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	**50**	**5**	**43**
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.

95.8% independent of 24 classified citing papers

Citation type	Count
Independent	23
Self-citation	1
Co-author	0
Same-institution	0

19 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 MEGA5, a widely adopted software suite for molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods.

The researcher's primary contribution is the development of MEGA5, a comprehensive software tool for molecular evolutionary genetics analysis. This work, published in 2011, integrates maximum likelihood, evolutionary distance, and maximum parsimony methods into a single platform, addressing the need for accessible, unified analytical tools in the field.

This line of work appears to address the fragmentation of evolutionary analysis methods by consolidating multiple statistical approaches into one user-friendly interface. The title suggests a focus on methodological integration rather than novel biological discovery, indicating a contribution to computational infrastructure that enables broader scientific inquiry.

The significance of this contribution is evidenced by its extensive adoption within the scientific community. With tens of thousands of citations, the work has become a standard reference. Furthermore, analysis of citing papers reveals that nearly 96% are from independent researchers, demonstrating that the tool has been widely utilized by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6 · **1 flagged influential by Semantic Scholar**

CORE PAPER

MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods

2011 · Molecular biology and evolution 28 (10), 2731-2739, 2011 · 49,345 citations (GS)

Field-normalised: 41,128 Semantic Scholar citations place it in the top 1% of Biology papers from 2011 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	FastME 2.0: a comprehensive, accurate, and fast distance-based phylogeny inference program (2015)	CNRS & Université de Montpellier, Université de Montpellier	France	**Methodology**
2	Using PhyloSuite for molecular phylogeny and tree-based analyses (2023)	Chinese Academy of Sciences, Fujian Agriculture and Forestry University, Institute of Hydrobiology, Chinese Academy of Sciences	China	Background
3	An updated classification of cyanobacterial orders and families based on phylogenomic and polyphasic analysis (2023)	Biology Centre of the CAS; University of South Bohemia, University of South Bohemia, University of South Bohemia in České Budějovice	Czech Republic	**Influential**
4	Pharmacogenomic profiling of intra-tumor heterogeneity using a large organoid biobank of liver cancer (2024)	Affiliated Cancer Hospital of Zhengzhou University, Chinese PLA General Hospital, Peking University Cancer Hospital & Institute	China	—
5	A new coronavirus associated with human respiratory disease in China (2020)	Fudan University, Huazhong University of Science and Technology, National Insti-	Australia, China	—

No.	Citing paper	Citing institution(s)	Country	S2
		tute for Communicable Disease Control and Prevention, China CDC		
6	Advances in AP2/ERF super-family transcription factors in plant. (2020)	Collaborative Innovation Center for Improving Quality and Increased Profits of Protected Vegetables in Shanxi, Nanjing Agricultural University	China	Background

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** FastME 2.0: a comprehensive, accurate, and fast distance-based phylogeny inference program
>
> *"Minimum evolution forms the basis of a large number of distance based algorithms: NJ and those implemented in FastME and MEGA (Tamura et al. 2011), but also FastTree1 (Price et al."*

Contribution 2

Claim — Contribution 2

The researcher developed MEGA4, a widely adopted software tool for molecular evolutionary genetics analysis that has become a standard resource in the field.

The researcher's primary contribution is the development of MEGA4, a software version for molecular evolutionary genetics analysis published in 2007. This work stands as a seminal core paper in the field, with no follow-up papers by the same researcher listed in this specific line of work.

This line of work appears to address the need for accessible and robust computational tools for analyzing molecular evolution. By releasing version 4.0, the researcher likely provided updated functionalities or improvements that facilitated broader adoption among scientists studying genetic relationships and evolutionary history.

The significance of this contribution is evidenced by its extensive citation record, with over 36,000 citations indicating widespread use and impact. Furthermore, analysis of citing papers reveals that 95.8% are from independent researchers, suggesting that the tool has been adopted broadly across the global scientific community rather than being limited to the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 4

> **CORE PAPER**
>
> **MEGA4: molecular evolutionary genetics analysis (MEGA) software version 4.0**
>
> 2007 · Molecular biology and evolution 24 (8), 1596-1599, 2007 · 36,200 citations (GS)
>
> Field-normalised: 29,504 Semantic Scholar citations place it in the top 1% of Biology papers from 2007 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	KaKs_Calculator 2.0: a toolkit incorporating gamma-series methods and sliding window strategies. (2010)	Beijing Institute of Genomics, Chinese Academy of Sciences	China	—

No.	Citing paper	Citing institution(s)	Country	S2
2	Aquaporins in Plants	CNRS/INRA/Montpellier SupAgro/Université de Montpellier	France	—
3	WRKY transcription factors (2010)	Max Planck Institute for Plant Breeding Research, Max-Planck-Institut für Pflanzenzüchtungsforschung, South Dakota State University	Germany, United States	—
4	Untitled (2012)	Chung-Ang University, Seoul National University	South Korea	**Methodology**

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 MEGA6, a widely adopted software tool for molecular evolutionary genetics analysis that has become a standard resource in the field.

