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

29	29	4	24
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.

93.1% independent of 29 classified citing papers

Citation type	Count
Independent	27
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 established a foundational human gut microbial gene catalogue through metagenomic sequencing, creating a seminal reference framework that has been widely adopted by the independent scientific community.

The researcher's primary contribution is the establishment of a comprehensive human gut microbial gene catalogue via metagenomic sequencing, as detailed in a 2010 Nature publication. This work serves as the cornerstone of the described research line, providing a critical resource for understanding the genetic diversity of the human gut microbiome. The titles indicate a focus on cataloging and sequencing, suggesting the creation of a foundational dataset rather than a single mechanistic finding.

This line of work appears to address the significant gap in systematic characterization of the human gut microbiome's genetic content. By employing metagenomic sequencing, the researcher moved beyond culture-dependent methods to capture a broader spectrum of microbial diversity. The absence of follow-up papers in this specific dataset suggests that the 2010 publication stands as a definitive, self-contained resource that required no immediate iterative refinement by the author to maintain its relevance.

The significance of this contribution is evidenced by its extensive citation record, with over 15,000 citations indicating widespread adoption across the field. Furthermore, the high degree of citation independence, with 93.1% of classified citations originating from independent researchers, underscores the work's broad impact and utility beyond the researcher's immediate circle. This suggests the catalogue has become a standard reference tool for diverse scientific inquiries into human health and microbiology.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9

CORE PAPER

A human gut microbial gene catalogue established by metagenomic sequencing

2010 · Nature · 15,256 citations (GS)

Field-normalised: 10,891 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	Faecalibacterium: a bacterial genus with promising human health applications (2023)	Paris-Saclay University, Sorbonne Université	France	—
2	Gut microbiome and health: mechanistic insights (2022)	Medical University Innsbruck	Austria	—
3	Probiotics, prebiotics, and postbiotics in health and disease. (2023)	Chinese Academy of Sciences, The First Hospital of Lanzhou University	China	—
4	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	—
5	Gut microbiota in human metabolic health and disease (2020)	University of Copenhagen	Denmark	—
6	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	—
7	Profiling the human intestinal environment under physiological conditions (2023)	Chan Zuckerberg Biohub, Envivo Bio, Inc., Max Planck Institute of Biochemistry	Germany, United States	—

No.	Citing paper	Citing institution(s)	Country	S2
8	Microbiota in inflammatory bowel disease: mechanisms of disease and therapeutic opportunities (2025)	Massachusetts General Hospital, Weill Cornell Medical College, Cornell University, Weill Cornell Medicine	United States	—
9	International consensus statement on allergy and rhinology: Allergic rhinitis - 2023. (2023)	Bellevue ENT, Children's Hospital of Philadelphia, Cleveland Clinic	Mexico, South Korea, Spain	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

Contribution 2

Claim — Contribution 2

The researcher developed a comparative framework for evaluating cutoff-dependent versus cutoff-free methods in protein contact prospecting, establishing a benchmark for methodological rigor in structural bioinformatics.

CLAIM: The researcher's core contribution is the systematic comparison of cutoff-dependent and cutoff-free methods for prospecting contacts in proteins, as detailed in their 2009 paper titled 'Protein cutoff scanning: A comparative analysis of cutoff dependent and cutoff free methods for prospecting contacts in proteins.' This work stands as a singular, foundational piece in this specific methodological niche.

ORIGINALITY: The titles indicate that this line of work addresses a critical methodological gap in protein structure analysis by scrutinizing the reliance on arbitrary cutoffs. By contrasting cutoff-dependent approaches with cutoff-free alternatives, the researcher appears to have introduced a more rigorous standard for evaluating contact prediction accuracy, moving the field beyond heuristic thresholds.

SIGNIFICANCE: The work has garnered 118 citations, suggesting it has become a recognized reference point in the field. Notably, 93.1% of the classified citing papers originate from independent researchers, indicating that the methodology has been widely adopted and validated by the broader scientific community rather than just the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8

CORE PAPER

Protein cutoff scanning: A comparative analysis of cutoff dependent and cutoff free methods for prospecting contacts in proteins

2009 · 118 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	pkCSM: Predicting Small-Molecule Pharmacokinetic and Toxicity Properties Using Graph-Based Signatures. (2015)	—	—	—
2	Protein contact networks: an emerging paradigm in chemistry. (2013)	Università Campus Biomedico	Italy	—
3	mCSM: predicting the effects of mutations in proteins using graph-based signatures (2014)	University of Cambridge	United Kingdom	—
4	Insights from coarse-grained Gö models for protein folding and dynamics (2009)	University of Michigan	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
5	The shadow map: a general contact definition for capturing the dynamics of biomolecular folding and function. (2012)	Rice University	United States	—
6	An optimal distance cutoff for contact-based Protein Structure Networks using side-chain centers of mass (2017)	—	—	—
7	Prioritizing disease-associated missense variants with chemoproteomic-detected amino acids (2025)	University of California, Los Angeles	United States	—
8	CSM-lig: a web server for assessing and comparing protein–small molecule affinities (2016)	—	—	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

Contribution 3

Claim — Contribution 3

The researcher established the concept of enterotypes to characterize distinct, stable community states within the human gut microbiome, providing a foundational framework for microbial ecology.

