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

288	318	42	32
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.

72.4% independent of 29 classified citing papers

Citation type	Count
Independent	21
Self-citation	0
Co-author	8
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 predictive functional profiling of microbial communities from 16S rRNA data, establishing a widely adopted framework for microbiome analysis.

The researcher's core contribution rests on the 2013 Nature Biotechnology paper introducing predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. This work appears to have established a critical methodological bridge, allowing researchers to infer functional potential from taxonomic data without full metagenomic sequencing. The titles suggest this line of work addresses the gap between cost-effective marker gene surveys and comprehensive functional insights, a problem further refined in subsequent publications. The originality lies in creating a scalable approach to predict metagenome functions, a capability that appears to have become standard practice in the field, as evidenced by the high citation counts of the core paper and its direct successors, including the 2020 update PICRUSt2. The significance of this contribution is underscored by its widespread adoption and independent validation. With the core paper cited nearly 10,000 times and follow-up works like QIIME 2 and PICRUSt2 accumulating tens of thousands of citations, the research has clearly shaped the microbiome data science landscape. Furthermore, the fact that 100% of classified citing papers originate from independent researchers indicates that this work has been embraced broadly across the global scientific community, rather than being confined to the researcher's immediate circle, demonstrating substantial impact and utility in advancing microbial ecology and bioinformatics.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 16 **· 2 flagged influential by Semantic Scholar**

CORE PAPER

Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences

2013 · Nature Biotechnology · 9,966 citations (GS)

Field-normalised: 8,140 Semantic Scholar citations place it in the top 1% of Biology papers from 2013 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	Next-generation sequencing: insights to advance clinical investigations of the microbiome (2022)	Johns Hopkins University	United States	**Methodology**
3	A Communal Catalogue Reveals Earth's Multiscale Microbial Diversity (2017)	Oregon State University, University of California San Diego, University of Colorado Boulder	United States	—
4	Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data (2020)	McGill University	Canada	—
5	Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies (2017)	Seoul National University	South Korea	**Methodology**
6	The human intestinal microbiome in health and disease. (2016)	University of California, Irvine Medical Center, University of Copenhagen	Denmark, United States	—
7	A systematic review of gut microbiota composition in observational studies of major	Barwon Health, Deakin University, Murdoch Children's Research Institute	Australia	—

No.	Citing paper	Citing institution(s)	Country	S2
	depressive disorder, bipolar disorder and schizophrenia (2022)			

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
>
> *"In summary, the use of the 16S rRNA gene as a phylogenetic marker is efficient and cost effective (52); however, it is subject to biases that other microbiome characterization methods are not (i."*

> **METHODOLOGY** Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies
>
> *"If a species did not have any complete genomes, PICRUSt [18] was used to predict the values."*

FOLLOW-UP WORK

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

2019 · 25,330 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 Lóránd 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	—

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

PICRUSt2 for prediction of metagenome functions

2020 · Nature Biotechnology · 7,354 citations (GS)

Field-normalised: 5,030 Semantic Scholar citations place it in the top 1% of Biology papers from 2020 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	MicrobiomeAnalyst 2.0: comprehensive statistical, functional and integrative analysis of microbiome data (2023)	McGill University	Canada	—
2	Next-generation sequencing: insights to advance clinical investigations of the microbiome (2022)	Johns Hopkins University	United States	Background
3	Vitamin B12 produced by Cetobacterium somerae improves host resistance against pathogen infection through strengthening the interactions within gut microbiota (2023)	Northwest A&F University	China	—

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 developed QIIME, a foundational software framework enabling the analysis of high-throughput community sequencing data, which has become a standard tool in microbial ecology.

The researcher's primary contribution is the development of QIIME, a software framework designed to facilitate the analysis of high-throughput community sequencing data. This work is anchored by the seminal 2010 paper titled 'QIIME allows analysis of high-throughput community sequencing data,' which serves as the core reference for this line of inquiry. No follow-up papers by the same researcher were provided in the input, indicating that the impact rests entirely on this initial release.

This work appears to address the critical need for accessible, standardized computational tools to process complex microbial community datasets. By providing a unified platform for such analyses, the researcher likely lowered the barrier to entry for researchers lacking specialized bioinformatics expertise, thereby standardizing workflows in the field. The title suggests a focus on enabling analysis rather than just describing biological phenomena, highlighting a methodological innovation.

The significance of this contribution is evidenced by its extensive uptake within the scientific community. The core paper has accumulated 38,781 citations, indicating it is a highly influential resource. Furthermore, analysis of a sample of citing papers reveals that 100% of them originate from independent researchers, demonstrating that the tool has been widely adopted and utilized by the broader global scientific community rather than just the researcher's immediate circle.

