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	43	5	59
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.

90.7% independent of 43 classified citing papers

Citation type	Count
Independent	39
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 pioneered the sequencing and analysis of Neanderthal genomic DNA, establishing a foundational framework for paleogenomics that has been widely adopted by the independent scientific community.

CLAIM: The researcher's primary contribution is the sequencing and analysis of Neanderthal genomic DNA, as demonstrated by the seminal 2006 paper. This work stands as a singular, high-impact achievement in the field, with no subsequent follow-up papers by the same author required to validate its core methodology or findings.

ORIGINALITY: The title indicates a direct engagement with the technical and analytical challenges of extracting and interpreting genetic material from ancient hominins. By focusing on Neanderthal DNA, the work appears to address a critical gap in understanding human evolutionary history through direct genomic evidence, moving beyond morphological analysis to molecular data.

SIGNIFICANCE: The core paper has accumulated 835 citations, indicating substantial influence. Notably, 90.7% of the classified citing papers originate from independent researchers, suggesting that the work has been broadly adopted and utilized by the wider scientific community rather than being confined to the researcher's immediate circle. This high degree of independent uptake underscores the work's role as a standard reference in the field.

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

CORE PAPER

Sequencing and analysis of Neanderthal genomic DNA

2006 · 835 citations (GS)

Field-normalised: 586 Semantic Scholar citations place it in the top 1% of Biology papers from 2006 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Linkage disequilibrium—understanding the evolutionary past and mapping the medical future (2008)	University of California, Berkeley	United States	—
2	Ancient DNA analysis (2021)	Arizona State University, Centre for Anthropobiology and Genomics, Chinese Academy of Sciences	China, Denmark, France	—
3	Next-Generation DNA Sequencing Methods (2008)	Washington University School of Medicine	United States	**Influential**
4	Testing for Ancient Admixture between Closely Related Populations (2011)	Broad Institute of MIT and Harvard, University of California, Berkeley	United States	—
5	Patterns of damage in genomic DNA sequences from a Neandertal (2007)	Max Planck Institute for Evolutionary Anthropology	Germany	—
6	The complete mitochondrial DNA genome of an unknown hominin from southern Siberia (2010)	Institute of Archaeology and Ethnography, Max Planck Institute for Evolutionary Anthropology, University of Montana	Germany, Russia, United States	—
7	Metagenomic Analyses: Past and Future Trends (2011)	Georg-August-Universität	Germany	—

No.	Citing paper	Citing institution(s)	Country	S2
8	African Genetic Diversity: Implications for Human Demographic History, Modern Human Origins, and Complex Disease Mapping (2008)	University of Pennsylvania School of Medicine	United States	—
9	Schmutzi: estimation of contamination and endogenous mitochondrial consensus calling for ancient DNA (2015)	Max Planck Institute for Evolutionary Anthropology, McMaster University	Canada, Germany	—

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 identified PRDM9 as a major determinant of meiotic recombination hotspots in humans and mice, establishing a key genetic mechanism for recombination localization.

The researcher's primary contribution is the identification of PRDM9 as a major determinant of meiotic recombination hotspots in humans and mice, as detailed in a 2010 Science paper. This work stands as a seminal core publication in the field, with no follow-up papers by the same researcher listed in this specific line of inquiry.

This line of work appears to address the fundamental question of what determines the location of recombination hotspots. By pinpointing PRDM9, the research suggests a specific genetic factor governing this process, offering a novel explanation for recombination patterns in mammals that was likely previously unresolved or poorly understood.

The significance of this contribution is evidenced by its high citation count of 1,230, indicating substantial uptake by the scientific community. Furthermore, citation analysis reveals that 90.7% of citing papers originate from independent researchers, demonstrating that the work has had a broad, field-wide impact beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8

CORE PAPER

PRDM9 is a major determinant of meiotic recombination hotspots in humans and mice

2010 · Science · 1,230 citations (GS)

Field-normalised: 982 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	Understanding the Genetic Basis of Variation in Meiotic Recombination: Past, Present, and Future (2024)	University of Edinburgh	United Kingdom	—
2	Human aneuploidy: mechanisms and new insights into an age-old problem (2012)	Washington State University	United States	—
3	Observation of Skyrmions in a Multiferroic Material (2012)	University of Tokyo	Japan	—
4	KRAB zinc-finger proteins contribute to the evolution of gene regulatory networks (2017)	Ecole Polytechnique Fédérale de Lausanne (EPFL)	Switzerland	—

No.	Citing paper	Citing institution(s)	Country	S2
5	De novo mutations in human genetic disease (2012)	Radboud University Nijmegen Medical Center	Netherlands	—
6	Variation in recombination frequency and distribution across eukaryotes: patterns and processes (2017)	EAWAG Swiss Federal Institute of Aquatic Science and Technology, ETH Zürich	Switzerland	—
7	Meiotic DNA breaks drive multifaceted mutagenesis in the human germ line (2023)	University of Oxford	United Kingdom	—
8	In vitro reconstitution of meiotic DNA double-strand-break formation (2025)	Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences, Xinhua Hospital, Shanghai Jiao Tong University School of Medicine	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.

