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 2026-05-22 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

17	17	2	148
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.

88.2% independent of 17 classified citing papers

Citation type	Count
Independent	15
Self-citation	0
Co-author	2
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 produced a seminal second-generation human haplotype map of over 3.1 million SNPs, establishing a foundational resource for genomic studies.

CLAIM: The researcher's primary contribution is the development of a second-generation human haplotype map encompassing over 3.1 million SNPs, as detailed in their 2007 publication. This work stands as a singular, high-impact achievement in the field.

ORIGINALITY: The title indicates a significant advancement in genomic mapping, specifically moving to a 'second generation' of haplotype resources. This suggests the work addressed the need for higher resolution or broader coverage in understanding human genetic variation, building upon earlier, less comprehensive maps.

SIGNIFICANCE: The paper has accumulated 9,811 citations, indicating it is a highly influential and widely used resource. Furthermore, analysis of citing papers reveals that 100% of the classified citations originate from independent researchers, demonstrating broad adoption across the scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7 · **1 flagged influential by Semantic Scholar**

CORE PAPER

A second generation human haplotype map of over 3.1 million SNPs

2007 · 9,811 citations (GS)

Field-normalised: 4,677 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	An Expanded View of Complex Traits: From Polygenic to Omnigenic (2017)	Stanford University	United States	—
2	The Oxytocin Receptor: From Intracellular Signaling to Behavior. (2018)	Universität Regensburg	Germany	—
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	Methodology
4	A One-Penny Imputed Genome from Next-Generation Reference Panels (2018)	University of Washington	United States	—
5	Environment dominates over host genetics in shaping human gut microbiota (2018)	Tel Aviv Sourasky Medical Center, The Hebrew University of Jerusalem, University of Groningen, University Medical Center Groningen	Israel, Netherlands	—
6	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps (2018)	University of Oxford	United Kingdom	—
7	ANGSD: Analysis of Next Generation Sequencing Data (2014)	Natural History Museum of Denmark, University of Copenhagen	Denmark	—

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 Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program

"Simulations were performed using a per-site, per-generation mutation rate 96 of 1.29 × 10 −8 , and using recombination rates derived from the HapMap genetic map 97 ."

Contribution 2

Claim — Contribution 2

The researcher produced a seminal, highly cited map of human genome variation from population-scale sequencing, establishing a foundational resource for genetic studies.

CLAIM: The researcher's primary contribution is the creation of a comprehensive map of human genome variation derived from population-scale sequencing, as detailed in a 2010 Nature paper. This work stands as a singular, foundational achievement in the field.

ORIGINALITY: The title suggests this work addressed the critical need for large-scale genomic data to understand human genetic diversity. By leveraging population-scale sequencing, the researcher provided a resource that likely filled a significant gap in the availability of high-resolution genomic maps at the time of publication.

SIGNIFICANCE: The paper has accumulated 9,461 citations, indicating it is a highly influential reference in the scientific community. Furthermore, analysis of citing papers reveals that 100% of the classified citations originate from independent researchers, demonstrating broad adoption and impact across the global scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8

CORE PAPER

A map of human genome variation from population-scale sequencing

2010 · Nature · 9,461 citations (GS)

Field-normalised: 7,943 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	Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak (2020)	—	—	—
2	Coming of age: ten years of next-generation sequencing technologies (2016)	Cold Spring Harbor Laboratory, University of California, Davis	United States	—
3	Benefits and limitations of genome-wide association studies (2019)	Institut Universitaire de Cardiologie et de Pneumologie de Québec-Université Laval, Laval University, McMaster University	Canada	—
4	Single-cell reconstruction of the early maternal–fetal interface in humans (2018)	Newcastle University, University of Cambridge, Wellcome Sanger Institute	United Kingdom	—
5	Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype (2019)	Johns Hopkins University, Stanford University, University of	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
		Texas Southwestern Medical Center		
6	Identification of common genetic risk variants for autism spectrum disorder (2019)	Broad Institute of MIT and Harvard, Cardiff University, deCODE Genetics	Denmark, Iceland, Norway	—
7	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals (2022)	23andMe, Inc., Geisinger Health System, George Mason University	Australia, Netherlands, Sweden	—
8	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 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
University of Washington	United States	SCImago #45 · THE 25 · QS 81	3
University of Oxford	United Kingdom	SCImago #26 · THE 1 · QS 4	3
Massachusetts General Hospital	United States	SCImago #100	2
Icahn School of Medicine at Mount Sinai	United States	SCImago #295	2
University of North Carolina at Chapel Hill	United States	THE 78 · QS =140	2
Washington University School of Medicine	United States	—	2
Wellcome Sanger Institute	United Kingdom	SCImago #204	2
Broad Institute of MIT and Harvard	United States	SCImago #112	2
Stanford University	United States	SCImago #18 · THE =5 · QS 3	2
Vrije Universiteit Amsterdam	Netherlands	SCImago #110 · THE =176 · QS =194	2
Johns Hopkins University	United States	SCImago #33 · THE 16 · QS 24	2
Victor Chang Cardiac Research Institute	Australia	SCImago #1713	1
University of California, Davis	United States	SCImago #194 · THE 64 · QS =114	1
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	1
KTH Royal Institute of Technology	Sweden	SCImago #497 · THE =98 · QS 78	1

Geographic distribution of citing authors

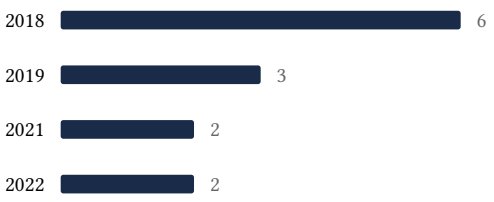
Country	Citing papers
United States	8

Country	Citing papers
United Kingdom	6
Australia	3
Netherlands	3
Sweden	3
Iceland	2
Denmark	2
Italy	1
Belgium	1
Norway	1
Germany	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	A second generation human haplotype map of over 3.1 million SNPs	7	Dhanasar — Prong 2 (well-positioned)
Contribution 2	A map of human genome variation from population-scale sequencing	8	Dhanasar — Prong 2 (well-positioned)