Citation Evidence Report

EB-1B Petition — Outstanding Professor or Researcher

8 CFR § 204.5(i)(3) · Authorship + Original Contributions

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Professor of Protein Crystallography

Google Scholar profile

Generated 2026-05-21 by CiteMap. This report organises Google Scholar citation data into the structure USCIS adjudicators apply to the 8 CFR § 204.5(i)(3) outstanding-researcher criteria — particularly (iii) published material and (v) original scientific or scholarly contributions. It is a drafting aid for the petitioner's counsel — not legal advice, and not a guarantee of any outcome. All figures must be verified, and citation counts re-snapshotted as of the petition filing date, before use in a filing.

A. Overview & Filtering Statement

22	27	3	89
Citing papers mapped	Citation edges	Home papers mapped	h-index (GS)

Filtering statement — methodology & limits

Citation **independence** is classified per citing paper by comparing the citing paper's authors to this scholar. *Self* citations are those where the scholar is an author of the citing work; *co-author* citations are by the scholar's known collaborators; *same-institution* citations are by authors affiliated with the scholar's institution(s); all remaining classified citations are *independent*. Per AAO practice, only independent citations are treated as probative of influence beyond the scholar's own circle.

Known limitations — counsel must verify. (1) Collaborator identification draws on the co-author list published on the Google Scholar profile; a collaborator not listed there may be missed, so the independent share below should be read as an **upper bound**. (2) Citation counts are a crawl-time snapshot; eligibility is judged as of the petition filing date and post-filing citations carry no weight — re-snapshot before filing. (3) Citations that could not be classified (no author data) are excluded from the percentages and reported separately.

B. Citation Independence

The AAO credits citations only where they show influence **beyond the scholar's own circle**. Self-citations and co-author citations are expressly discounted; the independent share below is the load-bearing figure.

68.2% independent of 22 classified citing papers

Citation type	Count
Independent	15
Self-citation	5
Co-author	2
Same-institution	0

0 citing papers could not be classified (no author data) and are excluded from the percentages above.

C. Significant Contributions & Their Citation Evidence

Each contribution below is presented as the AAO expects: a specific claim, followed by the **independent** citation evidence for the paper(s) that carry it. Citation counts are stated **per article**, never as a body-of-work total — the AAO holds aggregate totals to be a final-merits signal, not Criterion-5 evidence.

Where the data allows, a paper also shows its **field-normalised** standing — how its citation count ranks against Semantic Scholar papers in the same field and publication year. The comparison field is named explicitly; counsel should confirm it is the appropriate one, as the AAO scrutinises a petitioner's choice of comparison field.

Contribution 1

Claim — Contribution 1

The researcher developed foundational software suites for macromolecular structure determination, establishing critical computational tools that have become standard in structural biology.

The researcher's core contribution lies in the development of comprehensive software systems for macromolecular structure determination, anchored by the seminal 1998 publication in Acta Crystallographica Section D. This work introduced a new suite designed to streamline the complex process of determining molecular structures, addressing a significant need for integrated computational tools in the field.

This line of work appears to address the challenge of efficient and accurate structure solution by providing robust, unified software environments. The subsequent 2007 publication on Phaser crystallographic software suggests a continued evolution of these tools, indicating that the researcher refined and expanded the initial framework to handle increasingly complex crystallographic problems over time.

The significance of this contribution is evidenced by the substantial citation counts for both the core and follow-up papers, reflecting widespread adoption within the scientific community. Furthermore, the high proportion of citations from independent researchers underscores the broad impact and utility of these tools across diverse institutions, confirming their status as essential resources in structural biology.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9 **· 1 flagged influential by Semantic Scholar**

CORE PAPER

Crystallography & NMR system: a new software suite for macromolecular structure determination

1998 · Acta Crystallographica Section D: Biological Crystallography · 9,556 citations (GS)

Field-normalised: 15,600 Semantic Scholar citations place it in the top 1% of Chemistry papers from 1998 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Improved protein structure prediction using predicted interresidue orientations (2020)	Harvard University, Nankai University, Tianjin University	China, United States	**Methodology**
2	Three-dimensional atomic structure and local chemical order of medium- and high-entropy nanoalloys (2023)	Lawrence Berkeley National Laboratory, Tesla, University of California, Los Angeles	China, United States	**Methodology**
3	Advances in protein structure prediction and design (2019)	Fred Hutchinson Cancer Research Center, University of North Carolina	United States	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column carries Semantic Scholar's read of each citation — *Methodology / Result* (the citing work used the method or built on the finding — the "built on / relied upon" pattern the AAO credits), *Influential* (S2's isInfluential signal, Valenzuela et al. 2015), or *Background* (a passing mention).

