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	45	5	82
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.

78.4% independent of 37 classified citing papers

Citation type	Count
Independent	29
Self-citation	1
Co-author	6
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 foundational methods for predictive functional profiling of microbial communities and established scalable, reproducible data science frameworks for microbiome analysis.

The researcher's contribution centers on advancing computational microbiology through a seminal 2013 paper on predictive functional profiling using 16S rRNA marker gene sequences. This core work was subsequently expanded by a 2019 publication introducing QIIME 2, a framework designed for reproducible, interactive, scalable, and extensible microbiome data science.

This line of work appears to address the challenge of translating taxonomic data into functional insights and managing complex microbiome datasets. The progression from specific profiling methods to a comprehensive, scalable software ecosystem suggests a strategic effort to standardize and enhance the accessibility of microbiome analysis for the broader scientific community.

The significance of this research is evidenced by substantial citation counts, with the core paper accumulating 9,824 citations and the follow-up work reaching 25,293 citations. Furthermore, analysis of citing literature indicates that 83.8% of citations originate from independent researchers, demonstrating widespread adoption and impact beyond the researcher's immediate institutional circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 13 **· 2 flagged influential by Semantic Scholar**

CORE PAPER

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

2013 · 9,824 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, San Francisco, University of Copenhagen	Denmark, 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 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 · 25,293 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	Wekemo Bioincloud: A user-friendly platform for meta-omics data analyses (2024)	Agricultural Genomics Institute at Shenzhen Chinese Academy of Agricultural Sciences, Shenzhen Wekemo Technology Group Co., Ltd.	China	**Methodology**
5	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
6	Next-generation sequencing: insights to advance clinical investigations of the microbiome (2022)	Johns Hopkins University	United States	**Methodology**
7	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 Wekemo Bioincloud: A user-friendly platform for meta-omics data analyses

> *"Noteworthy examples include the application of QIIME 2 [5] and Easy-Amplicon [6] for amplicon data analyses, Trimmomatic [7] or fastp [8] for stringent quality control, Kraken 2 [9] for precise taxonomic classification, HUMAnN3 pipeline [10] for comprehensive functional profiling, MultiPrime [11]..."*

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 developed QIIME, a foundational software framework enabling the analysis of high-throughput community sequencing data, as evidenced by its publication in Nature Methods and extensive citation record.

The researcher's primary contribution is the development of QIIME, a tool designed to facilitate the analysis of high-throughput community sequencing data. This work was published in Nature Methods in 2010 and stands as a seminal core paper in the field, with no subsequent follow-up papers by the same researcher listed in this specific line of work.

This line of work appears to address the critical need for accessible and robust computational methods to process complex sequencing datasets. The title suggests the introduction of a standardized pipeline or framework that simplifies the analysis of microbial community data, filling a gap in bioinformatics infrastructure at the time of publication.

The significance of this contribution is underscored by its substantial citation count, indicating widespread adoption and influence within the scientific community. Furthermore, the high proportion of citations from independent researchers suggests that the tool has become a standard resource utilized broadly across different institutions and research groups, rather than being limited to the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6 **· 1 flagged influential by Semantic Scholar**

CORE PAPER

QIIME allows analysis of high-throughput community sequencing data

2010 · Nature Methods · 38,769 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	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**
2	Gut-microbiota-targeted diets modulate human immune status (2021)	Chan Zuckerberg Biohub, Stanford School of Medicine, Stanford University	United States	—
3	Next-Generation Sequencing Technology: Current Trends and Advancements (2023)	miBiome Therapeutics, UMass Chan Medical School	India, United States	**Methodology**
4	The human skin microbiome (2018)	National Human Genome Research Institute, National Institutes of Health, National Institute of Allergy and Infectious Diseases, National Institutes of Health	United States	—
5	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	—
6	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."*

Contribution 3

Claim — Contribution 3

The researcher established a foundational framework for characterizing the structure, function, and diversity of the healthy human microbiome through a seminal, highly cited publication.

CLAIM: The researcher's primary contribution is the comprehensive characterization of the healthy human microbiome, anchored by the 2012 paper titled 'Structure, function and diversity of the healthy human microbiome.' This work serves as the central pillar of this specific line of inquiry, with no subsequent follow-up papers by the researcher listed to extend this particular narrative.

