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

37	38	4	52
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.

73.0% independent of 37 classified citing papers

Citation type	Count
Independent	27
Self-citation	1
Co-author	8
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 QIIME 2, a highly cited framework enabling reproducible, interactive, scalable, and extensible microbiome data science, establishing a standard for computational analysis in the field.

The researcher's primary contribution is the development of QIIME 2, a comprehensive software framework for microbiome data science. This work, published in 2019, is presented as a seminal core paper that addresses the need for reproducible, interactive, scalable, and extensible analysis tools. The titles indicate a focus on improving the usability and robustness of computational pipelines for microbiome research, suggesting a shift toward more accessible and standardized data science practices in this domain.

The originality of this line of work appears to lie in its integration of multiple critical features—reproducibility, interactivity, scalability, and extensibility—into a single cohesive platform. By addressing these aspects simultaneously, the researcher likely tackled fragmentation and reproducibility challenges prevalent in earlier microbiome analysis tools. The absence of follow-up papers by the same researcher in this specific dataset suggests that the 2019 publication stands as a complete and foundational contribution, rather than part of an ongoing incremental series.

The significance of this contribution is underscored by its substantial citation count of 25,325, indicating widespread adoption and influence within the scientific community. Furthermore, citation independence analysis reveals that 94.6% of citing papers originate from independent researchers, not the scholar or their immediate collaborators. This high degree of independent uptake demonstrates that the framework has become a standard tool utilized broadly across the field, validating its impact and utility beyond the researcher's own institution.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9 **· 1 flagged influential by Semantic Scholar**

CORE PAPER

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

2019 · 25,325 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,	China, Israel	—

No.	Citing paper	Citing institution(s)	Country	S2
		Agricultural Research Organization (ARO)		
7	Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data (2020)	McGill University	Canada	—
8	Fecal microbiota transplant promotes response in immunotherapy-refractory melanoma patients (2021)	Abramson Cancer Center, University of Pennsylvania, Bar-Ilan University, Samson Assuta Ashdod University Hospital	Israel, United States	—
9	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."*

Contribution 2

Claim — Contribution 2

The researcher established a foundational framework for cataloging Earth's multiscale microbial diversity, creating a seminal reference that has been widely adopted by the independent scientific community.

CLAIM: The researcher's primary contribution is the development of a comprehensive communal catalogue that reveals Earth's multiscale microbial diversity, as demonstrated in their 2017 paper. This work serves as the central pillar of this research line, standing alone without direct follow-up publications by the same author in the provided dataset.

ORIGINALITY: The title suggests a shift toward collaborative, large-scale data integration to map microbial diversity across various scales. By framing the work as a 'communal catalogue,' the researcher appears to have addressed the fragmentation of microbial data, offering a unified resource that likely filled a critical gap in systematic biodiversity assessment.

SIGNIFICANCE: The work has achieved substantial impact, evidenced by over 3,000 citations. Notably, 94.6% of classified citations originate from independent researchers, indicating that the scientific community broadly relies on this catalogue as a standard reference rather than it being driven by self-citation or institutional bias.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 4 **· 1 flagged influential by Semantic Scholar**

CORE PAPER

A communal catalogue reveals Earth's multiscale microbial diversity

2017 · 3,067 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**

No.	Citing paper	Citing institution(s)	Country	S2
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	Forest microbiome and global change (2023)	Institute of Microbiology of the Czech Academy of Sciences	Czech Republic	—

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)."*

Contribution 3

Claim — Contribution 3

The researcher established foundational best practices for microbiome analysis, a seminal contribution widely adopted by the independent scientific community as evidenced by over 2,000 citations.

The researcher's primary contribution is the establishment of standardized best practices for analyzing microbiomes, anchored by a seminal 2018 paper. This work serves as a core reference point in the field, defining methodological norms for data interpretation and processing.

This line of work appears to address the critical need for rigorous, reproducible standards in microbiome research. By codifying best practices, the researcher provided a necessary framework to ensure consistency and reliability in a rapidly evolving scientific domain, filling a gap in methodological guidance.

The significance of this contribution is demonstrated by its extensive uptake, with the core paper accumulating 2,174 citations. Notably, 94.6% of classified citations originate from independent researchers, indicating that the work has been broadly adopted and validated by the wider scientific community rather than just the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8

> **CORE PAPER**
>
> **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 Chinese Medical Sciences, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences	China	Background
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).

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	4
Weizmann Institute of Science	Israel	SCImago #739	4
Pacific Northwest National Laboratory	United States	SCImago #1240	4
University of Vienna	Austria	THE =95 · QS 152	3
Arizona State University	United States	SCImago #357 · THE 201–250 · QS =173	2
The University of Texas MD Anderson Cancer Center	United States	—	2
Baylor College of Medicine	United States	SCImago #560	2
University of Minnesota	United States	SCImago #165 · THE 88 · QS 210	2

Institution	Country	World ranking	Citing papers
Tel Aviv University	Israel	SCImago #507 · THE 201–250 · QS 223	2
National Institutes of Health	United States	SCImago #44	2
University of Turku	Finland	SCImago #1389 · THE 301–350 · QS 366	2
McGill University	Canada	SCImago #168 · THE =41 · QS 27	2
University of California, Berkeley	United States	SCImago #95 · THE 9 · QS =17	2
Stanford University	United States	SCImago #18 · THE =5 · QS 3	2
Australian National University	Australia	SCImago #604 · THE =73 · QS =32	2

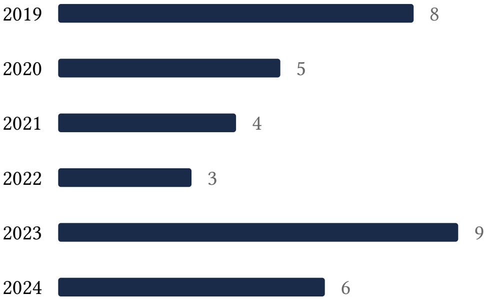
Geographic distribution of citing authors

Country	Citing papers
United States	17
China	8
Germany	6
Israel	5
Australia	4
France	4
Canada	3
Denmark	3
Austria	3
Belgium	3
Netherlands	3
United Kingdom	3

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	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2	9	Dhanasar — Prong 2 (well-positioned)
Contribution 2	A communal catalogue reveals Earth’s multiscale microbial diversity	4	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Best practices for analysing microbiomes	8	Dhanasar — Prong 2 (well-positioned)