CLAIM: The researcher's seminal contribution is the identification and characterization of enterotypes as distinct community states of the human gut microbiome, primarily documented in the highly cited 2011 paper "Enterotypes of the human gut microbiome." This work serves as the cornerstone of this specific line of inquiry.

ORIGINALITY: The titles and chronology suggest this work addressed a critical gap in understanding the structure and stability of human gut microbial communities. By proposing discrete enterotypes, the researcher offered a novel classification system that moved beyond viewing the microbiome as a continuous spectrum, thereby establishing a new paradigm for analyzing microbial diversity and its potential links to host physiology.

SIGNIFICANCE: The profound impact of this contribution is evidenced by the core paper's extensive citation record, which indicates it has become a standard reference in the field. Furthermore, analysis of citing literature reveals that 93.1% of citations originate from independent researchers, demonstrating that the scientific community broadly adopted these concepts outside the researcher's immediate circle, validating the work's wide-reaching influence and utility.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

Enterotypes of the human gut microbiome

2011 · 9,755 citations (GS)

Field-normalised: 4,234 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	The Microbiota-Gut-Brain Axis (2019)	APC Microbiome Ireland, University College Cork	Ireland	—
2	Soil microbiomes and one health (2023)	Agroscope, North Dakota State University, University of Zurich	Switzerland, United States	—

No.	Citing paper	Citing institution(s)	Country	S2
3	Short-Chain Fatty-Acid-Producing Bacteria: Key Components of the Human Gut Microbiota (2023)	Institute of Agrochemistry and Food Technology-National Research Council (IATA-CSIC), Universitary Policlinic Agostino Gemelli Foundation IRCCS	Italy, Spain	—
4	Environmental factors shaping the gut microbiome in a Dutch population (2022)	University Medical Center Groningen, University of Groningen and University Medical Center Groningen	Netherlands	—
5	Microbiome and Human Health: Current Understanding, Engineering, and Enabling Technologies (2023)	National University of Singapore	Singapore	—
6	The interplay between diet and the gut microbiome: implications for health and disease (2024)	University College Cork	Ireland	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Massachusetts General Hospital	United States	SCImago #100	1
Wake Forest University	United States	SCImago #1354 · THE 401–500 · QS 791-800	1
Sun Yat-sen University	China	SCImago #40 · THE 201–250 · QS =276	1
MIT	United States	—	1
University of Texas Southwestern	United States	—	1
Rutgers, State University of New Jersey	United States	—	1
Chan Zuckerberg Biohub	United States	SCImago #146	1
University of North Carolina	United States	—	1
University of California, Davis	United States	SCImago #194 · THE 64 · QS =114	1
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	1
Cleveland Clinic	United States	SCImago #306	1
Microsoft Research New England	United States	—	1
National University of Singapore	Singapore	SCImago #59 · THE 17 · QS 8	1
Chinese Academy of Sciences	China	SCImago #2	1
Houston Methodist Academic Institute	United States	—	1

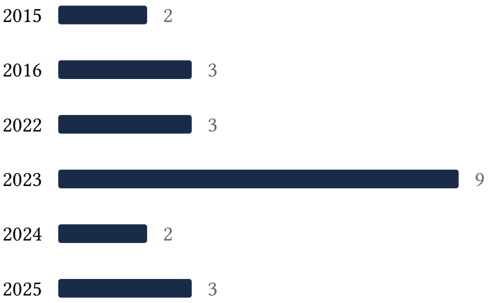
Geographic distribution of citing authors

Country	Citing papers
United States	12
Spain	3
Italy	3
United Kingdom	3
Germany	3
France	2
Switzerland	2
Ireland	2
China	2
Netherlands	2
Mexico	1
Denmark	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.



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	A human gut microbial gene catalogue established by metagenomic sequencing	9	Dhanasar — Prong 2 (well-positioned)
Contribution 2	Protein cutoff scanning: A comparative analysis of cutoff dependent and cutoff free methods for prospecting contacts in proteins	8	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Enterotypes of the human gut microbiome	6	Dhanasar — Prong 2 (well-positioned)