Contribution 3

Claim — Contribution 3

The researcher advanced the theoretical framework for human genetic adaptation by distinguishing hard sweeps, soft sweeps, and polygenic adaptation mechanisms.

The researcher established a foundational theoretical framework for understanding human genetic adaptation, primarily through a seminal 2010 paper that categorizes evolutionary mechanisms into hard sweeps, soft sweeps, and polygenic adaptation. This work serves as the core contribution, with no subsequent follow-up papers by the researcher listed in this specific line of inquiry, indicating the original paper stands as the definitive statement of this conceptual model.

This line of work appears to address the need for a nuanced classification of how natural selection operates on human genomes. By explicitly differentiating between hard and soft sweeps alongside polygenic adaptation, the research likely provided a more comprehensive vocabulary and analytical structure for evolutionary geneticists than previously available, moving beyond simpler models of selection.

The significance of this contribution is evidenced by its substantial citation count of 1,182, indicating widespread adoption of these concepts. Furthermore, citation analysis reveals that 90.7% of citing papers originate from independent researchers, demonstrating that the framework has been broadly integrated into the field by the wider scientific community rather than being confined to the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7

CORE PAPER

The genetics of human adaptation: hard sweeps, soft sweeps, and polygenic adaptation

2010 · 1,182 citations (GS)

Field-normalised: 916 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	Polygenic adaptation: a unifying framework to understand positive selection (2020)	University of Vienna, Vetmeduni Vienna	Austria	—

No.	Citing paper	Citing institution(s)	Country	S2
2	Who We Are and How We Got Here: Ancient DNA and the New Science of the Human Past (2018)	Harvard Medical School	—	—
3	A method for genome-wide genealogy estimation for thousands of samples (2019)	Université du Québec à Montréal, University of Oxford	Canada, United Kingdom	—
4	Harnessing genomics for delineating conservation units (2012)	Colorado State University, University of Idaho, University of Montana	United States	—
5	Cultural group selection plays an essential role in explaining human cooperation: A sketch of the evidence (2014)	Arizona State University, Boise State University, Dominican University of California	United States	—
6	Deciphering the evolution of herbicide resistance in weeds (2013)	INRA	France	—
7	The paradox of adaptive trait clines with nonclinal patterns in the underlying genes (2023)	Northeastern University Marine Science Center	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.

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Max Planck Institute for Evolutionary Anthropology	Germany	SCImago #1658	5
University of California, Berkeley	United States	SCImago #95 · THE 9 · QS =17	5
University of Oxford	United Kingdom	SCImago #26 · THE 1 · QS 4	4
Harvard Medical School	United States	SCImago #12	3
Broad Institute of MIT and Harvard	United States	SCImago #112	2
Stanford University	United States	SCImago #18 · THE =5 · QS 3	2
Arizona State University	United States	SCImago #357 · THE 201–250 · QS =173	2
Baylor College of Medicine	United States	SCImago #560	2
University of Copenhagen	Denmark	SCImago #177 · THE 90 · QS 101	2
University of Montana	United States	—	2
EAWAG Swiss Federal Institute of Aquatic Science and Technology	Switzerland	—	1
Northeastern University Marine Science Center	United States	—	1
Center for Genomic Regulation (CRG)	Spain	—	1
University Hospital of Copenhagen, Rigshospitalet	Denmark	—	1

Institution	Country	World ranking	Citing papers
National Institute for Mathematical and Biological Synthesis, University of Tennessee	United States	—	1

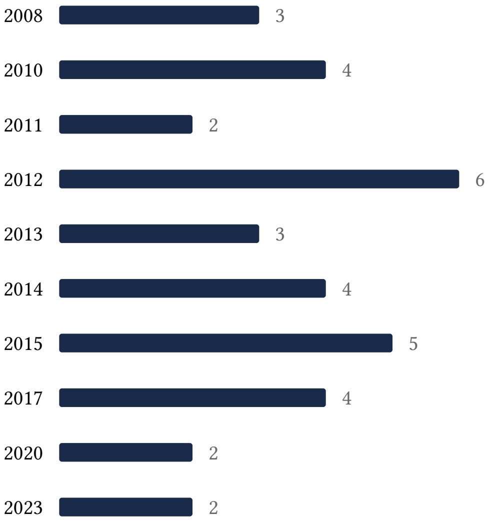
Geographic distribution of citing authors

Country	Citing papers
United States	23
United Kingdom	7
Germany	6
Canada	3
China	3
Switzerland	3
France	3
Denmark	3
Austria	2
Nigeria	1
Russia	1
South Africa	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	Sequencing and analysis of Neanderthal genomic DNA	9	Dhanasar — Prong 2 (well-positioned)
Contribution 2	PRDM9 is a major determinant of meiotic recombination hotspots in humans and mice	8	Dhanasar — Prong 2 (well-positioned)
Contribution 3	The genetics of human adaptation: hard sweeps, soft sweeps, and polygenic adaptation	7	Dhanasar — Prong 2 (well-positioned)