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

195	203	29	8
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.

89.0% independent of 73 classified citing papers

Citation type	Count
Independent	65
Self-citation	4
Co-author	4
Same-institution	0

122 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 identified a new class of antibacterial proteins by developing methods to predict peptidoglycan hydrolases, establishing a foundational framework for discovering novel antimicrobial targets.

CLAIM: The researcher's contribution centers on the 2016 paper titled 'Prediction of peptidoglycan hydrolases-a new class of antibacterial proteins,' which appears to establish a methodological approach for identifying this specific group of proteins as potential antibacterial agents.

ORIGINALITY: This work addresses the need for novel antibacterial strategies by focusing on peptidoglycan hydrolases, suggesting a shift toward predictive identification of these proteins as a distinct class of therapeutic targets. The titles indicate a focus on computational or predictive modeling to uncover these biological entities.

SIGNIFICANCE: The core paper has garnered 39 citations, with 89.0% of the 73 classified citations originating from independent researchers. This high degree of independent uptake suggests the work has been widely recognized and utilized by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9

CORE PAPER

Prediction of peptidoglycan hydrolases-a new class of antibacterial proteins

2016 · BMC genomics 17 (1), 411, 2016 · 39 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Peptidoglycan muropeptides: release, perception, and functions as signaling molecules	Umeå University	Sweden	—
2	One fold, many functions—M23 family of peptidoglycan hydrolases	Mossakowski Medical Research Institute, Polish Academy of Sciences	Poland	—
3	Phagocytosis-like cell engulfment by a planctomycete bacterium	University of Tsukuba	Japan	—
4	Engineering of chimeric enzymes with expanded tolerance to ionic strength	International Institute of Molecular and Cell Biology, Mossakowski Medical Research Institute, Polish Academy of Sciences	Poland	—
5	Ligilactobacillus-Derived Extracellular Vesicles Inhibit Growth and Virulence of Enteric Pathogens	University of Ottawa	Canada	—
6	Discovery of a novel antibacterial protein CB6-C to target methicillin-resistant Staphylococcus aureus	Jilin Agricultural University	China	—
7	Histidine auxotroph mutant is defective for cell separation and allows the identification of crucial factors for cell division in Brucella abortus	University of Namur	Belgium	Methodology

No.	Citing paper	Citing institution(s)	Country	S2
8	An exploration of mechanisms underlying Desemzia incerta colonization resistance to methicillin-resistant Staphylococcus aureus on the skin	Children's Hospital of Philadelphia, University of Pennsylvania	United States	—
9	Complete Genome Sequence of Lactic Acid Bacterium Pediococcus acidilactici Strain ATCC 8042, an Autolytic Anti-bacterial Peptidoglycan Hydrolase Producer	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).

Contribution 2

Claim — Contribution 2

The researcher developed a first-in-class fully modified miR-34a variant demonstrating superior stability, activity, and anti-tumor efficacy, establishing a novel therapeutic platform for oncology.

CLAIM: The researcher's primary contribution is the development of a first-in-class fully modified version of miR-34a, as detailed in a 2023 publication. This work presents a molecular entity characterized by outstanding stability, activity, and anti-tumor efficacy, positioning it as a significant advancement in microRNA-based therapeutics.

ORIGINALITY: The title indicates that this work addresses critical limitations in existing miR-34a formulations by introducing a fully modified structure. By achieving a first-in-class status, the research appears to overcome prior barriers related to molecular stability and therapeutic potency, offering a distinct improvement over previous iterations or unmodified versions of this microRNA.

SIGNIFICANCE: The core paper has accumulated 70 citations, suggesting strong engagement within the scientific community. Notably, 89.0% of the citing papers originate from independent researchers, indicating that the work has been widely adopted and validated by external groups rather than relying on self-citation or institutional bias. This high degree of independent uptake underscores the broad relevance and impact of the researcher's contribution to the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 17

CORE PAPER

A first-in-class fully modified version of miR-34a with outstanding stability, activity, and anti-tumor efficacy

2023 · Oncogene 42 (40), 2985-2999, 2023 · 70 citations (GS)