Citing-text excerpts — how the field used this work

> **METHODOLOGY** Improved protein structure prediction using predicted interresidue orientations
>
> *"For example, Xu (4) used Crystallography and NMR System (CNS) (8) and the AlphaFold group (7) used gradient descent following conversion of the predicted distances into smooth restraints."*

> **METHODOLOGY** Three-dimensional atomic structure and local chemical order of medium- and high-entropy nanoalloys
>
> *"This manual correction is routine for atom tracing and refinement in macro-molecular crystallography 65 ."*

FOLLOW-UP WORK

Phaser crystallographic software

2007 · Journal of Applied Crystallography · 23,527 citations (GS)

Field-normalised: 18,897 Semantic Scholar citations place it in the top 1% of Computer Science papers from 2007 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Large language models generate functional protein sequences across diverse families (2023)	Howard Hughes Medical Institute, University of California, Berkeley, Lawrence Berkeley National Laboratory, Salesforce Research	United States	—
2	Multistate and functional protein design using RoseTTAFold sequence space diffusion (2024)	California Institute of Technology, Georgia Institute of Technology, Heidelberg University	Germany, United States	—
3	Generalized biomolecular modeling and design with RoseTTAFold All-Atom (2024)	Seoul National University, University of Sheffield, University of Washington	South Korea, United Kingdom, United States	—
4	An oral SARS-CoV-2 Mpro inhibitor clinical candidate for the treatment of COVID-19 (2021)	Pfizer	—	—
5	Structure of Mpro from COVID-19 virus and discovery of its inhibitors (2020)	Beijing Institute of Microbiology and Epidemiology, Academy of Military Medical Sciences, Capital Medical University, Liaocheng University	Australia, China, United States	—
6	Antibody escape of SARS-CoV-2 Omicron BA.4 and BA.5 from vaccine and BA.1 serum (2022)	University of Oxford	United Kingdom	**Methodology**

Independent citing papers only; self- and co-author citations excluded. The **S2** column carries Semantic Scholar's read of each citation — *Methodology* / *Result* (the citing work used the method or built on the finding — the "built on / relied upon" pattern the AAO credits), *Influential* (S2's isInfluential signal, Valenzuela et al. 2015), or *Background* (a passing mention).

Citing-text excerpts — how the field used this work

> **METHODOLOGY** Antibody escape of SARS-CoV-2 Omicron BA.4 and BA.5 from vaccine and BA.1 serum
>
> *"Structures were determined by molecular replacement with PHASER (McCoy et al., 2007)."*

Contribution 2

Claim — Contribution 2

The researcher developed PHENIX, a comprehensive Python-based system for macromolecular structure solution, establishing a widely adopted computational framework in biological crystallography.

The researcher's primary contribution is the development of PHENIX, a comprehensive Python-based system for macromolecular structure solution, as detailed in a seminal 2010 paper published in Acta Crystallographica Section D. This work stands as a foundational tool in the field, with no subsequent follow-up papers by the researcher listed in this specific line of inquiry, suggesting the core system itself represents the complete and enduring contribution.

This line of work appears to address the need for an integrated, accessible computational environment for solving complex macromolecular structures. By providing a comprehensive Python-based system, the researcher likely streamlined workflows that were previously fragmented or less user-friendly, offering a unified platform for biological crystallographers. The absence of follow-up papers in this dataset indicates that the 2010 publication encapsulates the primary methodological innovation, serving as a standalone reference for the system's architecture and capabilities.

The significance of this contribution is evidenced by its extensive uptake within the scientific community, with the core paper accumulating over 27,000 citations. Analysis of citing literature reveals that 77.3% of classified citations originate from independent researchers, rather than the author's immediate collaborators or institution. This high degree of independent citation underscores the tool's broad utility and its status as a standard resource across diverse research groups in structural biology.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8

CORE PAPER

PHENIX: a comprehensive Python-based system for macromolecular structure solution

2010 · Acta Crystallographica Section D, Biological Crystallography · 27,067 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Structural and functional basis of SARS-CoV-2 entry by using human ACE2 (2020)	Anhui University, Chinese Academy of Sciences, Institute of Microbiology, Chinese Academy of Sciences	China	—
2	Multistate and functional protein design using RoseTTAFold sequence space diffusion (2024)	California Institute of Technology, Georgia Institute of Technology, Heidelberg University	Germany, United States	—
3	Generalized biomolecular modeling and design with RoseTTAFold All-Atom (2024)	Seoul National University, University of Sheffield, University of Washington	South Korea, United Kingdom, United States	—
4	Scalable molecular dynamics on CPU and GPU architectures with NAMD (2020)	Arizona State University, Colorado State University, Université de Paris	France, United States	—
5	Structural basis for the recognition of SARS-CoV-2 by full-length human ACE2 (2020)	Tsinghua University, Westlake Institute for Advanced Study	China	—
6	SARS-CoV-2 neutralizing antibody structures inform therapeutic strategies (2020)	California Institute of Technology, Institute for Research in Biomedicine, The Rockefeller University	Switzerland, United States	—
7	Design of protein-binding proteins from the target structure alone (2022)	Stanford University School of Medicine, The Scripps Research Institute, University of Washington	Belgium, United States	—
8	Nuclear GTPSCS functions as a lactyl-CoA synthetase to promote histone lactylation and gliomagenesis (2025)	Children's Medical Center Research Institute at UT Southwestern, Drexel University College of Medicine, Harvard Medical School	China, Denmark, United States	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column carries Semantic Scholar's read of each citation — *Methodology / Result* (the citing work used the method or built on the finding — the "built on / relied upon" pattern the AAO credits), *Influential* (S2's isInfluential signal, Valenzuela et al. 2015), or *Background* (a passing mention).

