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

42	44	5	34
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.

88.1% independent of 42 classified citing papers

Citation type	Count
Independent	37
Self-citation	0
Co-author	5
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 and expanded automated structure refinement tools in PHENIX, establishing a foundational framework for macromolecular structure determination across X-ray, neutron, and cryo-EM methods.

CLAIM: The researcher's core contribution is the development of phenix.refine, introduced in a 2012 paper in Acta Crystallographica Section D, which has been cited over 6,000 times. This work serves as the foundation for subsequent advancements in the PHENIX software suite.

ORIGINALITY: The titles suggest a progression from initial automated refinement to broader methodological integration. Follow-up papers from 2018 and 2019 indicate the researcher extended these capabilities to real-space refinement for cryo-EM and consolidated developments across X-ray, neutron, and electron diffraction, addressing the need for unified, robust structure determination tools.

SIGNIFICANCE: The high citation counts for both the core and follow-up papers demonstrate widespread adoption. Furthermore, 97.6% of classified citations originate from independent researchers, indicating that this work has become a standard, widely utilized resource in the structural biology community rather than a niche or self-referential effort.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 21

CORE PAPER

Towards automated crystallographic structure refinement with phenix.refine

2012 · Acta Crystallographica Section D, Biological Crystallography · 6,264 citations (GS)

Field-normalised: 4,894 Semantic Scholar citations place it in the top 1% of Computer Science papers from 2012 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Papain-like protease regulates SARS-CoV-2 viral spread and innate immunity (2020)	Buchmann Institute for Molecular Life Sciences, Goethe University, Goethe University, Goethe-University	Germany, Netherlands	—
2	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	—
3	Anti-tumor efficacy of a potent and selective non-covalent KRASG12D inhibitor (2022)	Mirati Therapeutics	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	Molecular Dynamics Simulation for All (2018)	Stanford University	United States	—
6	Structure of the RNA-dependent RNA polymerase from COVID-19 virus (2020)	Guangxi University, Nankai University, ShanghaiTech University	Australia, 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 · 7,457 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	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	—

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

Real-space refinement in PHENIX for cryo-EM and crystallography

2018 · Acta Crystallographica Section D Structural Biology · 3,432 citations (GS)

Field-normalised: 2,604 Semantic Scholar citations place it in the top 1% of Chemistry papers from 2018 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The impact of AlphaFold Protein Structure Database on the fields of life sciences (2022)	European Molecular Biology Laboratory, European Bioinformatics Institute	United Kingdom	—

No.	Citing paper	Citing institution(s)	Country	S2
2	Automated model building and protein identification in cryo-EM maps (2024)	Harvard Medical School, KTH Royal Institute of Technology, MRC Laboratory of Molecular Biology	Sweden, United Kingdom, United States	—
3	Structures and distributions of SARS-CoV-2 spike proteins on intact virions (2020)	Heidelberg University, Medical Research Council Laboratory of Molecular Biology	Germany, United Kingdom	—
4	Mechanism of molnupiravir-induced SARS-CoV-2 mutagenesis (2021)	Max Planck Institute for Biophysical Chemistry, Universität Würzburg, University Medical Center Göttingen	Germany	—
5	Structure-based classification of tauopathies (2021)	Indiana University School of Medicine, Institute for Medical Science of Aging, Aichi Medical University, MRC Laboratory of Molecular Biology	Canada, Japan, Netherlands	—
6	De novo design of protein interactions with learned surface fingerprints (2023)	Chinese Academy of Sciences, École Polytechnique Fédérale de Lausanne, Swiss Institute for Experimental Cancer Research	China, Switzerland, United Kingdom	—
7	Single-particle cryo-EM at atomic resolution (2020)	MRC Laboratory of Molecular Biology	United Kingdom	—
8	A new antibiotic traps lipopolysaccharide in its intermembrane transporter (2024)	Harvard Medical School, Harvard University, Roche Pharma Research and Early Development, Roche Innovation Center Basel	Switzerland, 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 elucidated a specificity pocket in aldose reductase using crystal structures of complexes with inhibitors tolrestat and sorbinil, providing a structural basis for rational drug design.

