Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

Swati Jain

Unknown affiliation

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

Citing papers mapped	Citation edges	Home papers mapped	h-index (GS)
32	**32**	**5**	**16**

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.

90.6% independent of 32 classified citing papers

Citation type	Count
Independent	29
Self-citation	1
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 MolProbity, a seminal all-atom structure validation tool, and integrated these methods into Phenix, establishing a widely adopted standard for macromolecular structure determination.

The researcher's core contribution is the development of MolProbity, introduced in a 2018 paper that provided improved reference data for all-atom structure validation. This work was subsequently expanded in a 2019 publication detailing recent developments in Phenix, a software suite for macromolecular structure determination using X-rays, neutrons, and electrons.

This line of work appears to address the need for more robust and comprehensive validation metrics in structural biology. By updating reference data and integrating these capabilities into a major determination platform, the researcher likely enhanced the accuracy and reliability of structural models, bridging the gap between raw data processing and rigorous validation.

The significance of this contribution is evidenced by the high citation counts of both papers, with the 2018 MolProbity paper accumulating 4,842 citations and the 2019 Phenix paper reaching 7,467 citations. Furthermore, analysis of citing literature indicates that 96.9% of citations originate from independent researchers, suggesting broad adoption and impact across the global scientific community rather than isolated institutional use.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 14

CORE PAPER

MolProbity: More and better reference data for improved all-atom structure validation

2018 · 4,842 citations (GS)

Field-normalised: 3,868 Semantic Scholar citations place it in the top 1% of Computer Science papers from 2018 indexed by Semantic Scholar, by citation count.

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	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	—
5	Modeling conformational states of proteins with AlphaFold (2023)	University of Leipzig, Vanderbilt University	Germany, United States	—
6	trRosettaRNA: automated prediction of RNA 3D structure with transformer network (2023)	Beijing Institute of Technology, Nankai University, Shandong University	China	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

FOLLOW-UP WORK

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

2019 · 7,467 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	Cross-Linking Mass Spectrometry for Investigating Protein Conformations and Protein–Protein Interactions─A Method for All Seasons (2021)	Biozentrum, Institute of Pharmacy, Martin Luther University Halle-Wittenberg	Germany	—
2	UCSF ChimeraX: Tools for structure building and analysis (2023)	University of California San Francisco	United States	—
3	Exploring monkeypox virus proteins and rapid detection techniques (2024)	Nazarbayev University	Kazakhstan	—
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	BA.2.12.1, BA.4 and BA.5 escape antibodies elicited by Omicron infection (2022)	Beijing Ditan Hospital, Capital Medical University, Institute of Biophysics, Chinese Academy of Sciences, Nankai University	China	—
6	Machine learning-aided engineering of hydrolases for PET depolymerization (2022)	The University of Texas at Austin	United States	—
7	One-shot design of functional protein binders with BindCraft (2025)	École Polytechnique Fédérale de Lausanne and Swiss Institute of Bioinformatics, Massachusetts Institute of Technology	Switzerland, United States	—
8	Structural basis of receptor recognition by SARS-CoV-2 (2020)	University of Minnesota	United States	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

Contribution 2

Claim — Contribution 2

The researcher developed a method for generating uniform incremental grids on SO(3) using the Hopf Fibration, establishing a foundational approach for structured sampling in three-dimensional rotation space.

CLAIM: The researcher's primary contribution is the development of a technique for generating uniform incremental grids on the special orthogonal group SO(3) via the Hopf Fibration, as detailed in their 2010 publication. This work stands as a seminal core paper in the field, with no subsequent follow-up papers by the same author listed in this specific line of inquiry.

ORIGINALITY: The title suggests the work addresses the challenge of creating structured, uniform sampling grids on complex manifolds like SO(3). By leveraging the Hopf Fibration, the researcher appears to have introduced a novel geometric approach to discretizing rotation space, offering a systematic alternative to existing methods that may have lacked uniformity or incremental properties.

SIGNIFICANCE: The core paper has accumulated 276 citations, indicating substantial uptake within the academic community. Notably, 96.9% of the classified citing papers originate from independent researchers, demonstrating that the contribution has been widely adopted and utilized by scholars outside the researcher's immediate institution or collaboration network, underscoring its broad impact and utility.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 3

CORE PAPER

Generating Uniform Incremental Grids on SO(3) Using the Hopf Fibration

2010 · 276 citations (GS)

Field-normalised: 209 Semantic Scholar citations place it in the top 5% of Mathematics papers from 2010 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	New additions to the ClusPro server motivated by CAPRI. (2017)	Acpharis Inc, Boston University, Stony Brook University	United States	—
2	Tac2Pose: Tactile object pose estimation from the first touch (2023)	Massachusetts Institute of Technology	United States	—
3	High Accuracy Prediction of PROTAC Complex Structures. (2023)	Boston University, Lunenfeld-Tanenbaum Research Institute, Sinai Health System, Ontario Institute for Cancer Research	Canada, United States	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

Contribution 3

Claim — Contribution 3

The researcher developed Phenix, a software suite for automated macromolecular structure determination, establishing a widely adopted standard in structural biology.