Field-normalised: 47 Semantic Scholar citations place it in the top 5% of Medicine papers from 2023 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	RNA chemistry and therapeutics	Icahn School of Medicine at Mount Sinai, University of Pennsylvania	United States	—
2	Frameworks for transformational breakthroughs in RNA-based medicines	Pfizer Inc	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
3	Utilizing Engineered Bacteria as “Cell Factories” In Vivo for Intracellular RNA-Loaded Outer Membrane Vesicles' Self-Assembly in Tumor Treatment	Peking University Third Hospital, Tianjin Children's Hospital, Tianjin University	China	—
4	Therapeutic potential of synthetic microRNA mimics based on the miR-15/107 consensus sequence	Asbestos and Dust Diseases Research Institute	Australia	—
5	Genomic landscape and preclinical models of angiosarcoma	Purdue University	United States	—
6	Recent advances in early diagnosis and treatment of T1D with miRNAs	Zhejiang Shuren University	China	—
7	miR-34 as a critical regulator in ovarian cancer	Ahvaz Jundishapur University of Medical Sciences	Iran	—
8	miRNA mediated mitochondrial function and gene regulation associated with Alzheimer's disease	University of North Texas Health Science Center	United States	—
9	MiRNA Stability and Degradation: Dynamic Regulators of Cellular Regulatory Networks	Jiangxi University of Chinese Medicine	China	—
10	miR147 promotes mucosal integrity and healing in intestinal inflammation	McGovern Medical School	United States	—
11	Hybrid Nanocarriers for Cancer Therapy: Advancements in Co-Delivery of Gene Therapy and Immunotherapy	Nazarbayev University	Kazakhstan	—
12	RNA Encapsulation in Metal–Organic Frameworks for Targeting Cancer-Causing Genes	Amity University	India	—
13	MiR-182 and MiR-34a regulate autophagy and apoptosis in tuberculosis and lung cancer	Islamic Azad University, Pasteur Institute of Iran, Tarbiat Modares University	Iran	—
14	MicroRNAs as Biomarkers and Therapeutic Targets in Treatment-Resistant Depression: Unveiling Diagnostic and Treatment Pathways	Lovely Professional University, Ras Al Khaimah Medical and Health Sciences University, The Hashemite University	India, Jordan, United Arab Emirates	—
15	Review of the Different Outcomes Produced by Genetic Knock Out of the Long Non-coding microRNA-host-gene MIR22HG versus Pharmacologic Antagonism of its ...	AptamiR Therapeutics, Inc., Pennington Biomedical Research Center	United States	—
16	Chemical Modifications in Nucleic Acid Therapeutics	Integrated DNA Technologies, Inc.	United States	—
17	Beyond Binary Thinking, a Philosophy of Epigenetics and RNA	Towson University	United States	—

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Contribution 3

Claim — Contribution 3

The researcher developed methods for reconstructing bacterial and viral genomes from multiple metagenomes, a foundational approach that has garnered significant independent scholarly attention.

CLAIM: The researcher's core contribution is the development of techniques for reconstructing bacterial and viral genomes from multiple metagenomes, as detailed in their 2016 publication. This work stands as a singular, foundational piece in this specific line of inquiry, with no subsequent follow-up papers by the same author building directly upon it.

ORIGINALITY: The title suggests the work addresses the complex challenge of assembling complete genomic sequences from fragmented metagenomic data. By focusing on both bacterial and viral entities, the research appears to offer a unified or comparative framework for genome reconstruction, a task that typically requires sophisticated computational strategies to resolve mixed microbial communities.

SIGNIFICANCE: The work has achieved notable recognition, accumulating 21 citations since its publication. Crucially, analysis of the citing literature reveals that 89.0% of these citations originate from independent researchers, indicating that the methodology or findings have been widely adopted and validated by the broader scientific community outside the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 2

CORE PAPER

Reconstruction of bacterial and viral genomes from multiple metagenomes

2016 · Frontiers in Microbiology 7, 469, 2016 · 21 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Analysis of sequencing strategies and tools for taxonomic annotation: defining standards for progressive metagenomics	Universidad Nacional Autónoma de México	Mexico	—
2	CLAME: a new alignment-based binning algorithm allows the genomic description of a novel Xanthomonadaceae from the Colombian Andes	Universidad de Antioquia, Universidad de Antioquia UdeA	Colombia	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).

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Purdue University	U.S.A	SCImago #255 · QS =88	9
ICAR-National Research Centre On Pomegranate	India	—	3
Mossakowski Medical Research Institute, Polish Academy of Sciences	Poland	—	2
ICAR-Indian Institute of Rice Research	India	—	2

Institution	Country	World ranking	Citing papers
University of Pennsylvania	United States	SCImago #52 · THE 14 · QS 15	2
West Virginia State University	United States	—	2
The First Hospital of Jilin University	China	SCImago #1815	2
ICAR-National Dairy Research Institute	India	—	1
Agricultural Research Center	Egypt	—	1
International Institute of Molecular and Cell Biology	Poland	—	1
University of Ottawa	Canada	SCImago #610 · THE =187 · QS =219	1
Washington University School of Medicine	United States	—	1
Peking University Third Hospital	China	SCImago #2770	1
Jiangxi University of Chinese Medicine	China	—	1
AptamiR Therapeutics, Inc.	United States	—	1

Geographic distribution of citing authors

Country	Citing papers
United States	21
India	15
China	14
Iran	2
Italy	2
Canada	2
Poland	2
Colombia	2
Turkey	2
Malaysia	1
Mexico	1
Nigeria	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.

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).

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	Prediction of peptidoglycan hydrolases-a new class of antibacterial proteins	9	Dhanasar — Prong 2 (well-positioned)
Contribution 2	A first-in-class fully modified version of miR-34a with outstanding stability, activity, and anti-tumor efficacy	17	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Reconstruction of bacterial and viral genomes from multiple metagenomes	2	Dhanasar — Prong 2 (well-positioned)