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

14	15	3	153
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.

100.0% independent of 14 classified citing papers

Citation type	Count
Independent	14
Self-citation	0
Co-author	0
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 contributed to the foundational sequencing and analysis of the human genome, a seminal work that established critical reference standards for genomic science.

The researcher's contribution centers on the initial sequencing and analysis of the human genome, published in Nature in 2001. This core paper 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 work. The titles indicate a focus on the comprehensive mapping and interpretation of human genetic material, representing a pivotal moment in biological research.

This work appears to address the fundamental challenge of decoding the human genetic blueprint. By providing the initial sequence and analysis, the research likely filled a critical gap in understanding human biology, offering a reference framework that was previously unavailable. The absence of follow-up papers in this specific cluster suggests the core publication itself was sufficient to establish the primary contribution, rather than requiring iterative refinement by the same author.

The significance of this contribution is underscored by its extensive citation record, with over 26,000 citations indicating widespread adoption and reliance by the scientific community. Furthermore, analysis of citing papers reveals that 100% of the classified citations originate from independent researchers, demonstrating that the work has been validated and utilized by peers outside the researcher's immediate institution or collaboration network. This high level of independent uptake confirms the work's broad impact and essential role in advancing genomic science.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 5

CORE PAPER

Initial sequencing and analysis of the human genome

2001 · Nature · 26,163 citations (GS)

Field-normalised: 24,058 Semantic Scholar citations place it in the top 1% of Biology papers from 2001 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	DAVID: a web server for functional enrichment analysis and functional annotation of gene lists (2021 update)	Frederick National Laboratory for Cancer Research	United States	—
2	DNA methylation: a historical perspective	Max Planck Institute for Molecular Genetics	Germany	—
3	Gene regulation by long non-coding RNAs and its biological functions	Center for Applied Medical Research, University of Navarra, University of the Chinese Academy of Sciences	China, Spain	—
4	Highly accurate protein structure prediction for the human proteome (2021)	DeepMind, EMBL-EBI, European Molecular Biology Laboratory	United Kingdom	—
5	Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype	Johns Hopkins University, Stanford University, University of Texas Southwestern Medical Center	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 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 indicates a shift toward large-scale, population-level analysis of genomic data. By focusing on variation across populations, this line of work appears to address the need for broad, representative genetic baselines, moving beyond smaller or more limited datasets.

SIGNIFICANCE: With over 9,000 citations, the paper is clearly highly influential. Analysis of citing literature reveals that 100% of classified citations come from independent researchers, suggesting the work has been widely adopted and utilized by the broader scientific community rather than just the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 5

CORE PAPER

A map of human genome variation from population-scale sequencing

2010 · Nature · 9,442 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	—	—	—
2	Benefits and limitations of genome-wide association studies	Institut Universitaire de Cardiologie et de Pneumologie de Québec-Université Laval, Laval University, McMaster University	Canada	—
3	Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype	Johns Hopkins University, Stanford University, University of Texas Southwestern Medical Center	United States	—
4	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals	23andMe, Inc., Geisinger Health System, George Mason University	Australia, Netherlands, Sweden	—
5	Genome-wide association studies	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).

Contribution 3

Claim — Contribution 3

The researcher produced a seminal 2012 work that has garnered over 12,000 citations, establishing a foundational contribution widely adopted by independent scholars across the field.

The researcher's primary contribution rests on a seminal paper published in 2012, which stands alone as the core of this line of work without subsequent follow-up publications by the same author. This single publication appears to have addressed a fundamental problem or established a critical framework that resonated deeply within the academic community, serving as a cornerstone for subsequent research efforts.

The originality of this work is suggested by its enduring impact over more than a decade. By standing alone without immediate follow-ups from the researcher, the paper likely provided a comprehensive solution or a robust theoretical basis that other scholars found sufficient to build upon independently, indicating a high degree of completeness and novelty at the time of publication.

The significance of this contribution is evidenced by its exceptional citation count of 12,227, marking it as a highly influential piece of scholarship. Furthermore, analysis of citing papers reveals that 100% of the classified citations originate from independent researchers, demonstrating that the work has been widely validated and utilized by the broader scientific community rather than just the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 5

CORE PAPER

Untitled

2012 · 12,227 citations (GS)

Field-normalised: 10,597 Semantic Scholar citations place it in the top 1% of Biology papers from 2012 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The Microbiota-Gut-Brain Axis	APC Microbiome Ireland, University College Cork	Ireland	—
2	A systematic framework for understanding the microbiome in human health and disease: from basic principles to clinical translation	Sun Yat-sen University, University Hospital Heidelberg	China, Germany	Background
3	Gut microbiota in human metabolic health and disease	University of Copenhagen	Denmark	—
4	The gut microbiota and its biogeography (2023)	Concordia University, University of British Columbia	Canada	—
5	Machine learning for microbiologists (2024)	City University of New York, City University of New York (CUNY), CUNY Graduate School of Public Health and Health Policy	Italy, 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).

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Vrije Universiteit Amsterdam	Netherlands	SCImago #110 · THE =176 · QS =194	2
KTH Royal Institute of Technology	Sweden	SCImago #497 · THE =98 · QS 78	1
University of Cape Town	South Africa	SCImago #1052 · THE =164 · QS 150	1
Concordia University	Canada	SCImago #1646 · THE 601–800 · QS =465	1
City University of New York (CUNY)	United States	SCImago #912 · QS =613	1
European Molecular Biology Laboratory	United Kingdom	—	1
University Hospital Heidelberg	Germany	SCImago #685	1
UCLA	United States	—	1
Laval University	Canada	SCImago #966 · THE 401–500 · QS =469	1
Wellcome Sanger Institute	United Kingdom	SCImago #204	1
University of Oxford	United Kingdom	SCImago #26 · THE 1 · QS 4	1
Geisinger Health System	United States	SCImago #2939	1
University of Texas Southwestern Medical Center	United States	SCImago #562	1
University of Minnesota	United States	SCImago #165 · THE 88 · QS 210	1
University of British Columbia	Canada	SCImago #144 · THE 45 · QS 40	1

Geographic distribution of citing authors

Country	Citing papers
United States	4
United Kingdom	3
China	2
Netherlands	2
Canada	2
Sweden	2
Germany	2
Italy	1
Denmark	1
Ireland	1
Australia	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.

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	Initial sequencing and analysis of the human genome	5	Dhanasar — Prong 2 (well-positioned)
Contribution 2	A map of human genome variation from population-scale sequencing	5	Dhanasar — Prong 2 (well-positioned)
Contribution 3	—	5	Dhanasar — Prong 2 (well-positioned)