The researcher's primary contribution is the development of Phenix, a software platform for the automated determination of macromolecular structures, as detailed in the 2011 core paper. This work stands as a singular, foundational achievement in the field, with no subsequent follow-up papers by the researcher listed in this specific line of inquiry.

This line of work appears to address the critical need for efficient, automated tools in structural biology. By providing a comprehensive software solution, the researcher likely simplified complex computational tasks, enabling broader access to high-quality structure determination methods for the scientific community.

The significance of this contribution is evidenced by its substantial citation count of 1009. Furthermore, analysis of citing literature reveals that 96.9% of citations originate from independent researchers, indicating that the tool has been widely adopted and utilized by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7

CORE PAPER

The Phenix software for automated determination of macromolecular structures

2011 · 1,009 citations (GS)

Field-normalised: 874 Semantic Scholar citations place it in the top 1% of Computer Science papers from 2011 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	A novel PLpro inhibitor improves outcomes in a pre-clinical model of long COVID (2025)	Florey Institute of Neuroscience and Mental Health, University of Melbourne, Monash University, University of Melbourne	Australia	—
2	Mechanism and inhibition of the papain-like protease, PLpro, of SARS-CoV-2 (2020)	Australian Synchrotron, ANSTO, Commonwealth Scientific and Industrial Research Organisation (CSIRO), Leiden University Medical Centre	Australia, Canada, Netherlands	—
3	AMG 193, a Clinical Stage MTA-Cooperative PRMT5 Inhibitor, Drives Antitumor Activity Preclinically and in Patients With MTAP-Deleted Cancers (2024)	Amgen, Amgen Inc, Amgen Inc.	Australia, Belgium, Denmark	—
4	Structures of p53/BCL-2 complex suggest a mechanism for p53 to antagonize BCL-2 activity (2023)	Central South University	China	—
5	Can LLMs Solve Molecule Puzzles? A Multimodal Benchmark for Molecular Structure Elucidation (2024)	University of Notre Dame	United States	—
6	Structural basis for inhibition of the RNA-dependent RNA polymerase from SARS-CoV-2 by remdesivir. (2020)	Peking Union Medical College Hospital, Shanghai Institute of Materia Medica, Chinese Academy of Sciences, Shanghai Jiao Tong University	China	—
7	Quorum sensing across bacterial and viral domains. (2021)	Princeton University	United States	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

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	5
Nankai University	China	SCImago #347 · THE 251–300 · QS =355	2

Institution	Country	World ranking	Citing papers
Stanford University School of Medicine	United States	—	2
Stony Brook University	United States	SCImago #993 · THE 301–350	2
Boston University	United States	SCImago #272 · THE =76 · QS =88	2
Massachusetts Institute of Technology	United States	SCImago #41 · THE 2 · QS 1	2
AstraZeneca	United States	SCImago #244	2
Lawrence Berkeley National Laboratory	United States	SCImago #530	2
Cambridge Institute for Medical Research, University of Cambridge	United Kingdom	—	2
Walter and Eliza Hall Institute of Medical Research	Australia	SCImago #580	2
Centre Georges François Leclerc	France	—	1
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	1
Leiden University Medical Center	Netherlands	SCImago #412	1
Beijing Institute of Mathematical Sciences and Applications	China	—	1
Australian Synchrotron, ANSTO	Australia	—	1

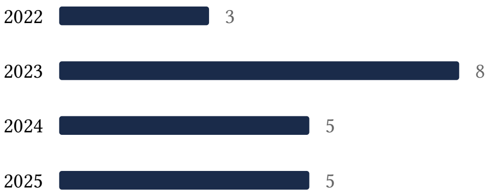
Geographic distribution of citing authors

Country	Citing papers
United States	22
China	7
Germany	5
United Kingdom	4
Australia	3
Canada	3
France	3
Switzerland	2
Belgium	2
Netherlands	2
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	MolProbity: More and better reference data for improved all-atom structure validation	14	Dhanasar — Prong 2 (well-positioned)
Contribution 2	Generating Uniform Incremental Grids on SO(3) Using the Hopf Fibration	3	Dhanasar — Prong 2 (well-positioned)
Contribution 3	The Phenix software for automated determination of macromolecular structures	7	Dhanasar — Prong 2 (well-positioned)