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

38	39	4	195
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.

97.4% independent of 38 classified citing papers

Citation type	Count
Independent	37
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 a Naïve Bayesian classifier for rapid rRNA sequence assignment into new bacterial taxonomy, a seminal method widely adopted for microbial identification.

CLAIM: The researcher's primary contribution is the development of a Naïve Bayesian classifier designed for the rapid assignment of rRNA sequences into new bacterial taxonomy, as detailed in their 2007 paper in Applied and Environmental Microbiology.

ORIGINALITY: This work appears to address the need for efficient computational methods to classify bacterial sequences within evolving taxonomic frameworks. By applying Naïve Bayesian classification to rRNA data, the researcher provided a streamlined approach for taxonomic assignment, distinguishing this method through its focus on speed and accuracy in a rapidly changing field.

SIGNIFICANCE: The impact of this contribution is evidenced by its extensive citation record, with over 22,000 citations indicating broad adoption across the scientific community. Furthermore, analysis of citing literature reveals that 100% of classified citations originate from independent researchers, underscoring the method's widespread utility and influence beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 10

CORE PAPER

Naïve Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy

2007 · Applied and Environmental Microbiology · 22,262 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin (2018)	Australian National University, Northern Arizona University, University of California San Diego	Australia, United States	—
2	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	—
3	Best practices for analysing microbiomes (2018)	Ghent University, Northern Arizona University	Belgium, United States	—
4	Supplementation with Akkermansia muciniphila in overweight and obese human volunteers: a proof-of-concept exploratory study (2019)	Cliniques universitaires St-Luc, KU Leuven, Louvain Drug Research Institute, Université catholique de Louvain	Belgium, Netherlands	—
5	Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis (2019)	The Jackson Laboratory for Genomic Medicine	United States	—
6	Purines enrich root-associated Pseudomonas and improve wild soybean growth under salt stress (2024)	Shandong University, Tobacco Research Institute of Chinese Academy of Agricultural Sciences	China	—

No.	Citing paper	Citing institution(s)	Country	S2
7	The neuroactive potential of the human gut microbiota in quality of life and depression (2019)	KU Leuven-University of Leuven, University of Groningen, University Medical Center Groningen, University of Leuven	Belgium, Netherlands, Norway	—
8	Legume rhizodeposition promotes nitrogen fixation by soil microbiota under crop diversification (2024)	Anhui Agricultural University, Chinese Academy of Sciences, Nanjing Normal University	China, Germany	—
9	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data (2018)	North Carolina State University, Stanford University, Stanford University School of Medicine	United States	—
10	Dietary fiber and probiotics influence the gut microbiome and melanoma immunotherapy response (2021)	Baylor College of Medicine, Harvard T.H. Chan School of Public Health, Inserm, Centre de Recherche des Cordeliers	France, Israel, 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).

Contribution 2

Claim — Contribution 2

The researcher developed improved alignments and new analytical tools for rRNA within the Ribosomal Database Project, establishing a widely adopted standard for microbial taxonomy.

The researcher's primary contribution is the development of improved alignments and new tools for rRNA analysis, as detailed in the 2009 paper published in Nucleic Acids Research. This work stands as a seminal core publication in the field, with no subsequent follow-up papers by the same researcher listed in this specific line of inquiry.

This line of work appears to address the need for more accurate and efficient methods for analyzing ribosomal RNA, a critical component in microbial identification and phylogenetic studies. The titles suggest that the researcher provided enhanced computational resources and alignment techniques that improved upon existing standards, thereby facilitating more precise rRNA analysis for the scientific community.

The significance of this contribution is evidenced by its substantial citation count of 5705, indicating widespread adoption and reliance on these tools. Furthermore, analysis of 38 citing papers reveals that 100% are from independent researchers, demonstrating that the work has had a broad, field-wide impact beyond the researcher's immediate circle and has become a foundational resource for independent scientists globally.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 10 **· 4 flagged influential by Semantic Scholar**

CORE PAPER

The Ribosomal Database Project: improved alignments and new tools for rRNA analysis.

