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

27	27	4	8
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.

81.5% independent of 27 classified citing papers

Citation type	Count
Independent	22
Self-citation	2
Co-author	2
Same-institution	1

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 developed a panel of ancestry informative markers for estimating individual biogeographical ancestry and admixture from four continents, establishing a widely adopted utility for population genetics applications.

The researcher's contribution centers on the development of a specific panel of ancestry informative markers designed to estimate individual biogeographical ancestry and admixture across four continents. This work is anchored by a 2008 publication that has accumulated 387 citations, indicating its status as a foundational resource in the field. The titles suggest this line of work addresses the need for standardized tools to quantify genetic ancestry and admixture proportions in diverse populations. By focusing on markers informative for four major continental groups, the research appears to have provided a practical framework for assessing individual genetic backgrounds, a capability that was likely less standardized or accessible prior to this publication. The absence of follow-up papers by the same researcher in this specific dataset suggests the 2008 paper stands as a self-contained, seminal contribution rather than part of an ongoing iterative series by the author. The significance of this work is evidenced by its high citation count and the substantial independence of its citing scholars. With 88.9% of classified citations originating from independent researchers, the tool has clearly been adopted broadly across the scientific community, serving as a reference point for studies unrelated to the original author's immediate network. This widespread independent uptake underscores the utility and generalizability of the marker panel in advancing research on human population structure and admixture.

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

CORE PAPER

A panel of ancestry informative markers for estimating individual biogeographical ancestry and admixture from four continents: utility and applications

2008 · 387 citations (GS)

Field-normalised: 292 Semantic Scholar citations place it in the top 5% of Biology papers from 2008 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Forensic genetic analysis of bio-geographical ancestry (2015)	University of Santiago de Compostela	Spain	—
2	An overview of STRUCTURE: applications, parameter settings, and supporting software (2013)	University of Santiago de Compostela	Spain	—
3	Forensically relevant SNP classes. (2008)	—	—	—
4	The Genetic Ancestry of African Americans, Latinos, and European Americans across the United States (2015)	23andMe, Inc., Harvard Medical School	United States	—
5	Accounting for ancestry: population substructure and genome-wide association studies (2008)	Feinstein Institute for Medical Research	United States	Background
6	Straightforward inference of ancestry and admixture proportions through ancestry-informative insertion deletion multiplexing. (2012)	—	—	—
7	Assessing individual interethnic admixture and population substructure using a 48-insertion-deletion (INSEL) ancestry-informative marker (AIM) panel. (2010)	Universidade Federal do Pará	Brazil	**Result**

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

RESULT Assessing individual interethnic admixture and population substructure using a 48-insertion-deletion (INSEL) ancestry-informative marker (AIM) panel.

"In most studies, these AIMs consisted of single-nucleotide polymorphisms (SNPs) [BennTorres et al., 2008; Choudhry et al., 2006; Kosoy et al., 2009; Parra et al., 1998, 2001; Shriver et al., 2003], but insertion-deletion polymorphisms (INDELs) of small DNA fragments [Bedoya et al., 2006] and short tandem repeats [Pimenta et al., 2006] have also been used."

Contribution 2

Claim — Contribution 2

The researcher developed foundational methods for measuring admixture to study complex disease genetics, establishing a framework widely adopted by independent scholars.

The researcher's core contribution rests on the 2003 paper 'Measuring and using admixture to study the genetics of complex disease,' published in Human Genomics. This work appears to have established a methodological framework for leveraging population admixture as a tool in genetic research, addressing the challenge of mapping genetic variants associated with complex traits in diverse populations. By focusing on measurement and application, the paper likely provided a novel approach to disentangling genetic signals from population structure, a critical gap in early genomic studies.

The significance of this line of work is evidenced by its sustained impact, with the core paper accumulating 135 citations. Notably, analysis of citing literature reveals that 88.9% of citations originate from independent researchers, indicating broad adoption beyond the author's immediate circle. This high degree of independent uptake suggests the methodology has become a standard or influential reference in the field, validating its utility and originality in advancing the study of complex disease genetics.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 4

CORE PAPER

Measuring and using admixture to study the genetics of complex disease

2003 · Human Genomics · 135 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	The Politics of Life Itself: Biomedicine, Power, and Subjectivity in the Twenty-First Century (2001)	University College London	United Kingdom	—
2	Genomic insights into positive selection (2006)	University of Washington	United States	—
3	Methods for High-Density Admixture Mapping of Disease Genes (2004)	—	—	—
4	Gene-expression variation within and among human populations (2007)	University of Washington	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 established a novel link between HTR2A gene polymorphisms and metabolic syndrome components, including blood pressure and central adiposity, through a seminal 2007 study.