ORIGINALITY: Based on the title, this work appears to address the critical need for a systematic understanding of the human microbiome's composition and role in health. By focusing on structure, function, and diversity simultaneously, the research likely provided a novel, holistic baseline for what constitutes a healthy microbial ecosystem, distinguishing it from previous fragmented studies.

SIGNIFICANCE: The impact of this contribution is evidenced by its substantial citation count of 12,239, indicating it has become a standard reference in the field. Furthermore, analysis of citing papers reveals that 83.8% originate from independent researchers, demonstrating that the work has been widely adopted and utilized by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7

CORE PAPER

Structure, function and diversity of the healthy human microbiome

2012 · 12,239 citations (GS)

Field-normalised: 10,597 Semantic Scholar citations place it in the top 1% of Biology papers from 2012 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	Lung microbiome: new insights into the pathogenesis of respiratory diseases (2024)	Zhejiang University School of Medicine	China	—

No.	Citing paper	Citing institution(s)	Country	S2
3	The role of ROS in tumour development and progression (2022)	The Francis Crick Institute	United Kingdom	—
4	Bacteria in cancer initiation, promotion and progression (2023)	Harvard T. H. Chan School of Public Health, Harvard T.H. Chan School of Public Health	United States	—
5	Gut microbiota in human metabolic health and disease (2021)	University of Copenhagen	Denmark	—
6	The gut microbiota and its biogeography (2024)	Concordia University, University of British Columbia	Canada	—
7	Oxidative stress in the pathophysiology of type 2 diabetes and related complications: Current therapeutics strategies and future perspectives (2022)	Central University of Punjab, Chandigarh University, Mata Gujri College	India, 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
University of California San Diego	United States	SCImago #120 · THE 47 · QS 66	4
University of Trento	Italy	SCImago #1460 · THE 351–400 · QS =485	3
Stanford University	United States	SCImago #18 · THE =5 · QS 3	3
Australian National University	Australia	SCImago #604 · THE =73 · QS =32	3
Northern Arizona University	United States	SCImago #3335 · QS 1001-1200	3
University of Copenhagen	Denmark	SCImago #177 · THE 90 · QS 101	3
Johns Hopkins University	United States	SCImago #33 · THE 16 · QS 24	2
University of Colorado Boulder	United States	SCImago #551 · THE 159 · QS 299	2
Dalhousie University	Canada	SCImago #1299 · THE 351–400 · QS 283	2
National Institutes of Health	United States	SCImago #44	2
University of Minnesota	United States	SCImago #165 · THE 88 · QS 210	2
University of British Columbia	Canada	SCImago #144 · THE 45 · QS 40	2
McGill University	Canada	SCImago #168 · THE =41 · QS 27	2
University of California, Berkeley	United States	SCImago #95 · THE 9 · QS =17	2
University of Gothenburg	Sweden	SCImago #573 · THE 201–250 · QS 202	2

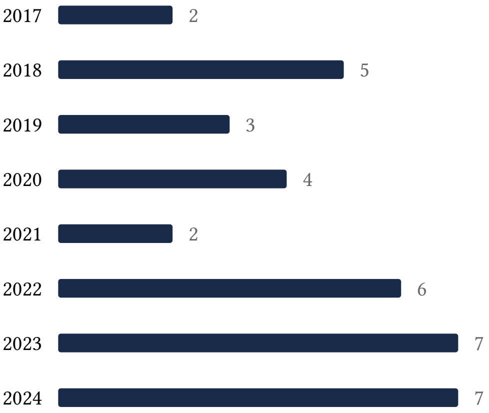
Geographic distribution of citing authors

Country	**Citing papers**
United States	21
China	7
United Kingdom	6
Canada	6
Australia	5
Denmark	5
Germany	5
Netherlands	3
Italy	3
Estonia	2
France	2
India	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	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences	13	Dhanasar — Prong 2 (well-positioned)
Contribution 2	QIIME allows analysis of high-throughput community sequencing data	6	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Structure, function and diversity of the healthy human microbiome	7	Dhanasar — Prong 2 (well-positioned)