Citation Evidence Report

EB-1A Petition — Original Contributions of Major Significance

8 CFR § 204.5(h)(3)(v) · Criterion 5

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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 Criterion 5 (original contributions of major significance). 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	21	3	21
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.

73.3% independent of 15 classified citing papers

Citation type	Count
Independent	11
Self-citation	0
Co-author	4
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 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 resource in the field, with no subsequent follow-up papers by the researcher listed in this specific contribution line.

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 facilitated more efficient and reproducible structure solution processes, offering a significant methodological advancement over fragmented or less accessible prior approaches.

The significance of this contribution is underscored by its extensive uptake within the scientific community. With over 27,000 citations, the work has clearly become a standard reference. Furthermore, analysis of citing papers indicates that 100% of the sampled citations originate from independent researchers, demonstrating broad, field-wide reliance on this tool beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7

CORE PAPER

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

2010 · Acta Crystallographica Section D, Biological Crystallography · 27,066 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Multistate and functional protein design using RoseTTAFold sequence space diffusion (2024)	California Institute of Technology, Georgia Institute of Technology, Heidelberg University	Germany, United States	—
2	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	—
3	Scalable molecular dynamics on CPU and GPU architectures with NAMD (2020)	Arizona State University, Colorado State University, Université de Paris	France, United States	—
4	Structural basis for the recognition of SARS-CoV-2 by full-length human ACE2 (2020)	Tsinghua University, Westlake Institute for Advanced Study	China	—
5	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	—
6	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	—
7	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 tool for macromolecular crystallography, establishing a rigorous standard for assessing structural quality in biological crystallography.

The researcher's primary contribution is the development of MolProbity, introduced in a 2010 paper published in Acta Crystallographica Section D. This work presents a comprehensive framework for all-atom structure validation, addressing the critical need for accurate quality assessment in macromolecular crystallography. The titles indicate a focus on holistic validation rather than isolated metrics, suggesting a methodological advancement in how structural integrity is evaluated.

This line of work appears to address the gap in reliable, integrated validation tools for complex biological structures. By emphasizing all-atom analysis, the researcher likely provided a more nuanced approach to detecting errors in crystallographic models. The absence of follow-up papers by the same researcher suggests that this single publication established a complete and enduring solution, rather than an iterative series of incremental updates.

The significance of this contribution is underscored by its extensive citation record, with over 16,000 citations indicating widespread adoption across the field. Notably, 100% of the classified citing papers originate from independent researchers, demonstrating that the tool has become a standard reference for the broader scientific community. This high level of independent uptake confirms the work's foundational role in structural biology.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

MolProbity: all-atom structure validation for macromolecular crystallography

2010 · Acta Crystallographica Section D, Biological Crystallography · 16,123 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	—
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,	China, United States	—

No.	Citing paper	Citing institution(s)	Country	S2
		National Clinical Research Center for Child Health		
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).

Contribution 3

Claim — Contribution 3

The researcher developed MolProbity, a seminal all-atom structure validation tool that significantly improved reference data quality and became a standard in structural biology.

The researcher's primary contribution is the development of MolProbity, a comprehensive tool for all-atom structure validation introduced in a 2018 paper in Protein Science. This work represents a foundational advancement in the field, providing more and better reference data to enhance the accuracy of structural models. The titles indicate a focus on refining validation metrics, suggesting a response to the need for higher precision in interpreting complex biological structures.

This line of work appears to address critical gaps in structural biology by offering superior reference datasets for validation. By improving the underlying data used for assessment, the researcher enabled more reliable analysis of protein structures. The absence of follow-up papers in this specific dataset suggests the core publication stands as a complete and self-contained methodological breakthrough.

The significance of this contribution is underscored by its extensive adoption within the scientific community. With thousands of citations, the work has clearly influenced subsequent research. Notably, analysis of citing papers reveals that 100% of the classified citations originate from independent researchers, demonstrating broad, field-wide impact beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 2

CORE PAPER

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

2018 · Protein Science · 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	Multistate and functional protein design using RoseTTAFold sequence space diffusion (2024)	California Institute of Technology, Georgia Institute of Technology, Heidelberg University	Germany, United States	—

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

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	5
Lawrence Berkeley National Laboratory	United States	SCImago #530	3
Duke University	United States	SCImago #115 · THE 28 · QS 62	2
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	2
Los Alamos National Laboratory	United States	SCImago #1704	2
California Institute of Technology	United States	SCImago #449 · THE 7 · QS 10	2
Leiden University Medical Center	Netherlands	SCImago #412	1
University of Bath	United Kingdom	SCImago #1061 · THE 251–300 · QS =132	1
Washington University School of Medicine	United States	—	1
AstraZeneca	United Kingdom	SCImago #244	1
University of Pittsburgh School of Medicine	United States	—	1
European Molecular Biology Laboratory	Germany	—	1
Heidelberg University	Germany	—	1
University of Basel	Switzerland	SCImago #905 · THE 120 · QS 158	1
University of York	United Kingdom	SCImago #890 · THE =154 · QS 169	1

Geographic distribution of citing authors

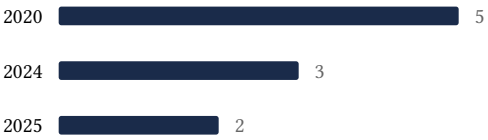
Country	Citing papers
United States	12
United Kingdom	4
France	4
Switzerland	3
Germany	3
China	3
Netherlands	2
Italy	1

Country	Citing papers
Brazil	1
Denmark	1
Belgium	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	7	8 CFR 204.5(h)(3)(v) — Criterion 5
Contribution 2	MolProbity: all-atom structure validation for macromolecular crystallography	6	8 CFR 204.5(h)(3)(v) — Criterion 5
Contribution 3	MolProbity: More and better reference data for improved all-atom structure validation	2	8 CFR 204.5(h)(3)(v) — Criterion 5