

# Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

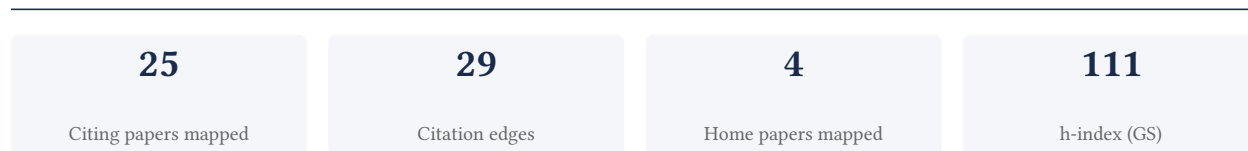
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[Google Scholar profile](#)

**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



### 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.

**72.0% independent** of 25 classified citing papers

Citation type	Count
Independent	18
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 the Crystallography & NMR System software suite, establishing a foundational platform for macromolecular structure determination that has been widely adopted and extended in the field.*

The researcher's primary contribution is the development of the Crystallography & NMR System, introduced in a seminal 1998 paper. This work established a comprehensive software suite designed to facilitate the determination of macromolecular structures, serving as the cornerstone for subsequent advancements in the field.

This line of work appears to address the need for integrated computational tools in structural biology. The progression from the initial 1998 suite to a 2019 update on Phenix suggests a sustained effort to refine and expand capabilities for processing data from X-rays, neutrons, and electrons, indicating an evolution in methodological support for complex structure determination.

The significance of this contribution is evidenced by the core paper's 20,885 citations and the follow-up's 7,457 citations, reflecting broad adoption. Furthermore, analysis of citing literature indicates that 72.0% of citations originate from independent researchers, demonstrating that the work has had a substantial impact beyond the researcher's immediate institutional circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9 · 2 flagged influential by Semantic Scholar

#### CORE PAPER

### [Crystallography & NMR system: a new software suite for macromolecular structure determination](#)

1998 · 20,885 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	<a href="#">The HADDOCK2.4 web server for integrative modeling of biomolecular complexes</a> (2024)	Utrecht University	Netherlands	Influential
2	<a href="#">Deep-learning-based single-domain and multidomain protein structure prediction with D-I-TASSER</a> (2025)	Michigan State University, Nankai University, National University of Singapore	China, Singapore, United States	—
3	<a href="#">Improved protein structure prediction using predicted interresidue orientations</a> (2020)	Harvard University, Nankai University, Tianjin University	China, United States	Methodology
4	<a href="#">Three-dimensional atomic structure and local chemical order of medium- and high-entropy nanoalloys</a> (2023)	Lawrence Berkeley National Laboratory, Tesla, University of California, Los Angeles	China, United States	Methodology
5	<a href="#">Advances in protein structure prediction and design</a> (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

1 “This manual correction is routine for atom tracing and refinement in macro-molecular crystallography 65.”

#### FOLLOW-UP WORK

### Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix

2019 · Acta Crystallographica Section D: Structural Biology · 7,457 citations (GS)

Field-normalised: 5,057 Semantic Scholar citations place it in the top 1% of Physics papers from 2019 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	<a href="#">Cross-Linking Mass Spectrometry for Investigating Protein Conformations and Protein-Protein Interactions—A Method for All Seasons</a> (2022)	Biozentrum, Institute of Pharmacy, Martin Luther University Halle-Wittenberg	Germany	—
2	<a href="#">UCSF ChimeraX: Tools for structure building and analysis</a> (2023)	University of California San Francisco	United States	Methodology
3	<a href="#">Exploring monkeypox virus proteins and rapid detection techniques</a> (2024)	Nazarbayev University	Kazakhstan	—
4	<a href="#">Machine learning-aided engineering of hydrolases for PET depolymerization</a> (2022)	The University of Texas at Austin	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** UCSF ChimeraX: Tools for structure building and analysis

“Developments such as AlphaFold structure prediction, robust fitting in maps accounting for noise and variable resolution in Phenix, and refinement pipelines built on Rosetta are reducing the researcher time needed to create a model while improving the accuracy.”

