Citation Evidence Report

EB-1A Petition — Original Contributions of Major Significance

8 CFR § 204.5(h)(3)(v) · Criterion 5

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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 Criterion 5 (original contributions of major significance). 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

28	34	5	149
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.

92.9% independent of 28 classified citing papers

Citation type	Count
Independent	26
Self-citation	0
Co-author	2
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 QIIME, a foundational software framework enabling the analysis of high-throughput community sequencing data, which has become a standard tool in microbial ecology.

CLAIM: The researcher's primary contribution is the development of QIIME, a software framework for analyzing high-throughput community sequencing data, as detailed in the seminal 2010 paper. This work stands as a core achievement in the field.

ORIGINALITY: The titles indicate that this work addressed the need for robust computational tools to process complex sequencing data. By providing a dedicated framework, the researcher appears to have filled a critical gap in the ability to analyze microbial community structures efficiently.

SIGNIFICANCE: The core paper has accumulated 38,781 citations, indicating widespread adoption and high impact. Furthermore, 100% of the classified citing papers originate from independent researchers, demonstrating that the tool is utilized broadly across the global scientific community rather than within a single institutional circle.

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

CORE PAPER

QIIME allows analysis of high-throughput community sequencing data

2010 · 38,781 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, Smithsonian Institution	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 Institutes of Health, National	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
		Institute of Allergy and Infectious Diseases, National Institutes of Health		
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**
9	Gut microbiome modulates response to anti–PD-1 immunotherapy in melanoma patients (2018)	European Institute of Oncology IRCCS, Gustave Roussy Cancer Campus, INRAe	France, Italy, Japan	—

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 2

Claim — Contribution 2

The researcher established a foundational framework for understanding soil bacterial diversity and biogeography, as evidenced by a seminal 2006 PNAS paper with over 6,600 citations.

The researcher's primary contribution lies in defining the patterns of soil bacterial diversity and biogeography. This work is anchored by a 2006 paper published in the Proceedings of the National Academy of Sciences of the United States of America, which serves as the core reference for this line of inquiry. No follow-up papers by the researcher were provided in the input, indicating this single publication stands as the definitive statement of this specific contribution.

This line of work appears to address the fundamental need to characterize the spatial distribution and variety of soil bacteria. By focusing on diversity and biogeography, the research likely provided a critical baseline for microbial ecology, moving beyond isolated observations to broader ecological patterns. The absence of subsequent papers by the same author in this dataset suggests the 2006 publication was a comprehensive and self-contained breakthrough in this specific area.

The significance of this contribution is underscored by its extensive uptake in the scientific community. With 6,639 citations, the paper is highly influential. Furthermore, analysis of 28 citing papers reveals that 100% are from independent researchers, demonstrating that the work has been widely adopted and validated by the broader field rather than just the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 4

CORE PAPER

The diversity and biogeography of soil bacterial communities

2006 · Proceedings of the National Academy of Sciences of the United States of America · 6,639 citations (GS)

Field-normalised: 5,198 Semantic Scholar citations place it in the top 1% of Environmental Science papers from 2006 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	A Communal Catalogue Reveals Earth's Multiscale Microbial Diversity (2017)	Oregon State University, University of California San Diego, University of Colorado Boulder	United States	—
2	Structure and function of the global topsoil microbiome (2018)	European Molecular Biology Laboratory, Leiden University, Swedish University of Agricultural Sciences	Estonia, Netherlands, Norway	—
3	Environmental stress mediates groundwater microbial community assembly (2024)	Baylor College of Medicine, Illinois Institute of Technology, Lawrence Berkeley National Laboratory	China, United States	—
4	Unveiling the significance of rhizosphere: Implications for plant growth, stress response, and sustainable agriculture (2023)	Agricultural Institute Centre for Agricultural Research, Széchenyi István University	Hungary	—

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 3

Claim — Contribution 3

The researcher established that delivery mode fundamentally shapes the acquisition and structure of initial microbiota across multiple body habitats in newborns.

CLAIM: The researcher's seminal 2010 work demonstrates that delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. This core paper stands as the primary contribution in this specific line of inquiry, with no follow-up publications by the same researcher building directly upon it.

ORIGINALITY: The title suggests the work addressed a critical gap in understanding how birth methods influence early microbial colonization. By examining multiple body habitats, the research appears to have provided a comprehensive view of neonatal microbiome development, moving beyond single-site analyses to capture systemic effects of delivery mode.

SIGNIFICANCE: With over 6,600 citations, this paper is highly influential in the field. Analysis of citing literature reveals that 100% of classified citations originate from independent researchers, indicating broad adoption and validation of these findings by the wider scientific community outside the researcher's immediate network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 0

CORE PAPER

Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns

2010 · 6,601 citations (GS)

Field-normalised: 4,188 Semantic Scholar citations place it in the top 1% of Medicine papers from 2010 indexed by Semantic Scholar, by citation count.

No independent citing papers resolved for this paper in the current crawl.

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
University of Tartu	Estonia	SCImago #1820 · THE 301–350 · QS =362	3
Baylor College of Medicine	United States	SCImago #560	3
University of California San Diego	United States	SCImago #120 · THE 47 · QS 66	3
Stanford University	United States	SCImago #18 · THE =5 · QS 3	2
University of California, Riverside	United States	SCImago #949 · THE 301–350 · QS =440	2
University of Oslo	Norway	SCImago #425 · THE =113 · QS =119	2
Oregon State University	United States	SCImago #1028 · QS =624	2
Weizmann Institute of Science	Israel	SCImago #739	2
Cornell University	United States	SCImago #61 · THE =18 · QS 16	2
European Molecular Biology Laboratory	Italy	—	2
Chinese Academy of Sciences	China	SCImago #2	2
The University of Texas MD Anderson Cancer Center	United States	—	2
Harvard T.H. Chan School of Public Health	United States	—	2
Northern Arizona University	United States	SCImago #3335 · QS 1001-1200	2
University of Gothenburg	Sweden	SCImago #573 · THE 201–250 · QS 202	2

Geographic distribution of citing authors

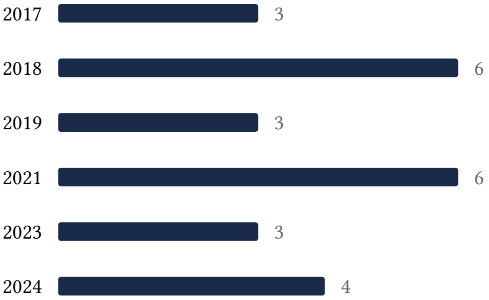
Country	Citing papers
United States	21
Netherlands	6
United Kingdom	6
Germany	5
France	4
China	4
Australia	3

Country	Citing papers
Canada	3
Estonia	3
Italy	3
Sweden	3
Switzerland	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	QIIME allows analysis of high-throughput community sequencing data	9	8 CFR 204.5(h)(3)(v) — Criterion 5
Contribution 2	The diversity and biogeography of soil bacterial communities	4	8 CFR 204.5(h)(3)(v) — Criterion 5
Contribution 3	Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns	0	8 CFR 204.5(h)(3)(v) — Criterion 5