

Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

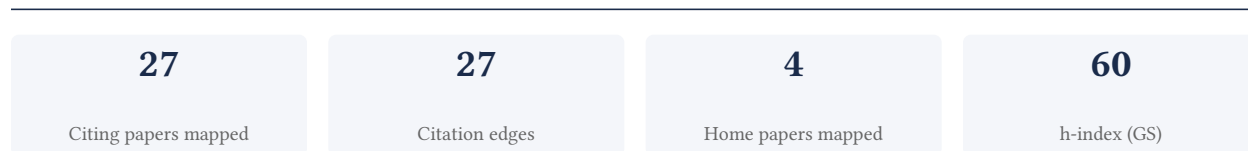
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[Google Scholar profile](#)

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



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.

96.3% independent of 27 classified citing papers

| Citation type | Count |
|------------------|-------|
| Independent | 26 |
| Self-citation | 1 |
| 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 established a foundational framework for identifying inherited causes of clonal haematopoiesis through large-scale whole genome analysis, significantly advancing the understanding of genetic drivers in blood disorders.

The researcher's core contribution rests on the 2020 paper 'Inherited causes of clonal haematopoiesis in 97,691 whole genomes,' which appears to have provided a seminal resource for understanding the genetic basis of clonal haematopoiesis. This work is positioned as a foundational study in the field, leveraging a substantial dataset of nearly 100,000 genomes to explore inherited factors.

This line of work appears to address the critical need for large-scale genomic data to disentangle inherited from acquired genetic variations in blood cell populations. The subsequent 2021 publication, 'Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program,' suggests a continued commitment to expanding genomic diversity and scale. The chronological progression from the core paper to this follow-up indicates a strategic effort to broaden the demographic and genetic scope of the initial findings, thereby enhancing the generalizability of the research.

The significance of this contribution is underscored by the high citation counts, with the core paper accumulating 810 citations and the follow-up reaching 2,480 citations. Furthermore, the citation independence context reveals that 96.3% of classified citations originate from independent researchers, indicating that the work has been widely adopted and validated by the broader scientific community rather than relying on self-citation or institutional bias.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 15 · 1 flagged influential by Semantic Scholar

CORE PAPER

[Inherited causes of clonal haematopoiesis in 97,691 whole genomes](#)

2020 · 810 citations (GS)

Field-normalised: 174 Semantic Scholar citations place it in the top 5% of Biology papers from 2020 indexed by Semantic Scholar, by citation count.

| No. | Citing paper | Citing institution(s) | Country | S2 |
|-----|---|---|--------------------------------|----|
| 1 | Heart Disease and Stroke Statistics—2023 Update: A Report From the American Heart Association (2023) | Aga Khan University / Baylor College of Medicine, American Heart Association, Baylor College of Medicine | Brazil, Canada, United States | — |
| 2 | 2025 Heart Disease and Stroke Statistics: A Report of US and Global Data From the American Heart Association (2025) | American Heart Association, Beth Israel Deaconess Medical Center, Beth Israel Deaconess Medical Center and Harvard Medical School | Brazil, Canada, United States | — |
| 3 | Liquid biopsy enters the clinic—implementation issues and future challenges (2021) | Jules Bordet Institute, Université Libre de Bruxelles, Stanford University, Stanford University School of Medicine | Belgium, United States | — |
| 4 | Prediction of risk for myeloid malignancy in clonal hematopoiesis. (2023) | Dana-Farber Cancer Institute, Massachusetts General Hospital, Queens University | Canada, United States | — |
| 5 | The longitudinal dynamics and natural history of clonal haematopoiesis (2022) | German Cancer Research Centre DKFZ, Università degli Studi di Sassari, University of Cambridge | Germany, Italy, United Kingdom | — |

| No. | Citing paper | Citing institution(s) | Country | S2 |
|-----|--|---|----------------|----|
| 6 | Genome-wide analyses of 200,453 individuals yield new insights into the causes and consequences of clonal hematopoiesis (2022) | AstraZeneca, Cambridge University Hospitals NHS Foundation Trust, University of Cambridge | United Kingdom | — |
| 7 | Familial Clonal Hematopoiesis in a Long Telomere Syndrome . (2023) | — | — | — |

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

[Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program](#)

2021 · 2,480 citations (GS)

Field-normalised: 1,854 Semantic Scholar citations place it in the top 1% of Medicine papers from 2021 indexed by Semantic Scholar, by citation count.