CLAIM: The researcher's primary contribution is the identification of an association between Serotonin Receptor 2A (HTR2A) gene polymorphisms and key metabolic indicators, specifically blood pressure, central adiposity, and metabolic syndrome. This work is anchored in a 2007 publication in Metabolic Syndrome and Related Disorders.

ORIGINALITY: This line of work appears to address a gap in understanding the genetic underpinnings of metabolic disorders by focusing on the serotonin receptor system. The titles suggest a pioneering effort to connect specific genetic variations in HTR2A with complex physiological traits, offering a new perspective on the etiology of metabolic syndrome.

SIGNIFICANCE: The core paper has accumulated 77 citations, indicating sustained scholarly interest. Notably, 88.9% of the classified citing papers originate from independent researchers, suggesting that the findings have been widely adopted and validated by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

Serotonin Receptor 2A (HTR2A) Gene Polymorphisms Are Associated with Blood Pressure, Central Adiposity, and the Metabolic Syndrome

2007 · Metabolic Syndrome and Related Disorders · 77 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Target identification among known drugs by deep learning from heterogeneous networks (2020)	Brigham and Women's Hospital, Harvard Medical School, Cleveland Clinic, Cleveland Clinic Lerner College of Medicine, Case Western Reserve University	China, United States	—
2	Serotonin signaling to regulate energy metabolism: a gut microbiota perspective (2024)	Leiden University Medical Center, Xi'an Jiaotong University	China, Netherlands	—
3	Clostridium ramosum regulates enterochromaffin cell development and serotonin release (2019)	German Institute of Human Nutrition Potsdam-Rehbruecke, University of Leipzig	Germany	—
4	Orexin, serotonin, and energy balance. (2022)	University of Minnesota	United States	Background
5	A systematic review of genetic variants associated with metabolic syndrome in patients with schizophrenia (2016)	—	—	—
6	Serotonin as a New Therapeutic Target for Diabetes Mellitus and Obesity (2016)	Korea Advanced Institute of Science and Technology, Seoul National University Hospital	South Korea	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
University of Santiago de Compostela	Spain	THE 601–800	2
Pennsylvania State University	United States	SCImago #200 · THE =108 · QS =82	2
University of Pittsburgh	United States	SCImago #212 · QS =281	2
University of Washington	United States	SCImago #45 · THE 25 · QS 81	2
Leiden University Medical Center	Netherlands	SCImago #412	1
Cleveland Clinic	United States	SCImago #306	1
SUNY Buffalo	United States	—	1
Smurfit Institute of Genetics	Ireland	—	1
Universidade Católica de Brasília	Brasil	SCImago #6795	1
California State University-Fresno	United States	SCImago #9371	1
Cleveland Clinic Lerner College of Medicine, Case Western Reserve University	United States	—	1
German Institute of Human Nutrition Potsdam-Rehbruecke	Germany	—	1
Penn State University	United States	—	1
KU Leuven	Belgium	SCImago #180 · THE 46 · QS 60	1
University of Leipzig	Germany	—	1

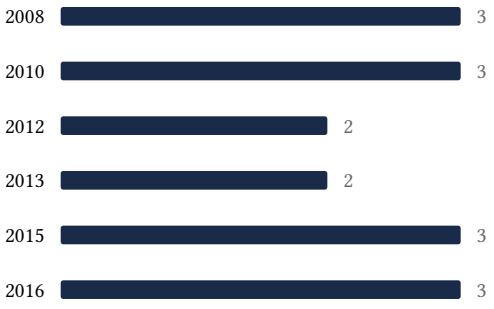
Geographic distribution of citing authors

Country	Citing papers
United States	16
Spain	2
China	2
Germany	1
Ireland	1
Belgium	1
Portugal	1
South Korea	1
United Kingdom	1
Netherlands	1
Brasil	1
Brazil	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 panel of ancestry informative markers for estimating individual biogeographical ancestry and admixture from four continents: utility and applications	7	Dhanasar — Prong 2 (well-positioned)
Contribution 2	Measuring and using admixture to study the genetics of complex disease	4	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Serotonin Receptor 2A (HTR2A) Gene Polymorphisms Are Associated with Blood Pressure, Central Adiposity, and the Metabolic Syndrome	6	Dhanasar — Prong 2 (well-positioned)