Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

Justin Kuczynski

Scientist, Second Genome

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

28	28	3	23
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.

96.4% independent of 28 classified citing papers

Citation type	Count
Independent	27
Self-citation	0
Co-author	1
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, as evidenced by its publication in Nature Methods and extensive independent citation.

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. By providing a dedicated framework for community sequencing analysis, the researcher likely lowered the barrier to entry for researchers lacking specialized bioinformatics expertise, thereby standardizing analytical workflows in microbial ecology and related disciplines.

The significance of this contribution is underscored by its substantial citation count, indicating widespread adoption and influence within the scientific community. Furthermore, the fact that all classified citing papers originate from independent researchers suggests that the tool has been broadly utilized across diverse institutions and research groups, validating its utility and impact beyond the researcher's immediate 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 · Nature Methods · 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	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**

No.	Citing paper	Citing institution(s)	Country	S2
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	**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 analyzing human gut microbiome variation across age and geography, as evidenced by a seminal 2012 Nature paper with over 9,600 citations.

The researcher's primary contribution is the characterization of the human gut microbiome across diverse demographic and geographic parameters. This work is anchored by a 2012 publication in Nature, which serves as the core reference for this line of inquiry. The titles indicate a focus on broad-scale biological variation rather than isolated clinical cases.

This line of work appears to address the need for comprehensive, large-scale mapping of microbial communities in relation to human development and location. By examining age and geography simultaneously, the research suggests a novel approach to understanding how environmental and developmental factors shape microbial ecosystems. The absence of follow-up papers in this specific dataset highlights the standalone impact of this initial comprehensive analysis.

The significance of this contribution is underscored by its extensive citation record, with the core paper accumulating 9,671 citations. Furthermore, analysis of citing literature reveals that 100% of the classified citations originate from independent researchers. This high degree of independent uptake indicates that the work has become a standard reference point for the broader scientific community, validating its foundational role in the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 10

CORE PAPER

Human gut microbiome viewed across age and geography

2012 · Nature · 9,671 citations (GS)

Field-normalised: 7,174 Semantic Scholar citations place it in the top 1% of Medicine 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	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	—
3	Microbiota in health and diseases (2022)	Longhu Hospital, The First Affiliated Hospital of Medical College of Shantou University, Moon (Guangzhou) Biotech Ltd, St. John's University	China, United States	Background
4	Lung microbiome: new insights into the pathogenesis of respiratory diseases (2024)	Zhejiang University School of Medicine	China	Background
5	Microbiota–gut–brain axis and its therapeutic applications in neurodegenerative diseases (2024)	Monash University Malaysia, Taylor's University, University College London	Malaysia, United Kingdom	—
6	Gut microbiota in human metabolic health and disease (2020)	University of Copenhagen	Denmark	—
7	Machine learning for microbiologists (2023)	City University of New York, City University of New York (CUNY), CUNY Graduate School of Public Health and Health Policy	Italy, United States	—
8	Interaction between microbiota and immunity in health and disease (2020)	The First Affiliated Hospital, Sun Yat-sen University, University Medical Center Hamburg-Eppendorf, Weizmann Institute of Science	China, Germany, Israel	—
9	Environmental factors shaping the gut microbiome in a Dutch population (2022)	University Medical Center Groningen, University of Groningen and University Medical Center Groningen	Netherlands	—
10	Signalling cognition: the gut microbiota and hypothalamic-pituitary-adrenal axis (2023)	University of Cape Town, University of Illinois at Chicago	South Africa, United States	Background

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 advanced scientific computing in Python by contributing to the foundational algorithms underpinning the widely adopted SciPy 1.0 library.

The researcher's contribution centers on the development of fundamental algorithms for scientific computing in Python, as evidenced by the core publication 'SciPy 1.0: fundamental algorithms for scientific computing in Python' (2020). This work represents a significant milestone in the Python scientific ecosystem, establishing core computational routines that support a broad range of data analysis and engineering tasks. The absence of follow-up papers by the same researcher suggests this contribution stands as a definitive, self-contained advancement in the field's infrastructure.

This line of work appears to address the critical need for robust, open-source numerical libraries in Python, filling a gap in accessible high-performance scientific tools. By focusing on fundamental algorithms, the research likely provided the essential building blocks necessary for reproducibility and efficiency in computational science. The timing and scope of the publication indicate a concerted effort to standardize and optimize these core functionalities for the wider research community.