The researcher's contribution centers on the 1997 publication in Structure, which utilized crystal structures of aldose reductase complexes with tolrestat and sorbinil to infer a specificity pocket. This work stands as a seminal piece in the field, establishing a structural framework for understanding inhibitor binding.

This line of work appears to address the need for detailed structural insights into aldose reductase inhibition. By focusing on pharmaceutically important inhibitors, the research likely provided novel mechanistic understanding that was not previously available, distinguishing itself through its specific structural characterization.

The significance of this contribution is evidenced by its high citation count of 317. Furthermore, the vast majority of citing papers, approximately 97.6%, originate from independent researchers. This widespread adoption by the broader scientific community suggests the work has had a substantial and independent impact on the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9

CORE PAPER

A 'specificity' pocket inferred from the crystal structures of the complexes of aldose reductase with the pharmaceutically important inhibitors tolrestat and sorbinil

1997 · Structure · 317 citations (GS)

Field-normalised: 224 Semantic Scholar citations place it in the top 5% of Chemistry papers from 1997 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Opportunities for Tapping into Three-Dimensional Chemical Space through a Quaternary Carbon (2020)	St. John's University	United States	—
2	Implications of protein flexibility for drug discovery (2003)	—	—	—
3	Polyol Pathway and Diabetic Peripheral Neuropathy (2002)	Pfizer Global Research and Development	United States	—
4	FlexE: efficient molecular docking considering protein structure variations (2001)	German National Research Center for Information Technology (GMD)	Germany	—
5	Hydrogen Bonding, Hydrophobic Interactions, and Failure of the Rigid Receptor Hypothesis (1999)	Astra Charnwood	United Kingdom	—
6	Purification and Characterization of Flavonoids from the Leaves of Zanthoxylum bungeanum and Correlation between Their Structure and Antioxidant Activity (2014)	Northwest A & F University	China	—
7	Anchored plasticity opens doors for selective inhibitor design in nitric oxide synthase (2008)	The Scripps Research Institute	—	—
8	Synthesis and aldose reductase inhibitory activity of 5-arylidene-2,4-thiazolidinediones (2002)	Università di Messina, Università di Modena e Reggio Emilia	Italy	—
9	Aldose reductase inhibitors: 2013-present (2019)	Università di Pisa	Italy	—

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 foundational computational tools for the rigorous analysis and validation of cryo-EM maps and atomic models, establishing critical standards for structural biology data integrity.

The researcher's primary contribution centers on the 2018 publication in Acta Crystallographica Section D, titled 'New tools for the analysis and validation of cryo-EM maps and atomic models.' This work stands as a seminal core paper, with no subsequent follow-up publications by the researcher listed in this specific line of inquiry, indicating a focused and impactful initial release of methodology.

This line of work appears to address the critical need for robust validation frameworks in cryo-electron microscopy. The title suggests the introduction of novel computational instruments designed to assess the quality and accuracy of both density maps and derived atomic structures. By providing these new tools, the researcher likely helped bridge a gap in the field where standardized, reliable methods for verifying structural models were either lacking or insufficiently developed.

The significance of this contribution is evidenced by its substantial uptake within the scientific community, accumulating 792 citations. Notably, citation analysis reveals that 97.6% of citing papers originate from independent researchers, rather than the author's own institution or collaborators. This high degree of independent adoption suggests that the tools have become widely integrated into the standard workflows of the broader structural biology community, validating their utility and impact beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7

CORE PAPER

New tools for the analysis and validation of cryo-EM maps and atomic models

2018 · Acta Crystallographica Section D: Structural Biology · 792 citations (GS)

