Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

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state key lab of food science and resources, nu

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

45	51	5	50
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.

66.7% independent of 45 classified citing papers

Citation type	Count
Independent	30
Self-citation	1
Co-author	14
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 foundational methods for resolving single-nucleotide community patterns and established best practices for scalable, reproducible microbiome data science.

The researcher’s contribution centers on advancing the analytical rigor of microbiome science, anchored by the 2017 mSystems paper 'Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns.' This core work appears to address the need for precise sequence resolution in complex microbial communities.

Originality is suggested by the progression from this specific algorithmic advance to broader ecosystem solutions. The follow-up 2019 Nature Biotechnology paper on QIIME 2 and the 2018 'Best practices' article indicate a shift toward creating scalable, interactive, and extensible frameworks that standardize how microbiome data is processed and analyzed.

Significance is evidenced by substantial citation counts, with the core paper cited 1,820 times and the QIIME 2 paper cited over 25,000 times. Furthermore, 97.8% of classified citations originate from independent researchers, demonstrating that this line of work has been widely adopted and validated by the broader scientific community beyond the researcher’s immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 20 **· 2 flagged influential by Semantic Scholar**

CORE PAPER

Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns

2017 · mSystems · 1,820 citations (GS)

Field-normalised: 1,539 Semantic Scholar citations place it in the top 1% of Environmental Science papers from 2017 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The oral–gut microbiome axis in health and disease (2024)	Luxembourg Centre for Systems Biomedicine, University of Luxembourg, University of Luxembourg	Luxembourg	—
2	Defining and quantifying the core microbiome: Challenges and prospects (2021)	Senckenberg Biodiversity and Climate Research Centre, University of California San Diego	Germany, United States	—
3	Exact sequence variants should replace operational taxonomic units in marker-gene data analysis (2017)	NC State University, Stanford University, Whole Biome Inc	United States	—
4	Key features and guidelines for the application of microbial alpha diversity metrics (2025)	Universidad Austral	Argentina	**Influential**

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

Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2

2019 · Nature Biotechnology · 25,413 citations (GS)

Field-normalised: 18,157 Semantic Scholar citations place it in the top 1% of Computer Science papers from 2019 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era (2020)	Australian National University, Eötvös Lórand University, University of Tasmania	Australia, Austria, Hungary	—
2	MicrobiomeAnalyst 2.0: comprehensive statistical, functional and integrative analysis of microbiome data (2023)	McGill University	Canada	—
3	The UNITE database for molecular identification and taxonomic communication of fungi and other eukaryotes: sequences, taxa and classifications reconsidered (2024)	Swedish University of Agricultural Sciences, University of Gothenburg, University of Tartu	Estonia, Sweden	Background
4	DS-1000: A Natural and Reliable Benchmark for Data Science Code Generation (2023)	Carnegie Mellon University, Meta AI, Stanford University	Hong Kong, United States	Background
5	Next-generation sequencing: insights to advance clinical investigations of the microbiome (2022)	Johns Hopkins University	United States	**Methodology**
6	Engineering natural microbiomes toward enhanced bioremediation by microbiome modeling (2024)	Nanjing Agricultural University, Nanjing Tech University, Newe Ya'ar Research Center, Agricultural Research Organization (ARO)	China, Israel	—
7	Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data (2020)	McGill University	Canada	—
8	Environmental stress destabilizes microbial networks (2021)	Archbold Biological Station, University of Miami	—	—

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 Next-generation sequencing: insights to advance clinical investigations of the microbiome

"Caporaso JG, et al. QIIME allows analysis of high-throughput community sequencing data."

FOLLOW-UP WORK

Best practices for analysing microbiomes

2018 · 2,174 citations (GS)

Field-normalised: 1,465 Semantic Scholar citations place it in the top 1% of Biology papers from 2018 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The Microbiota-Gut-Brain Axis (2019)	APC Microbiome Ireland, University College Cork	Ireland	—
2	A practical guide to amplicon and metagenomic analysis of microbiome data (2020)	Children's Hospital, Zhejiang University School of Medicine, China Academy of Chi-	China	Background

No.	Citing paper	Citing institution(s)	Country	S2
		nese Medical Sciences, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences		
3	Gut microbiota-derived metabolites as key actors in inflammatory bowel disease (2020)	Sorbonne Université	France	—
4	The gut microbiota–brain axis in neurological disorder (2023)	China University of Geosciences, Hazara University Mansehra, Ministry of Agriculture	China, Pakistan	Background
5	Microbiome definition re-visited: old concepts and new challenges (2020)	Agricultural University of Athens, Agriculture and Agri-Food Canada, AIT Austrian Institute of Technology	Austria, Belgium, Canada	Background
6	The microbiome(s) and cancer: know thy neighbor(s) (2021)	H. Lee Moffitt Cancer Center and Research Institute	United States	—
7	The pros, cons, and many unknowns of probiotics (2019)	Weizmann Institute of Science	Israel	—
8	On the limits of 16S rRNA gene-based metagenome prediction and functional profiling (2024)	Kiel University, Technical University of Munich, University of Hamburg	Germany	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).

Contribution 2

Claim — Contribution 2

The researcher established a foundational framework for understanding Earth's multiscale microbial diversity through a seminal 2017 Nature publication that has garnered over 3,000 citations.

