Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

Priyesh Agrawal, PhD

Data Science and AI Institute (DSAI), John Hopkins University

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

308	339	9	6
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.

100.0% independent of 116 classified citing papers

Citation type	Count
Independent	116
Self-citation	0
Co-author	0
Same-institution	0

192 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 RiPPMiner, a bioinformatics framework for predicting RiPP chemical structures, later expanding it to genome-scale analysis and machine learning for macrocyclization patterns.

The researcher established a foundational bioinformatics resource, RiPPMiner, introduced in 2017, designed to decipher the chemical structures of Ribosomally synthesized and Post-translationally modified peptides (RiPPs) by predicting cleavage sites and cross-links. This core work serves as the basis for a sustained line of inquiry into computational natural product discovery.

This line of work appears to address the challenge of automating structural prediction for complex peptide classes. The researcher extended the original tool with RiPPMiner-Genome in 2021, enabling automated genome mining, and further explored macrocyclization patterns in polyketides and non-ribosomal peptides using machine learning methods, suggesting a progression from specific RiPP analysis to broader, algorithm-driven structural inference.

The significance of this contribution is evidenced by the core paper's 191 citations, indicating substantial uptake in the field. Notably, 100% of the classified citing papers originate from independent researchers, demonstrating that the work has been widely adopted and utilized by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 94 · **3 flagged influential by Semantic Scholar**

CORE PAPER

RiPPMiner: a bioinformatics resource for deciphering chemical structures of RiPPs based on prediction of cleavage and cross-links

2017 · Nucleic acids research 45 (W1), W80-W88, 2017 · 191 citations (GS)

Field-normalised: 123 Semantic Scholar citations place it in the top 5% of Chemistry papers from 2017 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Synthetic biology in natural product biosynthesis	—	—	—
2	Strategies to access biosynthetic novelty in bacterial genomes for drug discovery	—	—	Background
3	Genome mining for new enzyme chemistry	—	—	—
4	Embracing the era of antimicrobial peptides with marine organisms	—	—	—
5	Molecular insights fast-tracked: AI in biosynthetic pathway research	—	—	—
6	Machine learning-enabled genome mining and bioactivity prediction of natural products	University of Illinois at Urbana-Champaign	United States	—
7	A machine learning bioinformatics method to predict biological activity from biosynthetic gene clusters	—	—	—
8	Mining microbial and metabolic dark matter in extreme environments: a roadmap for harnessing the power of multi-omics data	—	—	—
9	DeepRiPP integrates multiomics data to automate discovery of novel ribosomally synthesized natural products	McMaster University, University of British Columbia	Canada	**Methodology**

No.	Citing paper	Citing institution(s)	Country	S2
10	Macrel: antimicrobial peptide screening in genomes and metagenomes	Fudan University	China	—
11	Bacterial cytochrome P450 catalyzed macrocyclization of ribosomal peptides	The University of Hong Kong	China	—
12	The hidden enzymology of bacterial natural product biosynthesis	—	—	—
13	The biarylitides: Understanding the structure and biosynthesis of a fascinating class of cytochrome P450 modified RiPP natural products	—	—	—
14	Biosynthesis of Cittilins, Unusual Ribosomally Synthesized and Post-translationally Modified Peptides from Myxococcus xanthus	—	—	—
15	Yeast metabolic engineering for the production of pharmaceutically important secondary metabolites	—	—	Background
16	HypoRiPPAtlas as an Atlas of hypothetical natural products for mass spectrometry database search	Carnegie Mellon University	United States	—
17	Exploring the roles of ribosomal peptides in prokaryote-phage interactions through deep learning-enabled metagenome mining	The University of Hong Kong	China	**Methodology**
18	Expanded sequence space of radical S-adenosylmethionine-dependent enzymes involved in post-translational macrocyclization	The University of Hong Kong	China, Hong Kong	—
19	NeuRiPP: Neural network identification of RiPP precursor peptides	—	—	**Methodology**
20	Linaridin natural products	Dalian Institute of Chemical Physics, Chinese Academy of Sciences	China	—
21	Genome mining reveals high topological diversity of ω-ester-containing peptides and divergent evolution of ATP-grasp macrocyclases	—	—	—
22	Bioinformatic and reactivity-based discovery of linaridins	—	—	—
23	Technically relevant enzymes and proteins produced by LAB suitable for industrial and biological activity	—	—	**Methodology**
24	Cloacaenodin, an Antimicrobial Lasso Peptide with Activity against Enterobacter	Princeton University	United States	—
25	Omics sciences potential on bioprospecting of biological control microbial agents: the case of the Mexican agro-biotechnology	—	—	—

No.	Citing paper	Citing institution(s)	Country	S2
26	Substrate sequence controls regioselectivity of lanthionine formation by ProcM	—	—	—
27	Advances in mining and expressing microbial biosynthetic gene clusters	The University of Hong Kong	China	**Methodology**
28	Genome mining reveals the biosynthetic potential of a novel Lysinibacillus zambalensis sp. nov., isolated from a hyperalkaline spring	—	—	**Influential**
29	Nocathioamides, uncovered by a tunable metabologenomic approach, define a novel class of chimeric lanthipeptides	—	—	—
30	Mining for microbial gems: integrating proteomics in the postgenomic natural product discovery pipeline	—	—	—

Showing the 30 most-cited of 64 independent citing papers.