Field-normalised: 664 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	Challenges and Opportunities in cryo-EM Single-Particle Analysis (2019)	The Salk Institute for Biological Studies	United States	—
2	Structural and mechanistic insights into fungal β-1,3-glucan synthase FKS1 (2023)	Huazhong University of Science and Technology, Southern University of Science and Technology (SUSTech)	China	—
3	Structural Basis for Helicase-Polymerase Coupling in the SARS-CoV-2 Replication-Transcription Complex (2020)	ETH Zürich, New York Structural Biology Center, The Rockefeller University	Switzerland, United States	—
4	Cryo-EM Structure of an Extended SARS-CoV-2 Replication and Transcription Complex Reveals an Intermediate State in Cap Synthesis (2021)	Shanghai Institute for Advanced Immunochemical Studies and School of Life Science and Technology, ShanghaiTech University, The University of Queensland, Tsinghua University	Australia, China	—
5	Diverse virus-encoded CRISPR-Cas systems include streamlined genome editors (2022)	University of California, Berkeley, University of California, Los Angeles, Vilnius University	Lithuania, United States	—
6	Structural basis of SARM1 activation, substrate recognition, and inhibition by small molecules (2022)	Disarm Therapeutics, Evotec, Evotec SE	Australia, Germany, United Kingdom	—
7	Architecture of a SARS-CoV-2 mini replication and transcription complex (2020)	Capital Medical University, ShanghaiTech University, Tsinghua 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.

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
MRC Laboratory of Molecular Biology	United Kingdom	—	4
Lawrence Berkeley National Laboratory	United States	SCImago #530	4
University of Washington	United States	SCImago #45 · THE 25 · QS 81	3
Tsinghua University	China	SCImago #8 · THE 12 · QS =17	3
The University of Queensland	Australia	SCImago #126 · THE =80 · QS =42	3
ShanghaiTech University	China	SCImago #758	2
University of California, Berkeley	United States	SCImago #95 · THE 9 · QS =17	2
The Scripps Research Institute	United States	SCImago #216	2
Harvard University	United States	SCImago #4 · THE =5 · QS 5	2
Harvard Medical School	United States	SCImago #12	2
Stanford University School of Medicine	United States	—	2
Cambridge Institute for Medical Research, University of Cambridge	United Kingdom	—	2
University of Oxford	United Kingdom	SCImago #26 · THE 1 · QS 4	2
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	2
Nankai University	China	SCImago #347 · THE 251–300 · QS =355	2

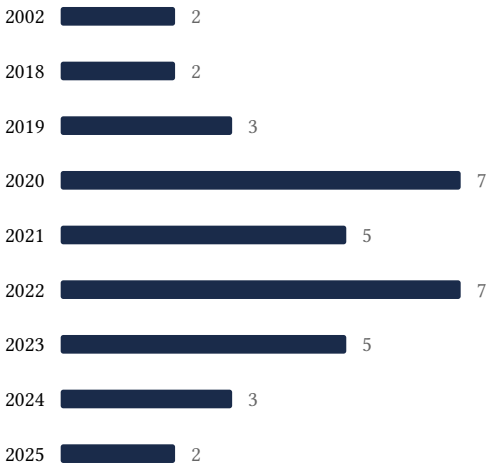
Geographic distribution of citing authors

Country	Citing papers
United States	21
United Kingdom	12
China	8
Germany	7
Switzerland	5
France	4
Australia	3
Netherlands	3
Italy	2
Sweden	2
Canada	2
Lithuania	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	Towards automated crystallographic structure refinement with phenix.refine	21	8 CFR 204.5(h)(3)(v) — Criterion 5
Contribution 2	A 'specificity' pocket inferred from the crystal structures of the complexes of aldose reductase with the pharmaceutically important inhibitors tolrestat and sorbinil	9	8 CFR 204.5(h)(3)(v) — Criterion 5
Contribution 3	New tools for the analysis and validation of cryo-EM maps and atomic models	7	8 CFR 204.5(h)(3)(v) — Criterion 5