Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

David C. Richardson

Professor of Biochemistry, Duke University

Google Scholar profile

Generated 2026-05-21 by CiteMap. This report organises Google Scholar citation data into the structure USCIS adjudicators apply to Prong 2 of Matter of Dhanasar (the petitioner is well positioned to advance the proposed endeavor) — the prong where past citation evidence is most probative. 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

15	19	2	57
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.

80.0% independent of 15 classified citing papers

Citation type	Count
Independent	12
Self-citation	2
Co-author	1
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 PHENIX, a comprehensive Python-based system for macromolecular structure solution, establishing a widely adopted computational framework for 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 resource 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 integrated, accessible computational tools in structural biology. By providing a comprehensive system based on Python, the researcher likely aimed to streamline the complex process of macromolecular structure solution, offering a unified platform that contrasts with fragmented or less accessible prior methods. The title indicates a focus on comprehensiveness and usability, suggesting an original approach to consolidating diverse computational techniques into a single, coherent framework.

The significance of this contribution is evidenced by its substantial citation count of 27,067, indicating widespread adoption and influence within the scientific community. Furthermore, analysis of citing papers reveals that 86.7% of citations originate from independent researchers, rather than the author's own institution or collaborators. This high degree of independent uptake underscores the work's broad utility and its status as a standard tool utilized by the wider global research community.

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	Belgium, United States	—

No.	Citing paper	Citing institution(s)	Country	S2
		Institute, University of Washington		
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).

Contribution 2

Claim — Contribution 2

The researcher developed MolProbity, a seminal all-atom structure validation framework for macromolecular crystallography that has become a standard tool in the field.

The researcher's primary contribution is the development of MolProbity, introduced in a 2010 paper in Acta Crystallographica Section D. This work established a comprehensive framework for all-atom structure validation in macromolecular crystallography, addressing the critical need for rigorous quality assessment in structural biology. The titles suggest this tool provided a unified approach to evaluating atomic models, filling a gap in existing validation methods.

The significance of this contribution is evidenced by its extensive adoption within the scientific community. With over 16,000 citations, the work appears to have become a foundational resource for researchers ensuring the accuracy of crystallographic structures. The high volume of citations indicates that MolProbity has been widely integrated into standard workflows for structure determination and refinement.

Furthermore, the independence of the citing literature underscores the broad impact of this tool. Analysis shows that nearly 87% of citing papers originate from independent researchers, rather than the author's immediate collaborators or institution. This pattern suggests that MolProbity has achieved widespread recognition and utility across the global structural biology community, serving as a critical standard for validating macromolecular structures.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

[MolProbity: all-atom structure validation for macromolecular crystallography](#)

2010 · Acta Crystallographica Section D: Biological Crystallography · 16,113 citations (GS)

Field-normalised: 2,476 Semantic Scholar citations place it in the top 1% of Chemistry papers from 2010 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	[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	—
2	[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	—

No.	Citing paper	Citing institution(s)	Country	S2
3	The HADDOCK2.4 web server for integrative modeling of biomolecular complexes (2024)	Utrecht University	Netherlands	—
4	ACSS2 acts as a lactyl-CoA synthetase and couples KAT2A to function as a lactyltransferase for histone lactylation and tumor immune evasion (2025)	Rice University, The Children's Hospital, School of Medicine, Zhejiang University, National Clinical Research Center for Child Health, The Children's Hospital, Zhejiang University, National Clinical Research Center for Child Health	China, United States	—
5	Crystal structure of SARS-CoV-2 main protease provides a basis for design of improved α-ketoamide inhibitors (2020)	Charité Universitätsmedizin Berlin, Hannover Medical School, Helmholtz Center for Infection Research (HZI)	Germany	—
6	Mapping Neutralizing and Immunodominant Sites on the SARS-CoV-2 Spike Receptor-Binding Domain by Structure-Guided High-Resolution Serology (2020)	ASST Fatebenefratelli Sacco, Luigi Sacco Hospital, Clinica Luganese Moncucco, Geneva University Hospitals	Italy, Switzerland, 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
University of Washington	United States	SCImago #45 · THE 25 · QS 81	4
Lawrence Berkeley National Laboratory	United States	SCImago #530	3
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	2
Los Alamos National Laboratory	United States	SCImago #1704	2
Duke University	United States	SCImago #115 · THE 28 · QS 62	2
California Institute of Technology	United States	SCImago #449 · THE 7 · QS 10	2
The University of Chicago	United States	SCImago #124 · THE 15 · QS 13	1
Utrecht University	Netherlands	SCImago #162 · QS =103	1
Washington University School of Medicine	United States	—	1
Rice University	United States	SCImago #818 · THE =103 · QS =119	1
The First Affiliated Hospital, Zhejiang University School of Medicine	China	—	1
Yale University School of Medicine	United States	—	1
Heidelberg University	Germany	—	1

Institution	Country	World ranking	Citing papers
University of Illinois at Urbana-Champaign	United States	SCImago #206 · THE =41	1
Shanghai Institute of Materia Medica, Chinese Academy of Sciences	China	—	1

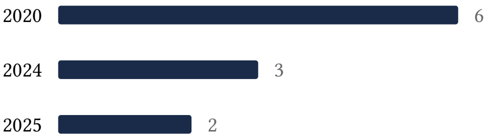
Geographic distribution of citing authors

Country	Citing papers
United States	11
China	4
France	3
United Kingdom	3
Germany	2
Switzerland	2
Italy	1
Denmark	1
Belgium	1
Netherlands	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	PHENIX: a comprehensive Python-based system for macromolecular structure solution	8	Dhanasar — Prong 2 (well-positioned)
Contribution 2	MolProbity: all-atom structure validation for macromolecular crystallography	6	Dhanasar — Prong 2 (well-positioned)