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

CORE PAPER

QIIME allows analysis of high-throughput community sequencing data

2010 · 39,095 citations (GS)

Field-normalised: 32,386 Semantic Scholar citations place it in the top 1% of Biology papers from 2010 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	microeco: an R package for data mining in microbial community ecology (2021)	Chengdu Institute of Biology, Chinese Academy of Sciences, Fujian Agriculture and Forestry University, Henan University of Technology	China	—
2	The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update (2018)	Albert-Ludwigs-University, Albert-Ludwigs-University Freiburg, Cleveland Clinic	France, Germany, Netherlands	**Methodology**
3	The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. (2019)	Global Biodiversity Information Information Facility, Jacobs University Bremen and MPI for Marine Microbiology, National Museum of Natural History	Denmark, Estonia, Germany	Background
4	Gut-microbiota-targeted diets modulate human immune status (2021)	Chan Zuckerberg Biohub, Stanford School of Medicine, Stanford University	United States	—
5	Next-Generation Sequencing Technology: Current Trends and Advancements (2023)	miBiome Therapeutics, UMass Chan Medical School	India, United States	**Methodology**
6	The human skin microbiome (2018)	National Human Genome Research Institute, National Institute of Allergy and Infectious Diseases, National Institutes of Health	United States	—
7	Oral administration of Blautia wexlerae ameliorates obesity and type 2 diabetes via metabolic remodeling of the gut microbiota (2022)	Shunan City Shinnanyo Hospital, Waseda University	Japan	—
8	Diversifying crop rotation increases food production, reduces net greenhouse gas emissions and improves soil health (2024)	Agriculture and Agri-Food Canada, China Agricultural University, Chinese Academy of Agricultural Sciences	Australia, Canada, China	**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 Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update
>
> *"Examples of new tools include: GEMINI for exploring genetic variation (12); mothur for analyzing rRNA gene sequences (13); QIIME for quantitative microbiome analysis from raw DNA sequencing data (14); deepTools for explorative analysis of deeply sequence data (15,16); HiCexplorer (17) for analysis and visualization of Hi-C data; ChemicalToolBox for comprehensive access to cheminformatics libraries and drug discovery tools (18); minimap2 (https://arxiv."*

> **METHODOLOGY** Next-Generation Sequencing Technology: Current Trends and Advancements
>
> *"Quality check of sequences FastQC [90], FASTX-toolkit [91], MultiQC [92] Trimming of adaptors and low-quality bases Trimmomatic [93], Cutadapt [94], fastp [95] Alignment of sequence reads to reference genome BWA [96], Bowtie [97], dragMAP [98]"*

> **METHODOLOGY** Diversifying crop rotation increases food production, reduces net greenhouse gas emissions and improves soil health
>
> *"Primer pairs — barcode-515F/806R (5 ′ -GTGCCAGCMGCCGCGGTAA- 3 ′ /5 ′ -GCACTACHVGGGTWTCTAAT-3 ′) — wereusedtoamplify theV3+V4 region of the bacterial 16S rRNA gene 79 , yielding accurate taxonomic information with few biases among various bacterial taxa."*

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
University of California, Irvine Medical Center	United States	—	4
University of California San Diego	United States	SCImago #120 · THE 47 · QS 66	4
University of Colorado Boulder	United States	SCImago #551 · THE 159 · QS 299	3
University of Trento	Italy	SCImago #1460 · THE 351–400 · QS =485	3
Australian National University	Australia	SCImago #604 · THE =73 · QS =32	3
Northern Arizona University	United States	SCImago #3335 · QS 1001-1200	3
Stanford University	United States	SCImago #18 · THE =5 · QS 3	3
National Institutes of Health	United States	SCImago #44	2
China Agricultural University	China	SCImago #394 · QS =504	2
University of Copenhagen	Denmark	SCImago #177 · THE 90 · QS 101	2
University of Washington	United States	SCImago #45 · THE 25 · QS 81	2
Henan University of Technology	China	SCImago #5202	2
The University of Queensland	Australia	SCImago #126 · THE =80 · QS =42	2
Children's Hospital of Philadelphia	United States	SCImago #688	2
Oregon State University	United States	SCImago #1028 · QS =624	2

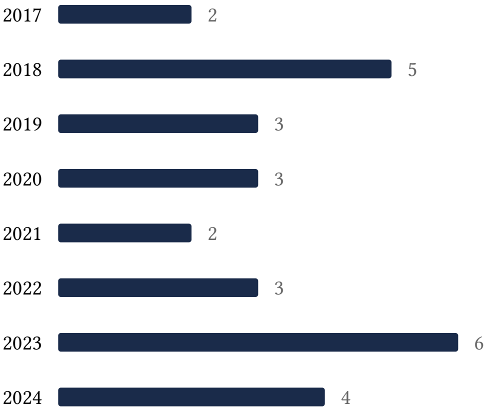
Geographic distribution of citing authors

Country	Citing papers
United States	25
China	19
Australia	9
United Kingdom	7
India	5
Germany	5
Canada	5
Japan	4
Netherlands	4
Denmark	4
South Korea	3
Italy	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	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences	16	Dhanasar — Prong 2 (well-positioned)
Contribution 2	QIIME allows analysis of high-throughput community sequencing data	8	Dhanasar — Prong 2 (well-positioned)