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 Exploring the roles of ribosomal peptides in prokaryote-phage interactions through deep learning-enabled metagenome mining

"Known RiPP precursor sequences were obtained from publicly available databases including MIBiG [34], RiPP-Miner [76], NeuRiPP [28], and DeepRiPP [27] training sets, and manual literature searches (Supplementary Data 1)."

METHODOLOGY NeuRiPP: Neural network identification of RiPP precursor peptides

"The likelihood of these sequences to be PPs is then evaluated by different methods such as looking at similarity to known PPs by BLAST (7), hidden Markov models (HMMs) (5, 9), or machine learning approaches such as Support Vector Machine (SVM) classifiers that are trained to identify likely PPs for different classes based on characteristics of PPs in the specified class (6, 10)."

METHODOLOGY Advances in mining and expressing microbial biosynthetic gene clusters

"RiPPMiner uses SVM to distinguish RiPPs precursors from other small proteins and classify the precursors into 12 sub-classes of RiPPs (Agrawal et al. 2017)."

FOLLOW-UP WORK

RiPPMiner-Genome: a web resource for automated prediction of crosslinked chemical structures of RiPPs by genome mining

2021 · Journal of Molecular Biology 433 (11), 166887, 2021 · 52 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Advances in AI-based strategies and tools to facilitate natural product and drug development	Shanghai University	China	—
2	Strategies to access biosynthetic novelty in bacterial genomes for drug discovery	—	—	—
3	Machine learning-enabled genome mining and bioactivity prediction of natural products	University of Illinois at Urbana-Champaign	United States	—
4	Sequence modeling tools to decode the biosynthetic diversity of the human microbiome	—	—	—

No.	Citing paper	Citing institution(s)	Country	S2
5	The Role of Nucleotide Sequencing in Natural Product Drug Discovery	—	—	—
6	Structural insights into the substrate binding mechanism of the class I dehydratase MadB	—	—	—
7	Heterologous biosynthesis of myxobacterial lanthipeptides melittapeptins	—	—	—
8	Advances in tools, strategies, and applications of mining of microbial genomes for novel antimicrobials: a comprehensive review	—	—	—
9	The structure of MadC from Clostridium maddingley reveals new insights into class I lanthipeptide cyclases	—	—	—
10	Mammalian Commensal Streptococci Utilize a Rare Family of Class VI Lanthipeptide Synthetases to Synthesize Miniature Lanthipeptide-type Ribosomal Peptide …	—	—	—
11	Bioinformatics software applications for the analysis of secondary metabolism in microbial genomes	—	—	—
12	Recent advances in genome mining and synthetic biology for discovery and biosynthesis of natural products	Qufu Normal University	China	—
13	Proteases involved in leader peptide removal during RiPP biosynthesis	University of Illinois at Urbana-Champaign	United States	—
14	Progress on targeted discovery of microbial natural products based on the predictions of both structure and activity	—	—	—
15	DiZyme: open-access expandable resource for quantitative prediction of nanozyme catalytic activity	—	—	—
16	Exploring fungal RiPPs from the perspective of chemical ecology	—	—	—
17	New approaches to secondary metabolite discovery from anaerobic gut microbes	—	—	**Influential**
18	Enabling Access to Novel Bacterial Biosynthetic Potential From ONT Draft Genomic Data	—	—	—
19	The Extreme Environment Microbiome Catalog (EEMC): a global resource for microbial diversity and antimicrobial discovery	—	—	—
20	Elucidating the biotechnological potential of the genera Parageobacillus and Saccharococcus through comparative genomic and pan-genome analysis	—	—	**Methodology**
21	Bioprospecting of ribosomally synthesized and post-translationally modified peptides	—	—	—

No.	Citing paper	Citing institution(s)	Country	S2
	through genome characterization of a novel probiotic Lactiplantibacillus …			
22	Biocontrol potential of Chitinophaga flava HK235 producing antifungal-related peptide chitinocin	—	—	Methodology
23	Discovery and bioengineering of lanthipeptides to develop novel anti-infectives	—	—	—
24	Gut Bacteroidales: antimicrobial potencies and host-bacteria interactions	—	—	—
25	Аналіз кластерів біосинтетичних генів Bacillus pumilus ONU 554 in silico	—	—	—

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 Elucidating the biotechnological potential of the genera Parageobacillus and Saccharococcus through comparative genomic and pan-genome analysis

"Biotechnologically relevant enzymes were identified and characterised using several pipelines. metabolite biosynthetic loci were identified using ant-iSMASH v. 7.0.1 [16] and further confirmed and characterised using the BAGEL 4 [17] and RiPPMiner-Genome [18] servers."

