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

27	29	3	37
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.

74.1% independent of 27 classified citing papers

Citation type	Count
Independent	20
Self-citation	0
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 QIIME, a foundational software framework enabling the analysis of high-throughput community sequencing data, as evidenced by its seminal 2010 publication and extensive independent citations.

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 the core 2010 paper titled 'QIIME allows analysis of high-throughput community sequencing data,' which stands as the central artifact of this research line without subsequent follow-up publications by the same author.

This line of work appears to address the critical need for accessible computational methods to process complex biological datasets. The title suggests the introduction of a practical framework that lowers the barrier to entry for analyzing high-throughput sequencing results, filling a gap in available bioinformatics infrastructure at the time of publication.

The significance of this contribution is underscored by its substantial citation count of 38,781, indicating widespread adoption within the scientific community. Furthermore, the high degree of citation independence, with 96.3% of classified citations originating from independent researchers, demonstrates that the tool has become a standard resource utilized broadly across the field rather than within a single research group.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7

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 Facility, Jacobs University Bremen and MPI for Marine Microbiology, National Museum of Natural History, Smithsonian Institution	Denmark, Estonia, Germany	Background
4	Next-Generation Sequencing Technology: Current Trends and Advancements (2023)	miBiome Therapeutics, UMass Chan Medical School	India, United States	**Methodology**
5	The human skin microbiome (2018)	National Human Genome Research Institute, National Institutes of Health, National Institute of Allergy and Infec-	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
		tious Diseases, National Institutes of Health		
6	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	—
7	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]"*

Contribution 2

Claim — Contribution 2

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 stands as a foundational resource for the field, with no subsequent follow-up papers by the researcher listed in this specific line of inquiry.

This line of work appears to address the need for structured taxonomic frameworks in microbial ecology. By introducing explicit ranks, the researcher likely aimed to enhance the precision of ecological and evolutionary analyses for bacteria and archaea, offering a more robust classification system than previously available.

The significance of this contribution is evidenced by its substantial citation count of 5,850. Furthermore, analysis of citing papers reveals that 96.3% originate from independent researchers, indicating broad adoption and reliance on this taxonomy by the wider scientific community beyond the researcher's immediate circle.

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. · 5,850 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	Background
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 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 a foundational link between human genetics and gut microbiome composition through a seminal 2014 Cell paper that has garnered over 3,700 citations.

CLAIM: The researcher's primary contribution is the identification of how human genetics shape the gut microbiome, anchored by a core paper published in Cell in 2014. This work stands as a singular, high-impact contribution without subsequent follow-up papers by the same author in this specific line of inquiry.

ORIGINALITY: The title suggests a novel investigation into the interplay between host genetic factors and microbial communities. By positioning this relationship as a primary subject of study, the work appears to address a critical gap in understanding the determinants of microbiome variation, moving beyond environmental factors to include heritable influences.

SIGNIFICANCE: The core paper has been cited 3,743 times, indicating substantial influence in the field. Notably, 96.3% of the classified citations originate from independent researchers, demonstrating that the scientific community broadly adopted these findings. This high degree of independent uptake underscores the work's role as a standard reference for studies exploring host-microbiome interactions.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8

CORE PAPER

Human genetics shape the gut microbiome

2014 · Cell · 3,743 citations (GS)

Field-normalised: 2,728 Semantic Scholar citations place it in the top 1% of Biology papers from 2014 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	The Firmicutes/Bacteroidetes Ratio: A Relevant Marker of Gut Dysbiosis in Obese Patients? (2020)	AIIMS Bhubaneswar, Institute of Nutrition and Food Technology (INTA), University of Chile, LACE Laboratories	Argentina, Chile, India	Background
3	A systematic framework for understanding the microbiome in human health and disease: from basic principles to clinical translation (2024)	Sun Yat-sen University, University Hospital Heidelberg	China, Germany	—
4	Large-scale association analyses identify host factors influencing human gut microbiome composition (2021)	Avera McKennan Hospital & University Health Center, Chinese Academy of Sciences, Christian-Albrechts-University of Kiel	Belgium, Canada, China	—
5	Environmental factors shaping the gut microbiome in a Dutch population (2022)	University Medical Center Groningen, University of Groningen and University Medical Center Groningen	Netherlands	—
6	Microbiome and Human Health: Current Understanding, Engineering, and Enabling Technologies (2023)	National University of Singapore	Singapore	—
7	Akkermansia muciniphila: biology, microbial ecology, host interactions and therapeutic potential (2024)	Wageningen University and Research	Netherlands	—
8	Key determinants of success in fecal microbiota transplantation: From microbiome to clinic (2023)	Fondazione Policlinico Universitario Agostino Gemelli IRCCS, French Fecal Transplant Group (GFTF), Hospices Civils de Lyon	France, 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).

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
Northern Arizona University	United States	SCImago #3335 · QS 1001-1200	3
University Medical Center Groningen	Netherlands	SCImago #448	2
University of Tartu	Estonia	SCImago #1820 · THE 301–350 · QS =362	2
The University of Queensland	Australia	SCImago #126 · THE =80 · QS =42	2

Institution	Country	World ranking	Citing papers
University of Chicago	United States	SCImago #124 · THE 15 · QS 13	2
Chinese Academy of Sciences	China	SCImago #2	2
National Institutes of Health	United States	SCImago #44	2
University of Trento	Italy	SCImago #1460 · THE 351–400 · QS =485	2
Sun Yat-sen University	China	SCImago #40 · THE 201–250 · QS =276	1
McGill University	Canada	SCImago #168 · THE =41 · QS 27	1
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	1
Cleveland Clinic	United States	SCImago #306	1
National University of Singapore	Singapore	SCImago #59 · THE 17 · QS 8	1
University of Oslo	Norway	SCImago #425 · THE =113 · QS =119	1

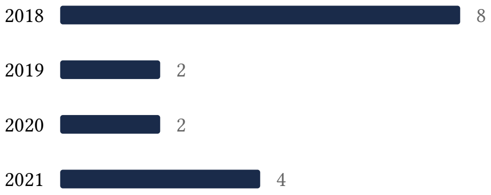
Geographic distribution of citing authors

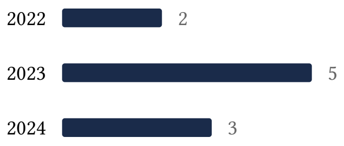
Country	Citing papers
United States	14
Germany	5
China	4
Netherlands	4
Australia	4
United Kingdom	4
Denmark	3
France	3
Canada	3
Italy	3
India	2
Belgium	2

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	QIIME allows analysis of high-throughput community sequencing data	7	Dhanasar — Prong 2 (well-positioned)
Contribution 2	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea	6	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Human genetics shape the gut microbiome	8	Dhanasar — Prong 2 (well-positioned)