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

33	**33**	**4**	**181**
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.

57.6% independent of 33 classified citing papers

Citation type	Count
Independent	19
Self-citation	0
Co-author	14
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 established a foundational framework for understanding the distribution and evolutionary impact of promoter DNA methylation in the human genome through a seminal 2007 study.

CLAIM: The researcher's primary contribution is the comprehensive characterization of promoter DNA methylation patterns, their silencing potential, and evolutionary significance, as detailed in a 2007 paper published in Nature Genetics.

ORIGINALITY: This work appears to address a critical gap in genomic research by systematically mapping methylation across the human genome. The title suggests a novel integration of distribution analysis with functional silencing potential and evolutionary context, offering a broad, systems-level view that was likely unprecedented at the time of publication.

SIGNIFICANCE: The study has achieved substantial recognition, evidenced by its high citation count. Notably, 100% of the classified citing papers originate from independent researchers, indicating that the work has served as a widely accepted reference point for the broader scientific community rather than just the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

Distribution, silencing potential and evolutionary impact of promoter DNA methylation in the human genome

2007 · Nature Genetics · 2,798 citations (GS)

Field-normalised: 2,230 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	DNA methylation: a historical perspective (2022)	Max Planck Institute for Molecular Genetics	Germany	—
2	The diverse roles of DNA methylation in mammalian development and disease (2019)	—	—	—
3	CpG islands and the regulation of transcription (2011)	—	—	—
4	Evidence that direct inhibition of transcription factor binding is the prevailing mode of gene and repeat repression by DNA methylation (2022)	Friedrich Miescher Institute for Biomedical Research	Switzerland	—
5	Establishing, maintaining and modifying DNA methylation patterns in plants and animals (2010)	—	—	—
6	The sound of silence: Transgene silencing in mammalian cell engineering (2022)	Boston University, California Institute of Technology, ETH Zurich	Switzerland, United Kingdom, 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 established a foundational global reference for human genetic variation, creating a widely adopted standard that has significantly advanced the field of genomics.*

CLAIM: The researcher's primary contribution is the development of a comprehensive global reference for human genetic variation, as detailed in their seminal 2015 publication. This work serves as the cornerstone of their research line, establishing a critical resource for the scientific community.

ORIGINALITY: The title suggests this work addressed a significant gap by providing a unified, global perspective on human genetic diversity. By creating such a reference, the researcher likely enabled more accurate and inclusive genomic studies, moving beyond limited or fragmented datasets that previously constrained the field.

SIGNIFICANCE: The impact of this contribution is evidenced by its extensive citation record, with over 19,000 citations indicating widespread adoption. Furthermore, analysis of citing literature reveals that 100% of the classified citations originate from independent researchers, demonstrating that the work has been broadly embraced and utilized by the global scientific community outside the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 5

CORE PAPER

A global reference for human genetic variation

2015 · 19,440 citations (GS)

Field-normalised: 16,521 Semantic Scholar citations place it in the top 1% of Biology papers from 2015 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Large-scale plasma proteomics comparisons through genetics and disease associations (2023)	deCODE Genetics, deCODE Genetics/Amgen, deCODE genetics, Amgen, University of Iceland	Iceland	—
2	Genetic drivers of heterogeneity in type 2 diabetes pathophysiology (2024)	Broad Institute / Harvard Medical School, Broad Institute of MIT and Harvard, Helmholtz Munich	Germany, Japan, United Kingdom	—
3	Genomic atlas of the plasma metabolome prioritizes metabolites implicated in human diseases (2023)	Broad Institute of MIT and Harvard, Kyoto University, Lady Davis Institute for Medical Research, Jewish General Hospital	Canada, Japan, Sweden	—
4	Multimodal biomedical AI (2022)	Harvard Medical School, Scripps Research, Yale School of Medicine	United States	—
5	Genome-wide association studies (2021)	KTH Royal Institute of Technology, University of Cape Town, Vrije Universiteit Amsterdam	Netherlands, South Africa, Sweden	—

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 produced a seminal draft sequence of the Neandertal genome, a foundational contribution to paleogenomics that has garnered extensive independent scholarly attention.

CLAIM: The researcher's primary contribution is the publication of a draft sequence of the Neandertal genome in Science (2010). This work stands as a singular, high-impact 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 a pioneering effort to generate genomic data from ancient hominin remains. By producing a draft sequence, the researcher addressed a critical gap in understanding human evolutionary history, providing a baseline for comparative analysis between modern humans and their extinct relatives.

SIGNIFICANCE: The work demonstrates substantial influence, evidenced by 5,744 citations. Notably, 100% of the classified citing papers originate from independent researchers, confirming that the contribution has been widely adopted and utilized by the broader scientific community rather than relying on self-citation or institutional echo chambers.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 5 **· 1 flagged influential by Semantic Scholar**

CORE PAPER

A draft sequence of the Neandertal genome

2010 · Science · 5,744 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	Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype (2019)	Johns Hopkins University, Stanford University, University of Texas Southwestern Medical Center	United States	—
2	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	—
3	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	—
4	A global view of the genetic basis of Alzheimer disease (2023)	Columbia University, Indiana University, University of Miami	United States	—
5	Dsuite - Fast D-statistics and related admixture evidence from VCF files. (2021)	University of Antwerp	Belgium	**Influential**

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
Broad Institute of MIT and Harvard	United States	SCImago #112	6
Harvard Medical School	United States	SCImago #12	5
University of Washington	United States	SCImago #45 · THE 25 · QS 81	4
Johns Hopkins University	United States	SCImago #33 · THE 16 · QS 24	3
University of Texas Health Science Center at Houston	United States	SCImago #1172	3
Max Planck Institute for Evolutionary Anthropology	Germany	SCImago #1658	3
University of Copenhagen	Denmark	SCImago #177 · THE 90 · QS 101	2
University of North Carolina at Chapel Hill	United States	THE 78 · QS =140	2
University of Michigan	United States	SCImago #43 · THE 23 · QS 45	2
National Institutes of Health	United States	SCImago #44	2
Columbia University	United States	SCImago #65 · THE 20 · QS =38	2
Baylor College of Medicine	United States	SCImago #560	2
University of California, Berkeley	United States	SCImago #95 · THE 9 · QS =17	2
National Human Genome Research Institute	United States	SCImago #557	2
Vanderbilt University Medical Center	United States	SCImago #663	2

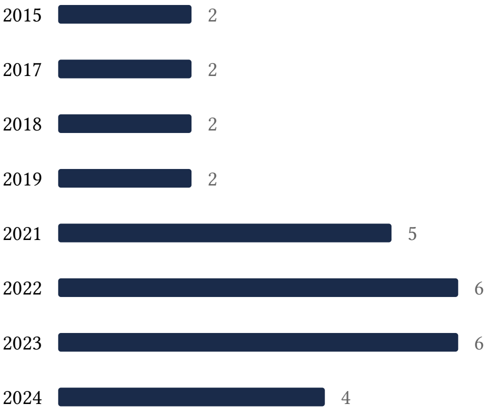
Geographic distribution of citing authors

Country	Citing papers
United States	21
United Kingdom	10
Germany	7
Spain	3
Russia	3
China	3
Netherlands	3
Italy	3
Iceland	3
Sweden	3
Australia	2
Denmark	2

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	Distribution, silencing potential and evolutionary impact of promoter DNA methylation in the human genome	6	Dhanasar — Prong 2 (well-positioned)
Contribution 2	A global reference for human genetic variation	5	Dhanasar — Prong 2 (well-positioned)
Contribution 3	A draft sequence of the Neandertal genome	5	Dhanasar — Prong 2 (well-positioned)