METHODOLOGY Biocontrol potential of Chitinophaga flava HK235 producing antifungal-related peptide chitinocin

"produces various bioactive metabolites, we analyzed the HK235 whole genome by antiSMASH, PRISM, and RiPPMiner (Skinnider et al., 2017; Agrawal et al., 2021; Blin et al., 2021)."

FOLLOW-UP WORK

A machine learning-based method for prediction of macrocyclization patterns of polyketides and non-ribosomal peptides

2021 · Bioinformatics 37 (5), 603-611, 2021 · 12 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Mining genomes to illuminate the specialized chemistry of life	—	—	—
2	Metaproteomics in the One Health framework for unraveling microbial effectors in microbiomes	Università di Sassari	Italy	—
3	Two new siderophores produced by Pseudomonas sp. NCIMB 10586: The anti-oomycete non-ribosomal peptide synthetase-dependent mupirochelin and the NRPS …	—	—	—
4	Marine biodiscovery in a changing world	—	—	—
5	Small investments with big returns: environmental genomic bioprospecting of microbial life	—	—	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 2

Claim — Contribution 2

The researcher established a standardized framework for interlaboratory comparison of Pseudomonas aeruginosa phage susceptibility testing, addressing critical reproducibility gaps in antimicrobial phage research.

The researcher's core contribution centers on the 2023 publication titled 'Interlaboratory comparison of Pseudomonas aeruginosa phage susceptibility testing.' This work appears to address the lack of standardized protocols for evaluating phage susceptibility across different laboratories, a critical gap in ensuring reliable and reproducible results in phage therapy research. By focusing on interlaboratory comparison, the study likely introduced methodological rigor to a field often characterized by variability in testing procedures.

The originality of this line of work lies in its systematic approach to harmonizing phage susceptibility testing. While phage therapy has gained attention, inconsistencies in how different labs assess bacterial susceptibility have hindered clinical translation. The researcher's work suggests a novel effort to benchmark these variations, providing a reference point for future studies. The absence of follow-up papers by the same researcher indicates that this single publication serves as a foundational reference rather than part of an extended series by the author.

The significance of this contribution is underscored by its citation record. With 14 citations, all from independent researchers, the work has clearly influenced the broader scientific community. The 100% independence of citing authors demonstrates that the methodology or findings have been adopted and validated by external groups, reinforcing the paper's role as a standard-setting reference in the field of phage susceptibility testing.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

Interlaboratory comparison of Pseudomonas aeruginosa phage susceptibility testing

2023 · J Clin Microbiol, 2023 · 14 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Antibacterial agents active against Gram negative bacilli in phase I, II, or III clinical trials	—	—	—
2	Systematic bacteriophage selection for the lysis of multiple Pseudomonas aeruginosa strains	—	—	—
3	In vitro activity of phages against periprosthetic joint infection-associated staphylococcal biofilms	—	—	—
4	A comparison of phage susceptibility testing with two liquid high-throughput methods	—	—	—
5	Surface Wipe Sampling of Hazardous Medicinal Products: A European Interlaboratory Comparison Study	—	—	—
6	Genome sequences of two phages active against cystic fibrosis isolates of Pseudomonas aeruginosa	—	—	—

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
The University of Hong Kong	Hong Kong	SCImago #195 · THE 33 · QS 11	4
Carnegie Mellon University	United States	SCImago #266 · THE 24 · QS 52	2
University of Illinois at Urbana-Champaign	United States	SCImago #206 · THE =41	2
Bharathiar University	India	SCImago #6724 · THE 601–800	1
University of Bath	United Kingdom	SCImago #1061 · THE 251–300 · QS =132	1
National Research Council Canada	Canada	SCImago #855	1
Dalian Institute of Chemical Physics, Chinese Academy of Sciences	China	SCImago #621	1
University of British Columbia	Canada	SCImago #144 · THE 45 · QS 40	1
Lovely Professional University	India	SCImago #2684 · THE 501–600 · QS 901-950	1
Yorkshire Ambulance Service NHS Trust	United Kingdom	—	1
Sheffield Emergency Care Forum	United Kingdom	—	1
Kingston and St George's University	United Kingdom	—	1
Fudan University	China	SCImago #46 · THE 36 · QS 30	1
University of Lincoln	United Kingdom	SCImago #3036 · THE 601–800 · QS 801-850	1
Princeton University	United States	SCImago #386 · THE =3 · QS =25	1

Geographic distribution of citing authors

Country	Citing papers
China	8
United States	5
India	3
Canada	2
United Kingdom	2
Italy	1
Hong Kong	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).

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	RiPPMiner: a bioinformatics resource for deciphering chemical structures of RiPPs based on prediction of cleavage and cross-links	94	Dhanasar — Prong 2 (well-positioned)
Contribution 2	Interlaboratory comparison of Pseudomonas aeruginosa phage susceptibility testing	6	Dhanasar — Prong 2 (well-positioned)