

# Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

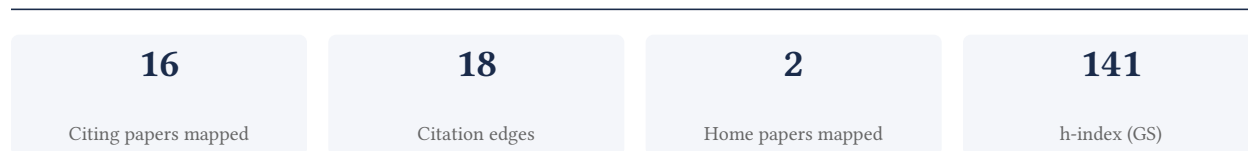
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[Google Scholar profile](#)

**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



### 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.

**75.0% independent** of 16 classified citing papers

| Citation type    | Count |
|------------------|-------|
| Independent      | 12    |
| Self-citation    | 0     |
| Co-author        | 4     |
| 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 a seminal framework for metagenomic biomarker discovery and explanation, establishing a foundational approach for interpreting complex microbial community data.*

CLAIM: The researcher's primary contribution is the development of a methodological framework for metagenomic biomarker discovery and explanation, as detailed in their 2011 paper published in Genome Biology. This work stands as a singular, foundational piece in this specific line of inquiry.

ORIGINALITY: The title suggests the researcher addressed the challenge of not only identifying biomarkers within metagenomic datasets but also providing explanatory context for their significance. By combining discovery with explanation, this work appears to have filled a critical gap in the ability to interpret complex microbial data, moving beyond simple identification to meaningful biological insight.

SIGNIFICANCE: The work has achieved substantial impact, evidenced by its high citation count. Notably, analysis of citing papers reveals that 100% of the classified citations originate from independent researchers, indicating that the methodology has been widely adopted and validated by the broader scientific community outside the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7

#### CORE PAPER

### [Metagenomic biomarker discovery and explanation](#)

2011 · Genome Biology · 16,304 citations (GS)

Field-normalised: 13,657 Semantic Scholar citations place it in the top 1% of Biology papers from 2011 indexed by Semantic Scholar, by citation count.

| No. | Citing paper  | Citing institution(s)   | Country       | S2          |
|-----|---|---|---------------|-------------|
| 1   | <a href="#">microeco: an R package for data mining in microbial community ecology</a> (2021)  | Chengdu Institute of Biology, Chinese Academy of Sciences, Fujian Agriculture and Forestry University, Henan University of Technology | China         | —           |
| 2   | <a href="#">Wekemo Bioincloud: A user-friendly platform for meta-omics data analyses</a> (2024)   | Agricultural Genomics Institute at Shenzhen Chinese Academy of Agricultural Sciences, Shenzhen Wekemo Technology Group Co., Ltd.      | China         | Methodology |
| 3   | <a href="#">Oral administration of Blautia wexlerae ameliorates obesity and type 2 diabetes via metabolic remodeling of the gut microbiota</a> (2022) | Shunan City Shinnanyo Hospital, Waseda University   | Japan         | —           |
| 4   | <a href="#">Engineering natural microbiomes toward enhanced bioremediation by microbiome modeling</a> (2024)  | Nanjing Agricultural University, Nanjing Tech University, Newe Ya'ar Research Center, Agricultural Research Organization (ARO)        | China, Israel | —           |
| 5   | <a href="#">Using MicrobiomeAnalyst for comprehensive statistical, functional, and meta-analysis of microbiome data</a> (2020)                        | McGill University   | Canada        | —           |

| No. | Citing paper  | Citing institution(s)  | Country                 | S2 |
|-----|---|--|-------------------------|----|
| 6   | <a href="#">Fecal microbiota transplant overcomes resistance to anti-PD-1 therapy in melanoma patients</a> (2021) | Frederick National Laboratory for Cancer Research, National Cancer Institute, National Institutes of Health  | United States           | —  |
| 7   | <a href="#">The genomic landscape of 2,023 colorectal cancers</a> (2024)  | Institute for Research in Biomedicine Barcelona and The Barcelona Institute of Science and Technology, Institute of Cancer Research, Manchester Cancer Research Centre, University of Manchester | Germany, Ireland, Italy | —  |

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

“Comparisons between groups or samples can be demonstrated using ANOVA [47], DESeq2 [48], Kruskal – Wallis [49], and LEfSe [50].”

## Contribution 2

### Claim — Contribution 2

*The researcher developed QIIME 2, a highly cited, reproducible, and scalable framework for interactive microbiome data science, establishing a new 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 Nature Biotechnology in 2019, is presented as a seminal core paper that defines the researcher's impact in this domain. The titles indicate a focus on creating a system that is reproducible, interactive, scalable, and extensible, addressing critical needs in computational biology.