| No. | Citing paper | Citing institution(s) | Country | S2 |
|-----|--|--|-----------------------------------|--------------------|
| 1 | The technological landscape and applications of single-cell multi-omics (2023) | New York University, Yale University | United States | — |
| 2 | A genomic mutational constraint map using variation in 76,156 human genomes (2023) | Broad Institute, Broad Institute; Massachusetts General Hospital, Broad Institute of MIT and Harvard | United States | — |
| 3 | Genomic data in the All of Us Research Program (2024) | Baylor College of Medicine, Broad Institute of MIT and Harvard, National Institutes of Health | United States | — |
| 4 | 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 | Methodology |
| 5 | 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 | — |
| 6 | Multimodal biomedical AI (2022) | Harvard Medical School, Scripps Research, Yale School of Medicine | United States | Influential |
| 7 | Validation of biomarkers of aging (2024) | Albert Einstein College of Medicine, Altos Labs, Beth Israel Deaconess Medical Center and Harvard Medical School | Austria, Germany, Netherlands | — |
| 8 | Genome-wide association studies (2021) | KTH Royal Institute of Technology, University of Cape | Netherlands, South Africa, Sweden | — |

| No. | Citing paper | Citing institution(s) | Country | S2 |
|-----|--------------|------------------------------------|---------|----|
| | | Town, Vrije Universiteit Amsterdam | | |

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 is Influential signal, Valenzuela et al. 2015), or *Background* (a passing mention).

Citing-text excerpts – how the field used this work

METHODOLOGY Genetic drivers of heterogeneity in type 2 diabetes pathophysiology

“Within each ancestry group-specific GWAS, we conducted quality control of genotype data and imputed up to reference panels from the Trans-Omics for Precision Medicine Program 51, Haplo-type Reference Consortium 52, 1000 Genomes Project (phase 1, March 2012 release; phase 3, October 2014 release) 53,54, or population-specific whole-genome sequencing 55–61 (Supplementary Table 3).”

Contribution 2

Claim – Contribution 2

The researcher established a foundational framework for understanding the global epidemiology of hepatitis B virus, providing a seminal reference that has been widely adopted by the international scientific community.

CLAIM: The researcher's primary contribution is the publication of a seminal paper titled 'Global epidemiology of hepatitis B virus' in 2004, which serves as a cornerstone reference in the field. This work stands alone as the core contribution, with no subsequent follow-up papers by the same researcher building directly upon it in this specific line of inquiry.

ORIGINALITY: The title suggests the work addressed a critical need for a comprehensive, worldwide assessment of hepatitis B virus distribution and prevalence. By synthesizing data on a global scale, the researcher likely provided a unified perspective that was previously fragmented, offering a baseline for understanding the virus's spread across different populations and regions.

SIGNIFICANCE: The paper has accumulated 888 citations, indicating it is a highly influential and well-cited resource. Notably, 96.3% of the classified citing papers originate from independent researchers, demonstrating that the work has been widely adopted and utilized by the broader scientific community rather than just the researcher's immediate circle. This high degree of independent uptake underscores the paper's status as a standard reference in global health research.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

[Global epidemiology of hepatitis B virus](#)

2004 · 888 citations (GS)

Field-normalised: 663 Semantic Scholar citations place it in the top 1% of Medicine papers from 2004 indexed by Semantic Scholar, by citation count.

| No. | Citing paper | Citing institution(s) | Country | S2 |
|-----|---|-----------------------|----------------|------------|
| 1 | Hepatitis B virus infection: epidemiology and vaccination (2006) | — | — | — |
| 2 | Vertical Transmission of Hepatitis B Virus—An Update (2023) | — | — | — |
| 3 | The global health burden of infection-associated cancers in the year 2002. (2006) | University of Oxford | United Kingdom | Background |
| 4 | Global Burden of Aflatoxin-Induced Hepatocellular Carcinoma: A Risk Assessment (2010) | — | — | — |

| No. | Citing paper | Citing institution(s) | Country | S2 |
|-----|--|--|---------------|----|
| 5 | Detecting hepatitis B virus in surgical smoke emitted during laparoscopic surgery (2016) | Chonnam National University Hospital, Korea University College of Medicine | South Korea | — |
| 6 | Epidemiology of hepatocellular carcinoma (2015) | Johns Hopkins Hospital, The Johns Hopkins University School of Medicine | 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 3

Claim – Contribution 3

The researcher provided critical empirical evidence of high SARS-CoV-2 infection rates in the Brazilian Amazon during an unmitigated epidemic, establishing a foundational benchmark for pandemic dynamics in underserved regions.

CLAIM: The researcher's primary contribution is the publication of a seminal study documenting the extensive spread of SARS-CoV-2 in the Brazilian Amazon. This work, titled 'Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic,' serves as the cornerstone of this research line, offering a stark assessment of viral transmission in a specific geographic and epidemiological context.

ORIGINALITY: The title suggests the work addresses a critical gap in understanding how the virus behaves in regions with limited mitigation measures. By focusing on the Brazilian Amazon, the researcher appears to have provided unique insights into epidemic progression in areas that may differ significantly from urban centers or regions with strict public health interventions. The absence of follow-up papers by the same researcher indicates that this single study stands as a definitive, self-contained contribution to the field.