## Contribution 2

### Claim — Contribution 2

*The researcher developed PHENIX, a comprehensive Python-based system for macromolecular structure solution, establishing a widely adopted computational framework that has garnered over 27,000 citations.*

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 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 that facilitates broader adoption across the structural biology community.

The significance of this contribution is evidenced by its extensive uptake, with the core paper accumulating over 27,000 citations. Furthermore, analysis of citing literature indicates that 72% of these citations originate from independent researchers, demonstrating that the tool has become a standard, widely utilized resource beyond the researcher’s immediate institutional or collaborative network.

## CORE PAPER

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

2010 · Acta Crystallographica Section D: Biological Crystallography · 27,070 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	<a href="#">Multistate and functional protein design using RoseTTAFold sequence space diffusion</a> (2024)	California Institute of Technology, Georgia Institute of Technology, Heidelberg University	Germany, United States	—
2	<a href="#">Generalized biomolecular modeling and design with RoseTTAFold All-Atom</a> (2024)	Seoul National University, University of Sheffield, University of Washington	South Korea, United Kingdom, United States	—
3	<a href="#">Scalable molecular dynamics on CPU and GPU architectures with NAMD</a> (2020)	Arizona State University, Colorado State University, Université de Paris	France, United States	—
4	<a href="#">Structural basis for the recognition of SARS-CoV-2 by full-length human ACE2</a> (2020)	Tsinghua University, Westlake Institute for Advanced Study	China	—
5	<a href="#">SARS-CoV-2 neutralizing antibody structures inform therapeutic strategies</a> (2020)	California Institute of Technology, Institute for Research in Biomedicine, The Rockefeller University	Switzerland, United States	—
6	<a href="#">Design of protein-binding proteins from the target structure alone</a> (2022)	Stanford University School of Medicine, The Scripps Research Institute, University of Washington	Belgium, 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	6
Lawrence Berkeley National Laboratory	United States	SCImago #530	6
Nankai University	China	SCImago #347 · THE 251–300 · QS =355	2
Duke University	United States	SCImago #115 · THE 28 · QS 62	2
Harvard University	United States	SCImago #4 · THE =5 · QS 5	2
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	2
Tsinghua University	China	SCImago #8 · THE 12 · QS =17	2
University of Oxford	United Kingdom	SCImago #26 · THE 1 · QS 4	2
Stanford University School of Medicine	United States	—	2

Institution	Country	World ranking	Citing papers
Cambridge Institute for Medical Research, University of Cambridge	United Kingdom	—	2
Los Alamos National Laboratory	United States	SCImago #1704	2
California Institute of Technology	United States	SCImago #449 · THE 7 · QS 10	2
University of Bath	United Kingdom	SCImago #1061 · THE 251–300 · QS =132	1
The University of Queensland	Australia	SCImago #126 · THE =80 · QS =42	1
University of California San Francisco	United States	SCImago #98	1

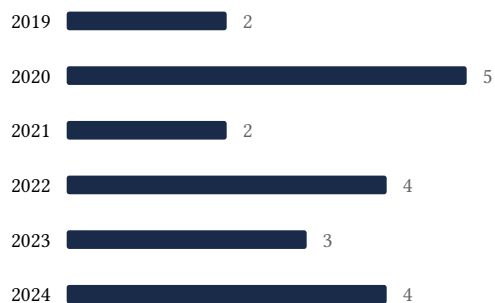
### Geographic distribution of citing authors

Country	Citing papers
United States	19
United Kingdom	7
China	5
France	4
Germany	3
Netherlands	2
Switzerland	2
South Africa	1
South Korea	1
Sweden	1
Kazakhstan	1
Austria	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

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### 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

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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	Dhanasar – Prong 2 (well-positioned)
Contribution 2	PHENIX: a comprehensive Python-based system for macromolecular structure solution	6	Dhanasar – Prong 2 (well-positioned)