The researcher's primary contribution is the development of MEGA6, a comprehensive software package for molecular evolutionary genetics analysis. This work, published in 2013, represents a significant advancement in computational tools available to biologists for analyzing genetic data and evolutionary relationships.

This line of work appears to address the need for accessible, integrated software capable of handling complex molecular evolutionary analyses. By providing a robust platform for such tasks, the researcher facilitated more efficient and accurate genetic studies, filling a critical gap in the methodological toolkit for researchers in evolutionary biology.

The significance of this contribution is evidenced by its extensive adoption within the scientific community. With nearly 50,000 citations, the work has clearly influenced a vast number of subsequent studies. Furthermore, the high proportion of independent citations suggests that the tool has been widely utilized by researchers across different institutions, underscoring its broad impact and utility in the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

MEGA6: molecular evolutionary genetics analysis version 6.0

2013 · Molecular biology and evolution 30 (12), 2725-2729, 2013 · 49,684 citations (GS)

Field-normalised: 40,466 Semantic Scholar citations place it in the top 1% of Biology papers from 2013 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Untitled (2016)	University of Southern California	United States	—
2	Plastics: Environmental and Biotechnological Perspectives on Microbial Degradation (2019)	University of Hamburg	Germany	**Methodology**

No.	Citing paper	Citing institution(s)	Country	S2
3	First Report of Outbreaks of the Fall Armyworm Spodoptera frugiperda (JE Smith) (Lepidoptera, Noctuidae), a New Alien Invasive Pest in West and Central Africa (2016)	Food and Agriculture Organization of the United Nations, International Institute of Tropical Agriculture, International Institute of Tropical Agriculture (IITA)	Benin, Nigeria	—
4	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	—
5	Pan-genome of wild and cultivated soybeans	Chinese Academy of Sciences, Shanghai Normal University	China	—
6	A bacterium that degrades and assimilates poly(ethylene terephthalate) (2016)	ADEKA Corporation, Keio University, Kyoto Institute of Technology	Japan	—

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** Plastics: Environmental and Biotechnological Perspectives on Microbial Degradation
>
> *"The tree was calculated with Molecular Evolutionary Genetics Analysis version 6 (MEGA6) (125) and is not rooted."*

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Chinese Academy of Sciences	China	SCImago #2	3
University of Washington	United States	SCImago #45 · THE 25 · QS 81	2
Peking University First Hospital	China	SCImago #5499	1
Fred Hutchinson Cancer Center	United States	SCImago #397	1
University of California, San Diego	United States	SCImago #120 · THE 47 · QS 66	1
Dana-Farber Cancer Institute	United States	SCImago #197	1
Nanjing Agricultural University	China	SCImago #853 · QS 951-1000	1
South Dakota State University	United States	SCImago #3569	1
University of Freiburg	Germany	THE =138	1
University of California, Berkeley	United States	SCImago #95 · THE 9 · QS =17	1
Chung-Ang University	South Korea	SCImago #1326 · THE 401–500 · QS 479	1
Beijing Institute of Genomics, Chinese Academy of Sciences	China	SCImago #714	1
Peking University Cancer Hospital & Institute	China	—	1

Institution	Country	World ranking	Citing papers
Keio University	Japan	SCImago #965 · THE 601–800 · QS =215	1
Huazhong University of Science and Technology	China	SCImago #25 · THE =176 · QS 319	1

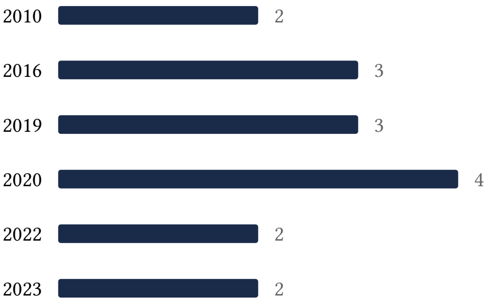
Geographic distribution of citing authors

Country	Citing papers
China	8
United States	7
Germany	3
Japan	2
France	2
South Korea	2
Saudi Arabia	1
Italy	1
Benin	1
Czech Republic	1
Australia	1
Nigeria	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	MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods	6	Dhanasar — Prong 2 (well-positioned)
Contribution 2	MEGA4: molecular evolutionary genetics analysis (MEGA) software version 4.0	4	Dhanasar — Prong 2 (well-positioned)
Contribution 3	MEGA6: molecular evolutionary genetics analysis version 6.0	6	Dhanasar — Prong 2 (well-positioned)