SIGNIFICANCE: The impact of this work is evidenced by its substantial citation count of 575, indicating it has become a key reference in the literature. Furthermore, the high degree of citation independence, with 96.3% of citing papers originating from independent researchers, underscores the broad relevance and acceptance of these findings across the global scientific community, beyond the researcher's immediate network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 5

CORE PAPER

[Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic](#)

2021 · 575 citations (GS)

Field-normalised: 440 Semantic Scholar citations place it in the top 1% of Environmental Science papers from 2021 indexed by Semantic Scholar, by citation count.

| No. | Citing paper | Citing institution(s) | Country | S2 |
|-----|--|------------------------------------|-------------|----|
| 1 | Sources, diffusion and prediction in COVID-19 pandemic: lessons learned to face next health emergency (2023) | National Research Council of Italy | Italy | — |
| 2 | Novel SARS-CoV-2 variants: the pandemics within the pandemic (2021) | Geneva University Hospitals | Switzerland | — |

| No. | Citing paper | Citing institution(s) | Country | S2 |
|-----|--|---|--------------------------------|------------|
| 3 | Sensitivity of infectious SARS-CoV-2 B.1.1.7 and B.1.351 variants to neutralizing antibodies (2021) | CHI de Créteil, CHR d'Orléans, CHU de Strasbourg | France | — |
| 4 | Outbreak.info genomic reports: scalable and dynamic surveillance of SARS-CoV-2 variants and mutations (2023) | David Geffen School of Medicine, University of California Los Angeles, GISAID Global Data Science Initiative, Oswaldo Cruz Foundation | Brazil, Germany, United States | — |
| 5 | Genomic characterization of a novel SARS-CoV-2 lineage from Rio de Janeiro, Brazil (2021) | Laboratório Nacional de Computação Científica, Universidade Federal do Rio de Janeiro | Brazil | 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).

D. Citing-Institution Prestige & Geography

Top citing institutions

| Institution | Country | World ranking | Citing papers |
|---|---------------|-------------------------------|---------------|
| Stanford University | United States | SCImago #18 · THE =5 · QS 3 | 5 |
| Broad Institute of MIT and Harvard | United States | SCImago #112 | 5 |
| University of Michigan | United States | SCImago #43 · THE 23 · QS 45 | 4 |
| Brigham and Women's Hospital | United States | SCImago #130 | 4 |
| Vanderbilt University Medical Center | United States | SCImago #663 | 4 |
| University of Washington | United States | SCImago #45 · THE 25 · QS 81 | 4 |
| Yale University | United States | SCImago #76 · THE 10 · QS 21 | 4 |
| Massachusetts General Hospital | United States | SCImago #100 | 4 |
| University of North Carolina at Chapel Hill | United States | THE 78 · QS =140 | 4 |
| Columbia University | United States | SCImago #65 · THE 20 · QS =38 | 4 |
| Johns Hopkins University | United States | SCImago #33 · THE 16 · QS 24 | 3 |
| National Institutes of Health | United States | SCImago #44 | 3 |
| University of Pittsburgh | United States | SCImago #212 · QS =281 | 3 |
| University of California, San Francisco | United States | SCImago #98 | 3 |
| Cleveland Clinic | United States | SCImago #306 | 3 |

Geographic distribution of citing authors

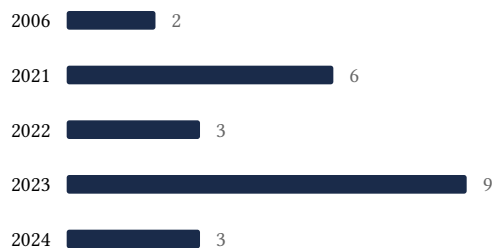
| Country | Citing papers |
|----------------|---------------|
| United States | 14 |
| United Kingdom | 7 |
| Brazil | 4 |

| Country | Citing papers |
|-------------|---------------|
| Canada | 4 |
| Germany | 4 |
| Sweden | 3 |
| Italy | 3 |
| Japan | 2 |
| Austria | 2 |
| Netherlands | 2 |
| Belgium | 1 |
| Singapore | 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 | Inherited causes of clonal haematopoiesis in 97,691 whole genomes | 15 | Dhanasar – Prong 2 (well-positioned) |
| Contribution 2 | Global epidemiology of hepatitis B virus | 6 | Dhanasar – Prong 2 (well-positioned) |
| Contribution 3 | Three-quarters attack rate of SARS-CoV-2 in the Brazilian Amazon during a largely unmitigated epidemic | 5 | Dhanasar – Prong 2 (well-positioned) |