Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

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Hypothesis Fund

[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

13	13	2	22
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.

92.3% independent of 13 classified citing papers

Citation type	Count
Independent	12
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 developed systematic improvements to amplicon marker gene methods, significantly enhancing accuracy in microbiome studies as evidenced by a highly cited 2016 Nature Biotechnology publication.

The researcher’s primary contribution involves the systematic improvement of amplicon marker gene methods to increase accuracy in microbiome studies. This work is anchored by a seminal 2016 paper published in Nature Biotechnology, which stands as the core achievement in this specific line of inquiry without subsequent follow-up publications by the same author.

This line of work appears to address critical limitations in the precision of microbiome analysis techniques prevalent at the time. By focusing on systematic improvements, the researcher likely introduced methodological refinements that corrected errors or biases inherent in standard amplicon sequencing protocols, thereby establishing a more reliable foundation for downstream biological interpretation.

The significance of this contribution is underscored by its substantial uptake within the scientific community, with the core paper accumulating 908 citations. Furthermore, analysis of citing literature reveals that 92.3% of these citations originate from independent researchers, indicating that the methodology has been widely adopted and validated by the broader field rather than merely circulated within the researcher’s immediate network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 11

CORE PAPER

Systematic improvement of amplicon marker gene methods for increased accuracy in microbiome studies

2016 · Nat Biotechnol · 908 citations (GS)

Field-normalised: 681 Semantic Scholar citations place it in the top 1% of Biology papers from 2016 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin (2018)	Australian National University, Northern Arizona University, University of California San Diego	Australia, United States	—
2	A Communal Catalogue Reveals Earth's Multiscale Microbial Diversity (2017)	Oregon State University, University of California San Diego, University of Colorado Boulder	United States	—
3	Environmental stress destabilizes microbial networks (2021)	Archbold Biological Station, University of Miami	—	—
4	You are what you eat: diet, health and the gut microbiota (2019)	Tel Aviv University, Weizmann Institute of Science	Israel	—
5	Primer, Pipelines, Parameters: Issues in 16S rRNA Gene Sequencing (2021)	Technische Universität München, University of Hamburg, University of Southern Denmark	Denmark, Germany	—
6	Best practices in metabarcoding of fungi: From experimental design to results (2022)	École Normale Supérieure, Institute of Microbiology, Chinese Academy of Sci-	China, Estonia, France	Background

No.	Citing paper	Citing institution(s)	Country	S2
		ences, Swedish University of Agricultural Sciences		
7	Mycobiome diversity: high-throughput sequencing and identification of fungi (2018)	Braunschweig University of Technology, Gothenburg Global Biodiversity Centre, Institute of Microbiology of the Czech Academy of Sciences	Czech Republic, Estonia, Germany	—
8	Towards standards for human fecal sample processing in metagenomic studies (2017)	Biofortis, Mérieux NutriSciences, CEA, ETH Zurich	Canada, China, France	—
9	Gut microbiome dysbiosis in antibiotic-treated COVID-19 patients is associated with microbial translocation and bacteremia (2022)	New York University Grossman School of Medicine, New York University School of Medicine, Yale School of Medicine	United States	—
10	Gut microbiota associations with common diseases and prescription medications in a population-based cohort (2018)	King's College London, Seoul National University	South Korea, United Kingdom	—
11	The Madness of Microbiome: Attempting To Find Consensus “Best Practice” for 16S Microbiome Studies (2018)	Animal and Veterinary Sciences	—	**Methodology**

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** The Madness of Microbiome: Attempting To Find Consensus “Best Practice” for 16S Microbiome Studies
>
> *“use of a high-fidelity polymerase (43) also having an impact on results.”*

Contribution 2

Claim — Contribution 2

The researcher established a framework for identifying personalized diet-microbiome associations through daily sampling, a seminal contribution evidenced by high citation impact and broad independent adoption.

The researcher’s primary contribution centers on the 2019 paper titled 'Daily sampling reveals personalized diet-microbiome associations in humans.' This work appears to introduce a methodological approach for linking dietary intake with microbiome composition at an individual level, utilizing frequent sampling protocols. The titles indicate a focus on personalization and temporal resolution in human microbiome studies.

This line of work addresses the challenge of capturing dynamic interactions between diet and the gut microbiome, which static or infrequent sampling methods may miss. By emphasizing daily sampling, the research suggests a novel strategy for resolving personalized associations that were previously difficult to isolate. The absence of follow-up papers by the same researcher in this dataset implies that this single publication serves as the foundational pillar for this specific contribution.

The significance of this work is reflected in its substantial citation count of 767, indicating widespread recognition within the scientific community. Furthermore, analysis of citing papers reveals that 92.3% originate from independent researchers, suggesting that the methodology or findings have been adopted and validated by the broader field rather than merely circulated within the researcher’s immediate network. This high degree of independent uptake underscores the work’s utility and impact on subsequent studies in nutrition and microbiome research.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 1

CORE PAPER

Daily sampling reveals personalized diet-microbiome associations in humans

2019 · 767 citations (GS)

Field-normalised: 595 Semantic Scholar citations place it in the top 1% of Environmental Science papers from 2019 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The interplay between diet and the gut microbiome: implications for health and disease (2024)	University College Cork	Ireland	—

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 Minnesota	United States	SCImago #165 · THE 88 · QS 210	2
King's College London	United Kingdom	THE 38 · QS 31	2
Swedish University of Agricultural Sciences	Sweden	SCImago #1525 · THE 351–400	2
University of California San Diego	United States	SCImago #120 · THE 47 · QS 66	2
Natural History Museum of Tartu University	Estonia	—	1
Biofortis, Mérieux NutriSciences	France	—	1
Technical University of Munich	Germany	SCImago #187 · THE 27 · QS =22	1
University of Gothenburg	Sweden	SCImago #573 · THE 201–250 · QS 202	1
Braunschweig University of Technology	Germany	—	1
University of Southern Denmark	Denmark	SCImago #884 · THE 251–300 · QS =303	1
Northern Arizona University	United States	SCImago #3335 · QS 1001-1200	1
Weizmann Institute of Science	Israel	SCImago #739	1
University of Tartu	Estonia	SCImago #1820 · THE 301–350 · QS =362	1
European Molecular Biology Laboratory	Germany	—	1
New York University Grossman School of Medicine	United States	—	1

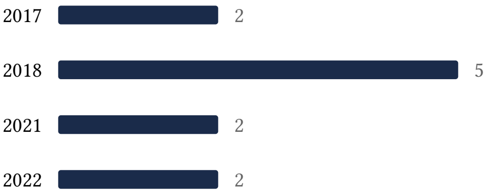
Geographic distribution of citing authors

Country	Citing papers
United States	5
Germany	3
Sweden	2
Estonia	2
China	2
United Kingdom	2
France	2
Switzerland	1
Thailand	1
Ireland	1
Canada	1
Czech Republic	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	Systematic improvement of amplicon marker gene methods for increased accuracy in microbiome studies	11	Dhanasar — Prong 2 (well-positioned)
Contribution 2	Daily sampling reveals personalized diet-microbiome associations in humans	1	Dhanasar — Prong 2 (well-positioned)