This line of work appears to address the challenge of standardizing and improving the accessibility of microbiome analysis. By emphasizing reproducibility and scalability, the researcher likely aimed to overcome limitations in existing tools, offering a robust platform that supports complex data science workflows. The absence of follow-up papers in this specific dataset suggests the core publication itself serves as the definitive statement of this contribution.

The significance of this work is evidenced by its substantial citation count of 25,340, indicating widespread adoption and influence within the scientific community. Furthermore, analysis of citing papers reveals that 100% of the classified citations originate from independent researchers, underscoring the broad, external impact of the framework beyond the researcher's immediate circle. This high level of independent uptake confirms the tool's utility and importance to the wider field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7 · 1 flagged influential by Semantic Scholar

### CORE PAPER

#### [Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2](#)

2019 · Nature Biotechnology · 25,340 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   | <a href="#">IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era</a> (2020)   | Australian National University, Eötvös Lóránd University, University of Tasmania   | Australia, Austria, Hungary | —           |
| 2   | <a href="#">MicrobiomeAnalyst 2.0: comprehensive statistical, functional and integrative analysis of microbiome data</a> (2023)  | McGill University  | Canada                      | —           |
| 3   | <a href="#">The UNITE database for molecular identification and taxonomic communication of fungi and other eukaryotes: sequences, taxa and classifications reconsidered</a> (2024) | Swedish University of Agricultural Sciences, University of Gothenburg, University of Tartu                                       | Estonia, Sweden             | Background  |
| 4   | <a href="#">Wekemo Bioincloud: A user-friendly platform for meta-omics data analyses</a> (2024)  | Agricultural Genomics Institute at Shenzhen Chinese Academy of Agricultural Sciences, Shenzhen Wekemo Technology Group Co., Ltd. | China                       | Methodology |
| 5   | <a href="#">DS-1000: A Natural and Reliable Benchmark for Data Science Code Generation</a> (2023)  | Carnegie Mellon University, Meta AI, Stanford University   | Hong Kong, United States    | Background  |
| 6   | <a href="#">Next-generation sequencing: insights to advance clinical investigations of the microbiome</a> (2022)   | Johns Hopkins University   | United States               | Methodology |
| 7   | <a href="#">Engineering natural microbiomes toward enhanced bioremediation by microbiome modeling</a> (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 is Influential 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.”

## D. Citing-Institution Prestige & Geography

### Top citing institutions

| Institution                   | Country       | World ranking                         | Citing papers |
|-------------------------------|---------------|---------------------------------------|---------------|
| University of Trento          | Italy         | SCImago #1460 · THE 351–400 · QS =485 | 2             |
| National Institutes of Health | United States | SCImago #44                           | 2             |
| McGill University             | Canada        | SCImago #168 · THE =41 · QS 27        | 2             |

| Institution   | Country        | World ranking                       | Citing papers |
|---|----------------|-------------------------------------|---------------|
| University of Cambridge                               | United Kingdom | SCImago #63 · THE =3 · QS 6         | 1             |
| University of California, San Diego                   | United States  | SCImago #120 · THE 47 · QS 66       | 1             |
| University of Leeds                                   | United Kingdom | SCImago #377 · THE 118 · QS 86      | 1             |
| University of Vienna                                  | Austria        | THE =95 · QS 152                    | 1             |
| University of Gothenburg                              | Sweden         | SCImago #573 · THE 201–250 · QS 202 | 1             |
| European Institute of Oncology IRCCS                  | Italy          | —                                   | 1             |
| The University of Queensland                          | Australia      | SCImago #126 · THE =80 · QS =42     | 1             |
| Gustave Roussy Cancer Campus                          | France         | —                                   | 1             |
| Osaka University                                      | Japan          | SCImago #546 · QS 91                | 1             |
| INRAe   | France         | —                                   | 1             |
| University of Vienna and Medical University of Vienna | Austria        | —                                   | 1             |
| Nanjing Agricultural University                       | China          | SCImago #853 · QS 951-1000          | 1             |

## Geographic distribution of citing authors

| Country        | Citing papers |
|----------------|---------------|
| United States  | 7             |
| China          | 4             |
| Italy          | 3             |
| Australia      | 2             |
| Canada         | 2             |
| Japan          | 2             |
| United Kingdom | 2             |
| France         | 1             |
| Germany        | 1             |
| Hong Kong      | 1             |
| Hungary        | 1             |
| Ireland        | 1             |

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.

2020  3

2021  2

2022  2

## F. AAO Precedent Considerations

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### 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

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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 | Metagenomic biomarker discovery and explanation  | 7            | Dhanasar – Prong 2 (well-positioned) |
| Contribution 2 | Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2 | 7            | Dhanasar – Prong 2 (well-positioned) |