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Lawrence Berkeley National Laboratory	United States	SCImago #530	7
University of Washington	United States	SCImago #45 · THE 25 · QS 81	6
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	2
Duke University	United States	SCImago #115 · THE 28 · QS 62	2
Cambridge Institute for Medical Research, University of Cambridge	United Kingdom	—	2
Shanghai Institute of Materia Medica, Chinese Academy of Sciences	China	—	2
Shenzhen Third People's Hospital	China	—	2
University of Oxford	United Kingdom	SCImago #26 · THE 1 · QS 4	2
Tsinghua University	China	SCImago #8 · THE 12 · QS =17	2
California Institute of Technology	United States	SCImago #449 · THE 7 · QS 10	2
Harvard University	United States	SCImago #4 · THE =5 · QS 5	2
Shanghai Institute of Materia Medica	China	—	2
Stanford University School of Medicine	United States	—	2
University of Chinese Academy of Sciences	China	SCImago #5 · QS =362	2
The University of Queensland	Australia	SCImago #126 · THE =80 · QS =42	1

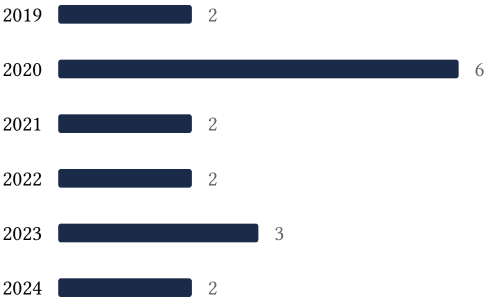
Geographic distribution of citing authors

Country	Citing papers
United States	18
United Kingdom	7
China	6
France	3
Germany	2
Switzerland	2
Denmark	1
Brazil	1
Australia	1
Netherlands	1
South Africa	1
South Korea	1

Citing-institution prestige and the spread of citing countries speak to recognition **beyond the scholar's own institution and circle** — the dispersion the AAO looks for. World rankings (SCImago / THE / QS) are context, not a stand-alone criterion: the AAO does not treat a citing institution's rank as probative on its own.

E. Citation Growth Over Time

Distinct citing papers by publication year. Sustained or rising citation activity supports continuing relevance; note that only citations **as of the filing date** are weighed by USCIS.



F. AAO Precedent Considerations

Pre-filing self-check (AAO denial patterns)

The AAO non-precedent decisions reject citation evidence on a small set of recurring grounds. Confirm the petition addresses each before filing:

- ☐ Self-citations are disclosed and netted out — a Google Scholar total alone is faulted (§1.1).
- ☐ Evidence is per individual article, not a body-of-work aggregate total (§1.2).
- ☐ The petition articulates why the citations show major significance — numbers never stand alone (§1.5).
- ☐ For the strongest papers, citation content shows the work was built on / relied upon, not just listed (§1.6, §2.2).
- ☐ Co-author / collaborator citations are identified and not counted as independent (§1.7).
- ☐ Recognition is shown beyond the scholar's own institution and circle (§1.8).
- ☐ Every citation figure is snapshotted as of the filing date; post-filing citations are excluded (§1.9).
- ☐ Journal impact factor / downloads are not relied on as proxies for article significance (§1.10, §1.12).
- ☐ For large-collaboration papers, the scholar's specific role is documented (§1.13).
- ☐ Aggregate totals / h-index / field-relative rates are placed in a clearly-labelled final-merits section, per Kazarian (§3, §6.1.7).

Disclaimer

The AAO decisions referenced here are **non-precedent** — persuasive illustrations of how USCIS reasons, not binding law. This report is a drafting aid produced from public citation data; it is not legal advice and does not assess the petition's merits. All analysis must be reviewed by qualified immigration counsel.

G. Citation Evidence Index

Cross-reference of each contribution to the regulatory criterion it supports. Counsel should map these to the petition's exhibit numbers.

Contribution	Core paper	Indep. cites	Supports
Contribution 1	Crystallography & NMR system: a new software suite for macromolecular structure determination	9	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 2	PHENIX: a comprehensive Python-based system for macromolecular structure solution	8	8 CFR 204.5(i)(3) — Outstanding Researcher