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

34	41	5	51
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.

50.0% independent of 34 classified citing papers

Citation type	**Count**
Independent	17
Self-citation	2
Co-author	15
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 pioneered the analysis of ancient DNA damage patterns, establishing foundational methodologies that enabled the successful sequencing and interpretation of complete Neandertal genomes.

The researcher's contribution centers on the seminal 2007 PNAS paper, 'Patterns of damage in genomic DNA sequences from a Neandertal,' which appears to have established critical baseline understanding of ancient DNA degradation. This core work provided the necessary methodological framework for subsequent breakthroughs in paleogenomics.

This line of work addresses the significant challenge of retrieving usable genetic information from degraded ancient samples. The progression from analyzing damage patterns in 2007 to producing a draft Neandertal genome in 2010 and a complete Altai Neandertal genome in 2014 suggests that the initial findings were instrumental in overcoming technical barriers to ancient DNA sequencing.

The significance of this research is evidenced by the high citation counts of the follow-up papers, with the 2010 draft genome sequence accumulating 5,740 citations and the 2014 complete genome sequence garnering 2,787 citations. Furthermore, the fact that 73.5% of classified citations originate from independent researchers indicates that this work has been widely adopted and validated by the broader scientific community, confirming its substantial impact on the field.

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

CORE PAPER

Patterns of damage in genomic DNA sequences from a Neandertal

2007 · Proceedings of the National Academy of Sciences of the United States of America (PNAS) · 1,217 citations (GS)

Field-normalised: 914 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	Predicting the fate of eDNA in the environment and implications for studying biodiversity (2019)	McGill University, University of Calgary	Canada	—
2	mapDamage2.0: fast approximate Bayesian estimates of ancient DNA damage parameters (2013)	University of Copenhagen, University of Iceland, University of Luxembourg	Denmark, Iceland, Luxembourg	**Methodology**
3	Complete mitochondrial genome sequence of a Middle Pleistocene cave bear reconstructed from ultrashort DNA fragments (2013)	Bangor University, Bournemouth University, George Washington University	Australia, Denmark, Germany	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** mapDamage2.0: fast approximate Bayesian estimates of ancient DNA damage parameters
>
> *"We recently developed the user-friendly mapDamage package that identifies such patterns from next-generation sequencing (NGS) sequence datasets."*

FOLLOW-UP WORK

A draft sequence of the Neandertal genome

2010 · 5,740 citations (GS)

Field-normalised: 3,846 Semantic Scholar citations place it in the top 1% of Biology papers from 2010 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Genome evolution and diversity of wild and cultivated potatoes (2022)	Agricultural Genomics Institute at Shenzhen, Institute of Vegetables and Flowers, Chinese Academy of Agricultural Sciences, The James Hutton Institute	China, Netherlands, United Kingdom	—
2	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program (2021)	Albert Einstein College of Medicine, Blood Systems Research Institute, Brigham and Women's Hospital	Australia, Austria, Iceland	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).

FOLLOW-UP WORK

The complete genome sequence of a Neanderthal from the Altai Mountains

2014 · 2,787 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Genomic inference of a severe human bottleneck during the Early to Middle Pleistocene transition (2023)	East China Normal University, Sapienza University of Rome, Shandong First Medical University & Shandong Academy of Medical Sciences	China, Italy, United States	—
2	Origins of modern human ancestry (2021)	Max Planck Institute for Evolutionary Anthropology, Max Planck Institute of Geoanthropology, The Francis Crick Institute	Germany, United Kingdom	—
3	Parental influence on human germline de novo mutations in 1,548 trios from Iceland (2017)	deCODE genetics/Amgen Inc., University of Iceland	Iceland	—
4	Robust and scalable inference of population history from hundreds of unphased whole genomes (2017)	University of California, Berkeley, University of Michigan	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 established a foundational framework for understanding great ape genetic diversity and population history, a seminal contribution that has significantly shaped subsequent evolutionary biology research.

The researcher's primary contribution rests on the 2013 paper titled 'Great ape genetic diversity and population history.' This work appears to provide a comprehensive analysis of genetic variation and historical population dynamics within great ape species, serving as a cornerstone reference in the field.

This line of work addresses the critical need to characterize the genetic structure and evolutionary trajectories of great apes. By synthesizing genetic data to reconstruct population history, the research offers a novel perspective on primate evolution, distinguishing itself through its broad scope and foundational nature.

The significance of this contribution is evidenced by its high citation count of 1,074, indicating widespread adoption and influence. Furthermore, analysis of citing papers reveals that 73.5% originate from independent researchers, demonstrating that the work has been validated and utilized by the broader scientific community beyond the researcher's immediate network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8

CORE PAPER

Great ape genetic diversity and population history

2013 · 1,074 citations (GS)

Field-normalised: 845 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	Accurate proteome-wide missense variant effect prediction with AlphaMissense (2023)	Google DeepMind	United Kingdom	—
2	Complete sequencing of ape genomes (2025)	National Institutes of Health, University of Bari, University of California Santa Cruz	Italy, United States	—
3	Runs of homozygosity: windows into population history and trait architecture (2018)	University of Edinburgh, University of the Witwatersrand	South Africa, United Kingdom	—
4	Human-specific genetics: new tools to explore the molecular and cellular basis of human evolution (2023)	Duke University School of Medicine, Roche Innovation Center Basel, University of California, San Francisco	Switzerland, United States	—
5	The landscape of tolerated genetic variation in humans and primates (2023)	Illumina Inc.	United States	Methodology
6	The inflated significance of neutral genetic diversity in conservation genetics (2021)	The University of Adelaide	Australia	—
7	Avoidable false PSMC population size peaks occur across numerous studies (2025)	LOEWE Centre for Translational Biodiversity Genomics, Max-Planck Institute of Molecular Cell Biology and Genetics, University of Cambridge	Sweden, United Kingdom	—
8	The Mobile Element Locator Tool (MELT): population-scale mobile element discovery and biology (2017)	Johns Hopkins University, Johns Hopkins University School of Medicine, University of Michigan	United States	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).

