Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

Daniel McDonald

American Gut, Knight Lab, Department of Pediatrics, UCSD

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	**46**	**5**	**75**
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	3
Co-author	5
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 and established scalable, reproducible data science frameworks for microbiome analysis.

The researcher's core contribution rests on the 2013 paper 'Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences,' which appears to introduce a method for inferring functional potential from marker gene data. This work was subsequently expanded by the 2019 publication in Nature Biotechnology, 'Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2,' suggesting a progression from specific analytical techniques to comprehensive, user-friendly software infrastructure.

This line of work appears to address the challenge of translating sparse 16S rRNA data into functional insights and the broader need for robust, standardized tools in microbiome research. The chronological development from a specific profiling method to a scalable data science platform indicates an effort to enhance reproducibility and accessibility in the field.

The significance of this work is evidenced by the high citation counts of both papers, with the 2013 core paper accumulating 9,821 citations and the 2019 follow-up reaching 25,270 citations. Furthermore, analysis of citing literature reveals that 86.5% of citations originate from independent researchers, indicating broad adoption and impact beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 12 **· 2 flagged influential by Semantic Scholar**

CORE PAPER

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

2013 · 9,821 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	**Influential**
3	Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data (2020)	McGill University	Canada	—
4	Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and whole-genome assemblies (2017)	Seoul National University	South Korea	—
5	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 flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

FOLLOW-UP WORK

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

2019 · Nature Biotechnology · 25,270 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	—
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	—
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	—
6	Next-generation sequencing: insights to advance clinical investigations of the microbiome (2022)	Johns Hopkins University	United States	**Influential**
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 flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

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 is anchored by a seminal 2010 paper published in Nature Methods, which stands as the core achievement in this line of research without subsequent follow-up publications by the same author.

This contribution appears to address the critical need for accessible computational methods to process complex microbial community data generated by emerging high-throughput sequencing technologies. By providing a dedicated framework, the work likely lowered barriers to entry for researchers analyzing large-scale genomic datasets, establishing a standard approach for the field.

The significance of this work 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 QIIME has become an essential, widely utilized resource across diverse institutions, validating its broad impact and utility beyond 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 · 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	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	—
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, Smithsonian Institution	Denmark, Estonia, Germany	—
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	—
6	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	—
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	**Influential**

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

Contribution 3

Claim — Contribution 3

The researcher developed an improved Greengenes taxonomy with explicit ranks, providing a standardized framework for ecological and evolutionary analyses of bacteria and archaea.

The researcher’s primary contribution is the development of an improved Greengenes taxonomy featuring explicit ranks, as detailed in a 2012 paper published in the ISME Journal. This work serves as the foundational element of this research line, establishing a structured approach for analyzing microbial diversity.

This line of work appears to address the need for clearer hierarchical classification in microbial ecology. By introducing explicit ranks, the researcher likely aimed to resolve ambiguities in existing taxonomic frameworks, thereby facilitating more precise ecological and evolutionary analyses of bacteria and archaea. The absence of follow-up papers by the same researcher suggests this contribution stands as a definitive, self-contained advancement in the field.

The significance of this work is evidenced by its substantial citation count of 5,846, indicating widespread adoption within the scientific community. Furthermore, analysis of citing papers reveals that 86.5% originate from independent researchers, demonstrating that the contribution has been broadly recognized and utilized by peers outside the researcher’s immediate network, underscoring its independent impact and utility.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea

2012 · ISME J. · 5,846 citations (GS)

Field-normalised: 4,705 Semantic Scholar citations place it in the top 1% of Environmental Science papers from 2012 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 Technology: Current Trends and Advancements (2023)	miBiome Therapeutics, UMass Chan Medical School	India, United States	—
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	The commensal microbiome is associated with anti–PD-1 efficacy in metastatic melanoma patients (2018)	University of Chicago	United States	—
5	Environmental stress destabilizes microbial networks (2021)	Archbold Biological Station, University of Miami	—	—
6	A complete domain-to-species taxonomy for Bacteria and Archaea (2020)	—	—	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2’s isInfluential signal, Valenzuela et al. 2015) — the “built on / relied upon” pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

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
University of Copenhagen	Denmark	SCImago #177 · THE 90 · QS 101	3
Northern Arizona University	United States	SCImago #3335 · QS 1001-1200	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
Oregon State University	United States	SCImago #1028 · QS =624	2
Dalhousie University	Canada	SCImago #1299 · THE 351–400 · QS 283	2
University of Minnesota	United States	SCImago #165 · THE 88 · QS 210	2
National Institutes of Health	United States	SCImago #44	2
University of Washington	United States	SCImago #45 · THE 25 · QS 81	2
University of Gothenburg	Sweden	SCImago #573 · THE 201–250 · QS 202	2
McGill University	Canada	SCImago #168 · THE =41 · QS 27	2

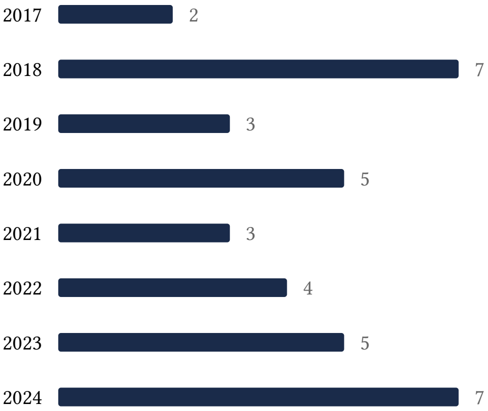
Geographic distribution of citing authors

Country	Citing papers
United States	19
China	7
Australia	6
Canada	6
Germany	5
Denmark	5
United Kingdom	5
Italy	3
Estonia	2
India	2
Netherlands	2
France	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	12	Dhanasar — Prong 2 (well-positioned)
Contribution 2	QIIME allows analysis of high-throughput community sequencing data	8	Dhanasar — Prong 2 (well-positioned)
Contribution 3	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea	6	Dhanasar — Prong 2 (well-positioned)