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 2026-06-10 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

15	15	3	88
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 13 classified citing papers

Citation type	Count
Independent	13
Self-citation	0
Co-author	0
Same-institution	0

2 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 ANNOVAR, a widely adopted tool for functional annotation of genetic variants from high-throughput sequencing data, establishing a standard for genomic analysis.

The researcher's primary contribution is the development of ANNOVAR, introduced in a 2010 paper titled 'ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data.' This work stands as a seminal core publication in the field, with no subsequent follow-up papers by the same researcher listed in this specific line of inquiry. The title suggests the tool addresses the critical need for efficient functional annotation of genetic variants derived from high-throughput sequencing, a task that was likely complex or fragmented prior to this release. By providing a dedicated solution for this specific bioinformatics challenge, the work appears to have filled a significant methodological gap in genomic data processing. The significance of this contribution is underscored by its extensive citation record, with the core paper accumulating 15,980 citations. Furthermore, analysis of citing literature reveals that 100% of the classified citations originate from independent researchers, indicating broad adoption and impact across the global scientific community rather than isolated institutional use. This high level of independent engagement suggests that ANNOVAR has become a foundational resource for researchers in genetics and genomics.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 5

CORE PAPER

ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data

2010 · 15,980 citations (GS)

Field-normalised: 13,300 Semantic Scholar citations place it in the top 1% of Computer Science papers from 2010 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	CADD v1.7: using protein language models, regulatory CNNs and other nucleotide-level scores to improve genome-wide variant predictions (2024)	Berlin Institute of Health at Charité – Universitätsmedizin Berlin, Berlin Institute of Health (BIH) at Charité – Universitätsmedizin Berlin, University of Lübeck	Germany	—
2	Allogeneic CD19-targeted CAR-T therapy in patients with severe myositis and systemic sclerosis	BRL Medicine Inc., East China Normal University, Nanjing University	China	—
3	Transplantation of chemically induced pluripotent stem-cell-derived islets under abdominal anterior rectus sheath in a type 1 diabetes patient (2024)	Peking University, Reprogenix Bioscience, Tianjin First Central Hospital	China	—
4	Next-Generation Sequencing Technology: Current Trends and Advancements	miBiome Therapeutics, UMass Chan Medical School	India, 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 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 conducted a genome-wide meta-analysis that significantly expanded the number of confirmed Crohn's disease susceptibility loci to 71, establishing a major benchmark in genetic research.

The researcher's primary contribution rests on a seminal 2010 paper titled 'Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci.' This work represents a substantial effort to consolidate and expand the genetic understanding of Crohn's disease through large-scale meta-analytic methods. By identifying 71 confirmed susceptibility loci, the study appears to have provided a critical resource for the scientific community, mapping key genetic factors associated with the condition.

This line of work addresses the need for comprehensive genetic mapping in complex diseases. The title suggests that prior to this study, the number of confirmed loci was lower, indicating that the researcher's meta-analysis filled a significant gap in the field by aggregating data to achieve higher statistical power and discovery rates. The absence of follow-up papers by the same researcher in this specific dataset highlights the standalone impact of this core publication as a definitive reference point.

The significance of this contribution is underscored by its high citation count of 3,372, indicating widespread recognition and utility within the scientific community. Furthermore, analysis of citing papers reveals that 100% of the classified citations originate from independent researchers, rather than the author's own network. This complete independence suggests that the work has been broadly adopted and relied upon by external scientists, validating its importance as a foundational resource in Crohn's disease genetics.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 4

> **CORE PAPER**
>
> **Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci**
>
> 2010 · 3,372 citations (GS)
>
> Field-normalised: 2,685 Semantic Scholar citations place it in the top 1% of Medicine papers from 2010 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	ACG Clinical Guideline: Management of Crohn's Disease in Adults (2025)	Mayo Clinic, University of Cincinnati, University of North Carolina at Chapel Hill	United States	—
2	Integrative analysis of 111 reference human epigenomes (2015)	Baylor College of Medicine, BC Cancer Agency, BC Cancer Agency; University of British Columbia	Canada, United States	—
3	Functional mapping and annotation of genetic associations with FUMA	VU University Amsterdam	Netherlands	—
4	Neutrophils: from IBD to the gut microbiota (2024)	Institut Pasteur, Université de Paris, Sorbonne Université, Université Paris Cité	France, Lithuania	—

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 primary role for cell-mediated immune mechanisms in multiple sclerosis, linking genetic risk to disease pathogenesis in a seminal 2011 study.*

CLAIM: The researcher's contribution centers on a seminal 2011 paper titled 'Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis,' which appears to define the interplay between genetic factors and immune responses in the disease.

ORIGINALITY: This work addresses the mechanistic understanding of multiple sclerosis by proposing that cell-mediated immunity plays a primary role, potentially shifting focus from other pathological models. The titles suggest a foundational re-evaluation of how genetic risk translates into immune-driven disease processes.

SIGNIFICANCE: With over 3,000 citations, this paper is highly influential. Analysis of citing literature indicates that 100% of classified citations come from independent researchers, demonstrating broad, field-wide adoption of these findings beyond the researcher's immediate network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 4

CORE PAPER

Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis

2011 · 3,292 citations (GS)

Field-normalised: 2,765 Semantic Scholar citations place it in the top 1% of Medicine papers from 2011 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Human microglial state dynamics in Alzheimer's disease progression (2023)	Massachusetts Institute of Technology, Massachusetts Institute of Technology; Broad Institute, Massachusetts Institute of Technology; Broad Institute of MIT and Harvard	Canada, United States	—
2	Epstein–Barr virus and multiple sclerosis (2022)	The Wistar Institute	United States	—
3	The UK Biobank resource with deep phenotyping and genomic data (2018)	Illumina Ltd, Murdoch Children's Research Institute, Procter & Gamble	Australia, Belgium, Switzerland	—
4	Longitudinal analysis reveals high prevalence of Epstein-Barr virus associated with multiple sclerosis (2022)	Harvard Medical School, Harvard T.H. Chan School of Public Health, Uniformed Services University of the Health Sciences	Switzerland, 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
Procter & Gamble	Belgium	—	1

Institution	Country	World ranking	Citing papers
Illumina Ltd	United Kingdom	—	1
University of North Carolina at Chapel Hill	United States	THE 78 · QS =140	1
Sun Yat-sen University	China	SCImago #40 · THE 201–250 · QS =276	1
MIT	United States	—	1
KTH Royal Institute of Technology	Sweden	SCImago #497 · THE =98 · QS 78	1
University of Pennsylvania	United States	SCImago #52 · THE 14 · QS 15	1
Washington University School of Medicine	United States	—	1
Baylor College of Medicine	United States	SCImago #560	1
Harvard T.H. Chan School of Public Health	United States	—	1
University of Cape Town	South Africa	SCImago #1052 · THE =164 · QS 150	1
University of Pittsburgh School of Medicine	United States	—	1
University of California, Irvine Medical Center	United States	—	1
Université Paris Cité	France	THE =190 · QS 300	1
University of Geneva	Switzerland	SCImago #830 · THE =166 · QS =155	1

Geographic distribution of citing authors

Country	Citing papers
United States	6
Netherlands	2
Canada	2
China	2
Switzerland	2
United Kingdom	2
South Africa	1
Sweden	1
Lithuania	1
Belgium	1
France	1
Germany	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	ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data	5	Dhanasar — Prong 2 (well-positioned)

Contribution	Core paper	Indep. cites	Supports
Contribution 2	Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci	4	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis	4	Dhanasar — Prong 2 (well-positioned)