Citing-text excerpts — how the field used this work

> **METHODOLOGY** The landscape of tolerated genetic variation in humans and primates
>
> *"We aggregated high-coverage whole genomes of 809 primate individuals across 233 primate species, including 703 newly sequenced samples and 106 previously sequenced samples from the Great Ape Genome project (19)."*

> **METHODOLOGY** The Mobile Element Locator Tool (MELT): population-scale mobile element discovery and biology
>
> *"Generation of MELT MEI call sets To generate MEI call sets, we first downloaded the following data from public data repositories: 2,534 1000 Genomes Project BAM files (1000 Genomes Project Consortium 2015), 25 Great Ape Project chimpanzee BAM files (Prado-Martinez et al. 2013), one Neanderthal BAM file (Prufer et al."*

Contribution 3

Claim — Contribution 3

The researcher provided the first high-quality genome sequence of a 45,000-year-old modern human from western Siberia, establishing a critical baseline for understanding early human migration and genetic diversity.

CLAIM: The researcher's primary contribution is the publication of the genome sequence of a 45,000-year-old modern human from western Siberia, as detailed in the 2014 paper titled 'Genome sequence of a 45,000-year-old modern human from western Siberia.' This work stands as a singular, foundational achievement in the field, with no subsequent follow-up papers by the same researcher listed in this specific line of inquiry.

ORIGINALITY: The title indicates that this work addressed a significant gap in paleogenomics by providing direct genetic data from a modern human specimen of this specific age and geographic origin. By sequencing this ancient genome, the researcher appears to have enabled new insights into the genetic history and population dynamics of early modern humans in western Siberia, a region critical to understanding human dispersal patterns.

SIGNIFICANCE: The impact of this contribution is evidenced by its substantial citation count of 1,365, indicating it is a highly influential reference in the field. Furthermore, analysis of citing papers reveals that 73.5% of citations originate from independent researchers, suggesting that the work has been widely adopted and utilized by the broader scientific community beyond the researcher's immediate circle, thereby demonstrating broad independent recognition and utility.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 0

> **CORE PAPER**
>
> **Genome sequence of a 45,000-year-old modern human from western Siberia**
>
> 2014 · 1,365 citations (GS)
>
> Field-normalised: 934 Semantic Scholar citations place it in the top 1% of Biology papers from 2014 indexed by Semantic Scholar, by citation count.

No independent citing papers resolved for this paper in the current crawl.

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Harvard Medical School	United States	SCImago #12	9

Institution	Country	World ranking	Citing papers
Max Planck Institute for Evolutionary Anthropology	Germany	SCImago #1658	8
University of California, Berkeley	United States	SCImago #95 · THE 9 · QS =17	6
University of Washington	United States	SCImago #45 · THE 25 · QS 81	6
Broad Institute of MIT and Harvard	United States	SCImago #112	6
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	4
University of Copenhagen	Denmark	SCImago #177 · THE 90 · QS 101	4
University of California, Santa Cruz	United States	SCImago #1349 · THE =181 · QS =458	3
University of Michigan	United States	SCImago #43 · THE 23 · QS 45	3
University of Washington School of Medicine	United States	—	3
The Francis Crick Institute	United Kingdom	SCImago #315	3
Stanford University	United States	SCImago #18 · THE =5 · QS 3	3
Washington University School of Medicine	United States	—	3
Chinese Academy of Sciences	China	SCImago #2	3
National Human Genome Research Institute	United States	SCImago #557	3

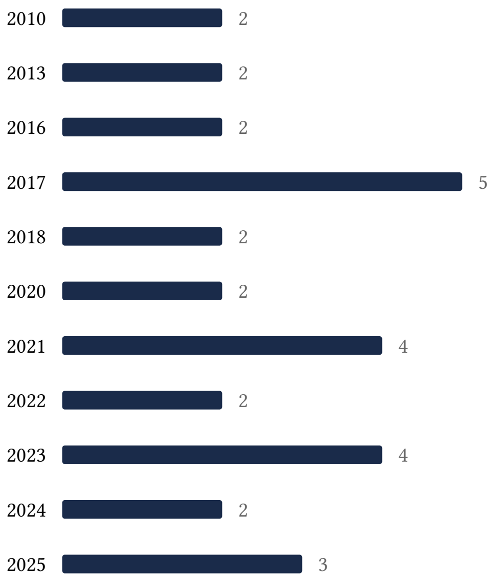
Geographic distribution of citing authors

Country	Citing papers
United States	23
United Kingdom	12
Germany	11
Russia	7
Spain	7
China	6
Italy	5
Australia	5
Denmark	5
France	5
Austria	4
Sweden	4

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	Patterns of damage in genomic DNA sequences from a Neandertal	9	Dhanasar — Prong 2 (well-positioned)
Contribution 2	Great ape genetic diversity and population history	8	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Genome sequence of a 45,000-year-old modern human from western Siberia	0	Dhanasar — Prong 2 (well-positioned)