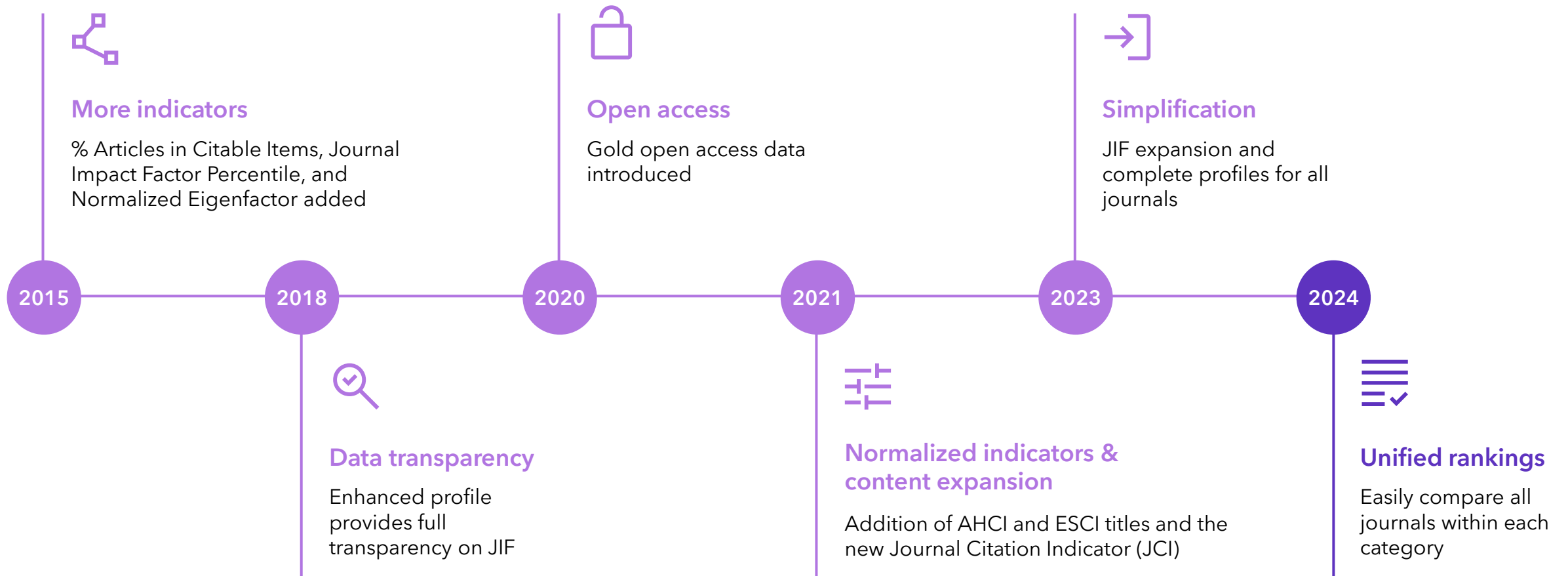
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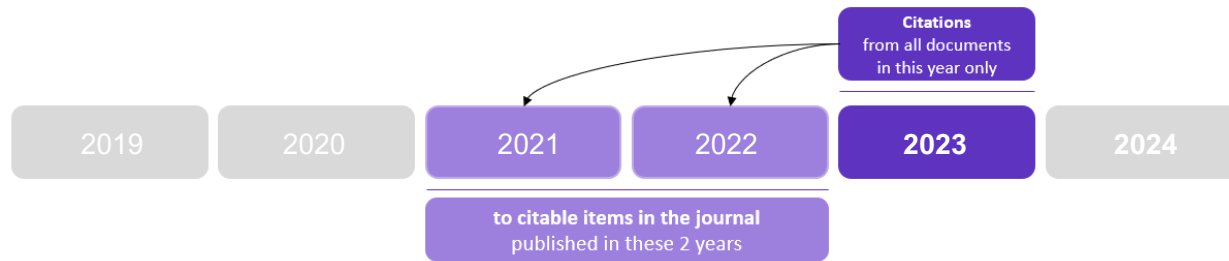


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Journal Impact Factor (JIF)

Metric for Journal level

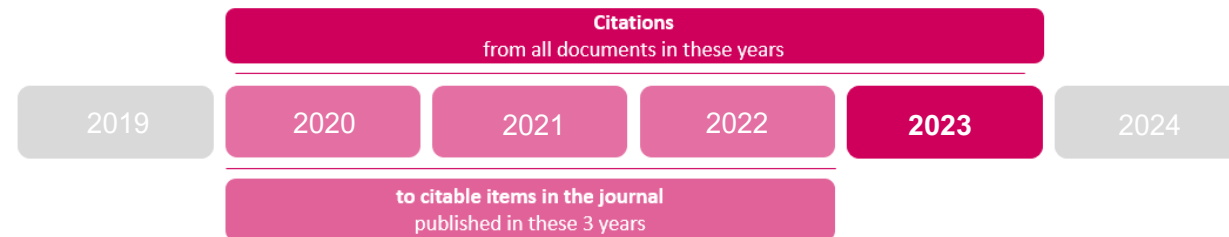
JIF can be used to compare journals within **the same research discipline**



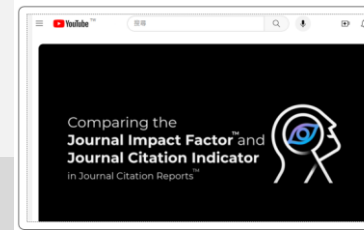
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Metric for Journal level-Normalized

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the **Normalized** citation impact of a journal compared to its peer group.