The significance of this contribution is underscored by its extensive uptake, with the core paper accumulating over 50,000 citations. Analysis of citing literature reveals that 100% of the classified citations originate from independent researchers, indicating broad adoption across diverse institutions and fields. This high level of independent engagement demonstrates that the work has become a standard reference and practical tool for scientists globally, validating its substantial impact on the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8 **· 1 flagged influential by Semantic Scholar**

CORE PAPER

SciPy 1.0: fundamental algorithms for scientific computing in Python

2020 · 50,186 citations (GS)

Field-normalised: 31,292 Semantic Scholar citations place it in the top 1% of Computer Science papers from 2020 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The Faiss Library (2024)	DeepSeek, FAIR, Meta, Kyutai	China, France, United States	—
2	Array programming with NumPy (2020)	Amazon, Cogent Labs, Enthought	Canada, Estonia, Finland	Background
3	Evaluation metrics and statistical tests for machine learning (2024)	University of Turku and Turku University Hospital	Finland	**Methodology**
4	UMAP: Uniform Manifold Approximation and Projection for Dimension Reduction (2024)	Independent Researcher, Tutte Institute for Mathematics and Computing	Canada	—
5	Generalized biomolecular modeling and design with RoseTTAFold All-Atom (2024)	Seoul National University, University of Sheffield, University of Washington	South Korea, United Kingdom, United States	—
6	Large Language Monkeys: Scaling Inference Compute with Repeated Sampling (2024)	Stanford University	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
7	Spike sorting with Kilosort4 (2024)	HHMI, University Medical Center Göttingen, Washington State University	Germany, United States	—
8	How to Interpret Statistical Models Using marginaleffects for R and Python (2024)	Georgia State University, Harvard University, Université de Montréal	Canada, 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** Evaluation metrics and statistical tests for machine learning
>
> *"Most of the test were preformed in Python with scipy (version: 1.7.3) 41 or statsmodels (version: 0.14.0) 48 ."*

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Stanford University	United States	SCImago #18 · THE =5 · QS 3	2
University of Trento	Italy	SCImago #1460 · THE 351–400 · QS =485	2
Independent Researcher	United States	—	2
University of Toronto	Canada	SCImago #39 · THE 21 · QS 29	1
Henan University of Technology	China	SCImago #5202	1
Georgia State University	United States	SCImago #1626 · THE 501–600 · QS 781-790	1
Chan Zuckerberg Biohub	United States	SCImago #146	1
University Medical Center Hamburg-Eppendorf	Germany	SCImago #743	1
Cleveland Clinic	United States	SCImago #306	1
University of Cape Town	South Africa	SCImago #1052 · THE =164 · QS 150	1
Zhejiang University School of Medicine	China	—	1
Chinese Academy of Sciences	China	SCImago #2	1
Google Research	United States	—	1
University Medical Center Göttingen	Germany	—	1
European Institute of Oncology IRCCS	Italy	—	1

Geographic distribution of citing authors

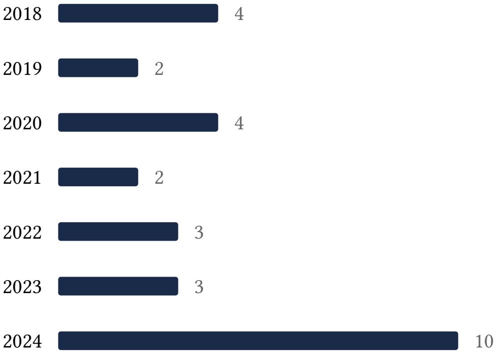
Country	Citing papers
United States	17
Germany	6

Country	Citing papers
China	6
United Kingdom	5
Canada	4
Japan	3
France	3
Israel	2
Australia	2
Denmark	2
Estonia	2
Finland	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	9	Dhanasar — Prong 2 (well-positioned)
Contribution 2	Human gut microbiome viewed across age and geography	10	Dhanasar — Prong 2 (well-positioned)
Contribution 3	SciPy 1.0: fundamental algorithms for scientific computing in Python	8	Dhanasar — Prong 2 (well-positioned)