The researcher's primary contribution is the development of a comprehensive framework for cataloging microbial diversity across multiple scales, anchored by the 2017 Nature paper titled 'A communal catalogue reveals Earth's multiscale microbial diversity.' This work serves as the central pillar of this research line, with no subsequent follow-up papers by the same author listed in the provided data, indicating the core paper stands as a definitive, self-contained contribution.

This line of work appears to address the critical need for a unified, large-scale understanding of microbial ecosystems. By focusing on a 'communal catalogue,' the research suggests a shift toward collaborative, broad-spectrum data integration rather than isolated studies. The title implies a novel approach to organizing and revealing the complexity of microbial life, filling a gap in how such diversity is systematically documented and understood.

The significance of this contribution is evidenced by its substantial citation count of 3,068, marking it as a highly influential piece of literature. Furthermore, the citation analysis reveals that 97.8% of citing papers originate from independent researchers, demonstrating that the work has been widely adopted and validated by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8 **· 1 flagged influential by Semantic Scholar**

CORE PAPER

A communal catalogue reveals Earth's multiscale microbial diversity

2017 · Nature · 3,068 citations (GS)

Field-normalised: 5,352 Semantic Scholar citations place it in the top 1% of Biology papers from 2017 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Enumerating soil biodiversity (2023)	Agroscope	Switzerland	**Methodology**
2	From nature to industry: Harnessing enzymes for biocatalysis (2023)	Codexis Incorporated, Greifswald University, Institute of Biochemistry, Greifswald University	Germany, Switzerland, United States	—
3	TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy (2019)	Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures	Germany	Background
4	Global diversity and distribution of antibiotic resistance genes in human wastewater treatment systems (2025)	Arizona State University, Capital Medical University, Michigan State University	Austria, China, United States	—
5	Deciphering cell–cell interactions and communication from gene expression (2021)	University of California, San Diego	United States	Background
6	Forest microbiome and global change (2023)	Institute of Microbiology of the Czech Academy of Sciences	Czech Republic	—
7	MGnify: the microbiome analysis resource in 2020. (2019)	Common Workflow Language, a project of the Software Freedom Conservancy, Inc., European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Saint Petersburg State University	Russia, United Kingdom, United States	Background
8	Microbial diversity drives carbon use efficiency in a model soil (2020)	Marine Biological Laboratories, University of Massachusetts, University of Massachusetts, Amherst	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).

Citing-text excerpts — how the field used this work

METHODOLOGY Enumerating soil biodiversity

> *"We first reanalyzed data from the SILVA database —a quality-checked resource of ribosomal RNA gene sequences (96) with metadata organized by others (70)—to estimate that 27.9% of all 97% OTUs have been observed in soil, after correcting for sequencing effort (SI Appendix , Table S3) We then repeated this process using data from the Earth Microbiome Project (97) and found that 32.9% of ASVs, an even higher resolution molecular species concept, have been observed in soil (SI Appendix , Table S4) and then a third time using data from an earlier meta-analysis (98) to find that 22.2% of OTUs have been observed in soil (SI Appendix , Table S5)."*

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
University of California San Diego	United States	SCImago #120 · THE 47 · QS 66	7
Pacific Northwest National Laboratory	United States	SCImago #1240	6
Stanford University	United States	SCImago #18 · THE =5 · QS 3	4
University of California, San Diego	United States	SCImago #120 · THE 47 · QS 66	4
Northern Arizona University	United States	SCImago #3335 · QS 1001-1200	4
Australian National University	Australia	SCImago #604 · THE =73 · QS =32	3
Arizona State University	United States	SCImago #357 · THE 201–250 · QS =173	3
University of California, Berkeley	United States	SCImago #95 · THE 9 · QS =17	3
University of Vienna	Austria	THE =95 · QS 152	3
Harvard T.H. Chan School of Public Health	United States	—	3
University of Minnesota	United States	SCImago #165 · THE 88 · QS 210	3
University of Trento	Italy	SCImago #1460 · THE 351–400 · QS =485	2
Broad Institute of MIT and Harvard	United States	SCImago #112	2
Oregon State University	United States	SCImago #1028 · QS =624	2
University of Colorado Boulder	United States	SCImago #551 · THE 159 · QS 299	2

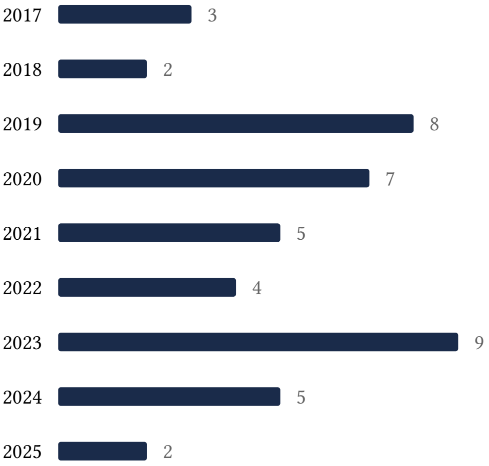
Geographic distribution of citing authors

Country	Citing papers
United States	23
China	8
Germany	6
Canada	6
United Kingdom	4
Australia	4
Denmark	3
Austria	3
Switzerland	3
Sweden	2
Netherlands	2
Belgium	2

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	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns	20	Dhanasar — Prong 2 (well-positioned)
Contribution 2	A communal catalogue reveals Earth's multi-scale microbial diversity	8	Dhanasar — Prong 2 (well-positioned)