A JCI of 1.0 indicates average performance.

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Journal Citation Reports data

Journal Impact Factor Quartile

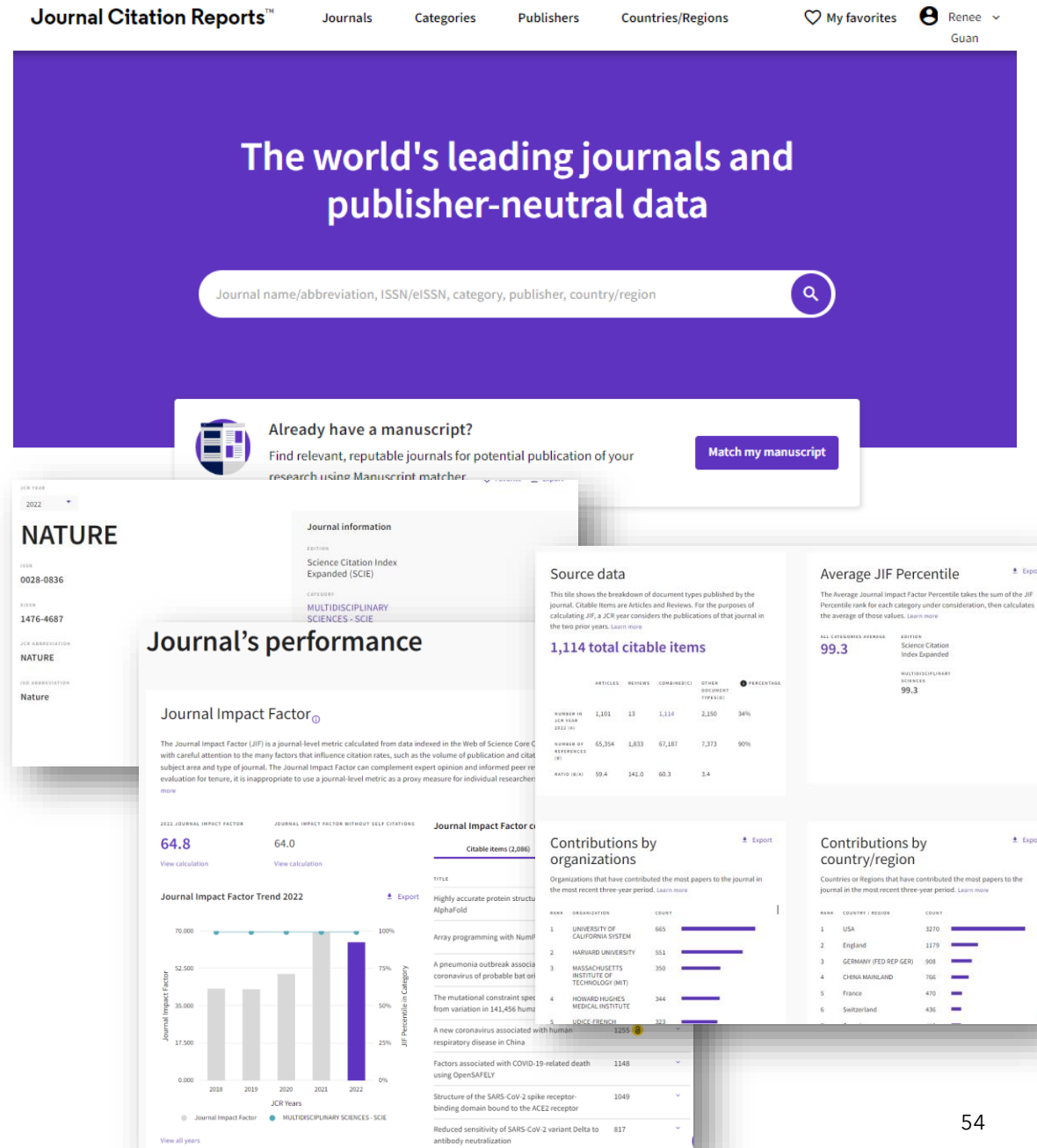
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A square QR code with a black and white pixelated pattern. In the center of the QR code is a small, stylized silhouette of a dinosaur, possibly a T-Rex, facing right.

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