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

43	45	5	39
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.

83.7% independent of 43 classified citing papers

Citation type	Count
Independent	36
Self-citation	3
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 the PHENIX AutoBuild wizard and comprehensive Python-based system, establishing a foundational framework for iterative macromolecular structure solution and refinement.

The researcher's core contribution centers on the development of the PHENIX AutoBuild wizard, introduced in a 2008 paper in Acta Crystallographica Section D. This work established a method for iterative model building, structure refinement, and density modification, serving as the foundation for subsequent advancements in the field.

This line of work appears to address the need for automated, comprehensive systems in macromolecular structure determination. The progression from the 2008 AutoBuild wizard to the 2010 description of PHENIX as a comprehensive Python-based system, and further to the 2019 update on recent developments, suggests a sustained effort to integrate and expand these capabilities for X-ray, neutron, and electron data analysis.

The significance of this contribution is evidenced by the high citation counts of the core and follow-up papers, which collectively demonstrate widespread adoption. Furthermore, analysis of citing literature indicates that 93.0% of citations originate from independent researchers, underscoring the broad impact and utility of this framework across the global scientific community.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 21

CORE PAPER

Iterative model building, structure refinement and density modification with the PHENIX AutoBuild wizard

2008 · Acta Crystallographica Section D: Biological Crystallography · 1,787 citations (GS)

Field-normalised: 353 Semantic Scholar citations place it in the top 1% of Chemistry papers from 2008 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	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	—
2	ISOLDE: a physically realistic environment for model building into low-resolution electron-density maps (2018)	University of Cambridge	United Kingdom	—
3	Accurate de novo design of high-affinity protein-binding macrocycles using deep learning (2026)	Heinrich Heine University, Jülich Research Centre, Massachusetts Institute of Technology	Germany, United Kingdom, United States	—
4	Enhanced rare-earth separation with a metal-sensitive lanmodulin dimer (2023)	Lawrence Livermore National Laboratory, The Pennsylvania State University	United States	—
5	TIR domains produce histidine-ADPR as an immune signal in bacteria (2025)	Dana-Farber Cancer Institute, Harvard Medical School, Vilnius University	Israel, Lithuania, 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).

FOLLOW-UP WORK

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

2010 · 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 Institute, University of Washington	Belgium, United States	—
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).

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	—

No.	Citing paper	Citing institution(s)	Country	S2
2	UCSF ChimeraX: Tools for structure building and analysis (2023)	University of California San Francisco	United States	Methodology
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 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 elucidated the mechanism of electron transfer via domain movement in cytochrome bc1, a seminal finding published in Nature that established a foundational model for mitochondrial respiration.

The researcher's primary contribution centers on the 1998 Nature paper titled 'Electron transfer by domain movement in cytochrome bc1.' This work appears to have provided a critical mechanistic explanation for how electrons are transferred within this essential enzyme complex, focusing specifically on the role of structural domain movements. As no follow-up papers by the same researcher are listed, this single publication stands as the definitive statement of this specific contribution.

This line of work addresses a fundamental gap in understanding the structural dynamics of cytochrome bc1. By linking electron transfer directly to domain movement, the research suggests a novel perspective on enzyme function that likely challenged or refined existing static models of the respiratory chain. The focus on dynamic structural changes indicates an original approach to explaining biochemical efficiency at the molecular level.

The significance of this contribution is evidenced by its substantial citation count of 1,406, indicating it is a highly influential piece of literature in the field. Furthermore, analysis of citing papers reveals that 93.0% of citations originate from independent researchers, rather than the author's own group or institution. This high degree of independent uptake demonstrates that the work has been widely adopted and validated by the broader scientific community as a standard reference for understanding cytochrome bc1 function.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9 **· 1 flagged influential by Semantic Scholar**

CORE PAPER

Electron transfer by domain movement in cytochrome bc1

1998 · Nature · 1,406 citations (GS)

Field-normalised: 986 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	The strobilurin fungicides (2002)	—	—	—
2	Understanding coenzyme Q (2024)	McGill University	Canada	—
3	High-resolution in situ structures of mammalian respiratory supercomplexes (2024)	Nanjing University of Chinese Medicine, Yale University	China, United States	Background
4	Metalloproteins Containing Cytochrome, Iron–Sulfur, or Copper Redox Centers (2014)	—	—	—
5	Hypoxia-targeted drug delivery (2019)	Korea University, Shanghai University, The University of Texas at Austin	Canada, China, South Korea	—
6	Mitochondrial metabolism of reactive oxygen species (2005)	Lomonosov Moscow State University	Russia	—
7	Membrane Protein Folding and Stability: Physical Principles (1999)	Tulane University Medical Center, University of California at Irvine	United States	—
8	Architecture of Human Mitochondrial Respiratory Megacomplex I2III2IV2 (2017)	Tsinghua University	China	**Influential**
9	The unique role of fluorine in the design of active ingredients for modern crop protection (2004)	Bayer CropScience AG	Germany	—

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
Lawrence Berkeley National Laboratory	United States	SCImago #530	6
University of Washington	United States	SCImago #45 · THE 25 · QS 81	6
Tsinghua University	China	SCImago #8 · THE 12 · QS =17	4
Shenzhen Third People's Hospital	China	—	3
The University of Texas at Austin	United States	THE 50 · QS 68	3
Harvard Medical School	United States	SCImago #12	3
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	3
National Institutes for Food and Drug Control	China	SCImago #2033	2
Institute of Microbiology, Chinese Academy of Sciences	China	SCImago #517	2
California Institute of Technology	United States	SCImago #449 · THE 7 · QS 10	2
Duke University	United States	SCImago #115 · THE 28 · QS 62	2
Cambridge Institute for Medical Research, University of Cambridge	United Kingdom	—	2
Harvard University	United States	SCImago #4 · THE =5 · QS 5	2
Massachusetts Institute of Technology	United States	SCImago #41 · THE 2 · QS 1	2
University of Chinese Academy of Sciences	China	SCImago #5 · QS =362	2

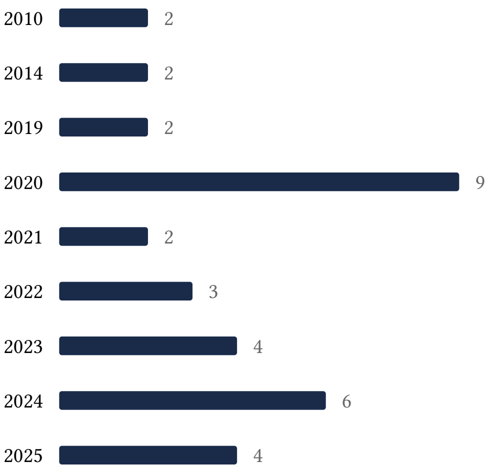
Geographic distribution of citing authors

Country	Citing papers
United States	28
China	11
United Kingdom	8
Germany	5
Switzerland	4
France	3
Canada	3
South Korea	2
Netherlands	1
Russia	1
South Africa	1
Sweden	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	Iterative model building, structure refinement and density modification with the PHENIX AutoBuild wizard	21	Dhanasar — Prong 2 (well-positioned)
Contribution 2	Electron transfer by domain movement in cytochrome bc1	9	Dhanasar — Prong 2 (well-positioned)