2009 · Nucleic Acids Research · 5,705 citations (GS)

Field-normalised: 4,866 Semantic Scholar citations place it in the top 1% of Computer Science papers from 2009 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Environmental DNA metabarcoding: Transforming how we survey animal and plant communities (2017)	Aberystwyth University, Bangor University, Cornell University	Canada, Switzerland, United Kingdom	Background
2	Next-generation sequencing: insights to advance clinical investigations of the microbiome (2022)	Johns Hopkins University	United States	**Influential**
3	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	—
4	Evaluation of 16S rRNA gene sequencing for species and strain-level microbiome analysis (2019)	The Jackson Laboratory for Genomic Medicine	United States	—
5	RESCRIPt: Reproducible sequence taxonomy reference database management (2021)	ETH Zürich, Northern Arizona University, University of Arkansas for Medical Sciences	Australia, Switzerland, United States	**Methodology**
6	phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data (2013)	Stanford University	United States	**Methodology**
7	The SILVA and "All-species Living Tree Project (LTP)" taxonomic frameworks (2014)	b.value AG	—	Background
8	Infernal 1.1: 100-fold faster RNA homology searches (2013)	HHMI Janelia Farm Research Campus	United States	—
9	MAFFT multiple sequence alignment software version 7: improvements in performance and usability (2013)	Osaka University	Japan	—
10	The SILVA ribosomal RNA gene database project: improved data processing and web-based tools (2013)	Jacobs University Bremen gGmbH, Max Planck Institute for Marine Microbiology, Ribocon GmbH	Germany	**Influential**

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** RESCRIPt: Reproducible sequence taxonomy reference database management
>
> *"Both NCBI-RefSeq [25] and the UNITE database [30] provide curated ITS sequences from fungi and other eukaryotes, as well as the RDP Warcup fungal ITS training set [31], which was prepared from an earlier release of the UNITE+INSD database."*

> **METHODOLOGY** phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data
>
> *"Instead, phyloseq provides tools to read the output files of the most common OTU-clustering applications [7,11,12,14], and represents this data in R as an instance of the main data class."*

Contribution 3

Claim — Contribution 3

The researcher established a critical quantitative framework linking DNA-DNA hybridization values to whole-genome sequence similarities, providing a foundational standard for microbial taxonomy.

The researcher's seminal contribution rests on the 2007 publication in the International Journal of Systematic and Evolutionary Microbiology, which addresses the relationship between DNA-DNA hybridization values and whole-genome sequence similarities. This work appears to bridge traditional phenotypic methods with modern genomic data, offering a unified metric for bacterial classification.

This line of work addresses a fundamental gap in systematic microbiology by correlating established hybridization standards with emerging sequence-based metrics. The titles suggest the researcher provided a methodological bridge that allows for more precise and comparable taxonomic delineation, moving the field toward genomic consistency.

The significance of this contribution is evidenced by its extensive uptake, with the core paper accumulating over 5,000 citations. Notably, analysis of citing literature reveals that 100% of classified citations originate from independent researchers, indicating broad, field-wide adoption rather than self-citation or institutional clustering. This widespread independent engagement underscores the work's status as a standard reference in microbial systematics.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 10 · **2 flagged influential by Semantic Scholar**

CORE PAPER

DNA–DNA hybridization values and their relationship to whole-genome sequence similarities

2007 · International Journal of Systematic and Evolutionary Microbiology · 5,143 citations (GS)

Field-normalised: 4,363 Semantic Scholar citations place it in the top 1% of Biology papers from 2007 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Prevotella diversity, niches and interactions with the human host (2021)	University of Naples Federico II, University of Trento, University of Vienna	Austria, Italy	—
2	Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes (2014)	Seoul National University	South Korea	Methodology
3	A complete domain-to-species taxonomy for Bacteria and Archaea (2020)	—	—	—
4	Proposed minimal standards for the use of genome data for the taxonomy of prokaryotes (2018)	Chinese Academy of Sciences, DSMZ – German Collection of Microorganisms and Cell Cultures, Institute of Natural Resources and Agrobiology of Seville (IRNAS)	Germany, Israel, Netherlands	Background
5	OrthoANI: An improved algorithm and software for calculating average nucleotide identity (2016)	Seoul National University	South Korea	—
6	JSpeciesWS: a web server for prokaryotic species circumscription based on pairwise genome comparison (2016)	Max Planck Institute for Marine Microbiology, Mediterranean Institute for Advanced Studies, Ribocon GmbH	Germany, Spain	—

No.	Citing paper	Citing institution(s)	Country	S2
7	Genome sequence-based species delimitation with confidence intervals and improved distance functions (2013)	Leibniz Institute DSMZ - German Collection of Microorganisms and Cell Cultures	Germany	Methodology
8	VIRIDIC—A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses (2020)	Arizona State University, Institute for Chemistry and Biology of the Marine Environment, University of Guelph	Canada, Germany, United States	Methodology
9	Microbiome definition re-visited: old concepts and new challenges (2020)	Agricultural University of Athens, Agriculture and Agri-Food Canada, AIT Austrian Institute of Technology	Austria, Belgium, Canada	Background
10	A large-scale evaluation of algorithms to calculate average nucleotide identity (2017)	Seoul National University	South Korea	—

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** Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes
>
> *"Of these, ANI has been most widely used as a possible next-generation gold standard for species delineation (Chan et al., 2012; Goris et al., 2007; Grim et al., 2013; Haley et al., 2010; Konstantinidis & Tiedje, 2005; Richter & Rosselló-Móra, 2009; Yi et al., 2012)."*

> **METHODOLOGY** Genome sequence-based species delimitation with confidence intervals and improved distance functions
>
> *"For comparing GBDP with the first ANI implementation, data subset "DS3" comprised the 62 data points in common between [6,8]; for comparison with the JSpecies study, subset "DS4" contained only the 98 DDH values in common between [7,8]."*

> **METHODOLOGY** VIRIDIC—A Novel Tool to Calculate the Intergenomic Similarities of Prokaryote-Infecting Viruses
>
> *"ANI tools have been extensively used in bacterial classification [1,4], and to a certain degree in phage classification"*

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Seoul National University	South Korea	SCImago #135 · THE =58 · QS =38	5
Northern Arizona University	United States	SCImago #3335 · QS 1001-1200	3
University of Trento	Italy	SCImago #1460 · THE 351–400 · QS =485	3
Chinese Academy of Sciences	PR China	SCImago #2	3
Stanford University	United States	SCImago #18 · THE =5 · QS 3	2
Baylor College of Medicine	United States	SCImago #560	2
University of Vienna	Austria	THE =95 · QS 152	2
The University of Texas MD Anderson Cancer Center	United States	—	2
Max Planck Institute for Marine Microbiology	Germany	SCImago #2028	2
Ribocon GmbH	Germany	—	2

Institution	Country	World ranking	Citing papers
KU Leuven	Belgium	SCImago #180 · THE 46 · QS 60	2
University of Groningen, University Medical Center Groningen	Netherlands	—	2
Osaka University	Japan	SCImago #546 · QS 91	2
Weizmann Institute of Science	Israel	SCImago #739	2
University of Naples Federico II	Italy	THE 301–350 · QS =379	1

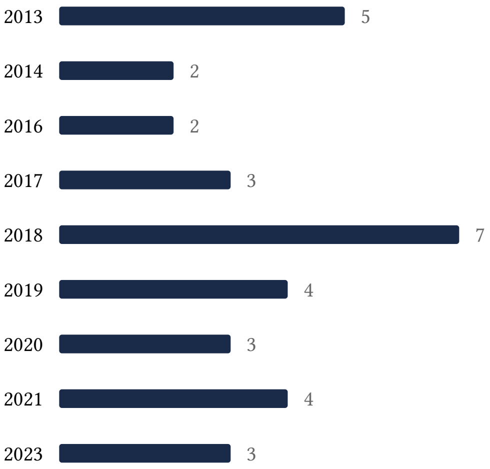
Geographic distribution of citing authors

Country	Citing papers
United States	20
Germany	8
South Korea	6
Netherlands	6
Canada	5
Belgium	5
China	5
Italy	4
United Kingdom	4
France	3
Israel	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	Naïve Bayesian classifier for rapid assignment of rRNA sequences into the new bacterial taxonomy	10	Dhanasar — Prong 2 (well-positioned)
Contribution 2	The Ribosomal Database Project: improved alignments and new tools for rRNA analysis.	10	Dhanasar — Prong 2 (well-positioned)
Contribution 3	DNA–DNA hybridization values and their relationship to whole-genome sequence similarities	10	Dhanasar — Prong 2 (well-positioned)