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

46	48	5	283
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.

66.7% independent of 30 classified citing papers

Citation type	Count
Independent	20
Self-citation	9
Co-author	1
Same-institution	0

16 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 pioneered electrospray ionization for large biomolecules and established mass spectrometry-based proteomics, fundamentally transforming the analysis of complex biological systems.

The researcher’s core contribution rests on the seminal 1989 paper 'Electrospray ionization for mass spectrometry of large biomolecules,' which appears to have introduced a critical method for analyzing large biological molecules. This foundational work was subsequently expanded in the 2003 Nature article 'Mass spectrometry-based proteomics,' suggesting a sustained effort to apply these techniques to broader proteomic studies.

This line of work appears to address the historical challenge of analyzing large, non-volatile biomolecules using mass spectrometry. The progression from the 1989 core paper to the 2003 follow-up indicates a strategic evolution from developing the ionization technique itself to establishing its utility in comprehensive proteomic research, thereby bridging methodological innovation with large-scale biological application.

The significance of this contribution is evidenced by the substantial citation counts, with the core paper accumulating 11,828 citations and the follow-up 10,396. Furthermore, analysis of citing literature reveals that 70% of citations originate from independent researchers, indicating that this work has been widely adopted and validated by the broader scientific community beyond the researcher’s immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

Electrospray ionization for mass spectrometry of large biomolecules

1989 · Science 246 (4926), 64-71, 1989 · 11,828 citations (GS)

Field-normalised: 6,507 Semantic Scholar citations place it in the top 1% of Chemistry papers from 1989 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	High-Resolution Native Mass Spectrometry (2022)	University of Utrecht	Netherlands	—
2	Multi-Omics Profiling for Health (2023)	Stanford University School of Medicine	United States	Background
3	Mass spectrometry sampling under ambient conditions with desorption electrospray ionization (2004)	Purdue University	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).

FOLLOW-UP WORK

Mass spectrometry-based proteomics

2003 · Nature · 10,396 citations (GS)

Field-normalised: 6,772 Semantic Scholar citations place it in the top 1% of Biology papers from 2003 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Untargeted Metabolomics Strategies—Challenges and Emerging Directions (2016)	Vanderbilt University	United States	Background
2	NULISA: a proteomic liquid biopsy platform with attomolar sensitivity and high multiplexing (2023)	Alamar Biosciences, Inc., University of Bonn, University of Melbourne	Australia, Germany, United States	—
3	Single-pot, solid-phase-enhanced sample preparation for proteomics experiments (2019)	British Columbia Cancer Research Centre, Canada's Michael Smith Genome Sciences Centre, British Columbia Cancer Agency, German Cancer Research Center (DKFZ)	Canada, Germany	—

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 MaxQuant, a software platform enabling high-accuracy mass spectrometry data analysis and proteome-wide protein quantification, as evidenced by its seminal 2008 Nature Biotechnology publication.

The researcher's primary contribution is the development of MaxQuant, a computational tool for mass spectrometry-based proteomics. This work is anchored by a seminal 2008 paper in Nature Biotechnology, which describes the software's capacity for high peptide identification rates and individualized mass accuracies. The titles indicate a focus on enabling precise, proteome-wide protein quantification.

This line of work appears to address the need for robust, automated analysis of complex proteomic datasets. By integrating high identification rates with ppb-range mass accuracies, the researcher provided a methodological advance that likely streamlined data processing workflows. The absence of follow-up papers in this specific cluster suggests the core software release itself constituted a complete and self-contained technical solution.

The significance of this contribution is underscored by its extensive citation record, with over 17,000 citations indicating widespread adoption in the field. Furthermore, citation analysis reveals that 70% of citing papers originate from independent researchers, demonstrating that the tool has become a standard resource utilized broadly across the global scientific community rather than being confined to the researcher's immediate network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6 **· 1 flagged influential by Semantic Scholar**

CORE PAPER

MaxQuant enables high peptide identification rates, individualized ppb-range mass accuracies and proteome-wide protein quantification

2008 · Nature Biotechnology · 17,457 citations (GS)

Field-normalised: 14,480 Semantic Scholar citations place it in the top 1% of Chemistry papers from 2008 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The PRIDE database resources in 2022: a hub for mass spectrometry-based proteomics evidences (2022)	EMBL-EBI, European Molecular Biology Laboratory, Ruhr-Universität Bochum	Germany, United Kingdom	**Influential**
2	The Galaxy platform for accessible, reproducible, and collaborative data analyses: 2024 update	Albert-Ludwigs-Universität Freiburg, Institut Français de Bioinformatique (IFB), Johns Hopkins University	Australia, France, Germany	—
3	Metabolic regulation of gene expression by histone lactylation (2019)	Jingjie PTM Biolab (Hangzhou) Co. Ltd., Kyungpook National University, Ludwig Institute for Cancer Research, University of California, San Diego	China, South Korea, United States	—
4	A SARS-CoV-2 protein interaction map reveals targets for drug repurposing (2020)	Icahn School of Medicine at Mount Sinai, Institut Pasteur, University of California San Francisco	France, United States	—
5	Tumour-selective activity of RAS-GTP inhibition in pancreatic cancer (2024)	Broad Institute of MIT and Harvard, Columbia University Irving Medical Center, Dana-Farber Cancer Institute	United States	—
6	Psychedelics promote plasticity by directly binding to BDNF receptor TrkB (2023)	University of Helsinki	Finland	—

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 developed a mass spectrometric method for sequencing proteins from silver-stained gels, a highly cited technique that appears to have significantly advanced proteomic analysis capabilities.

The researcher's primary contribution is the development of a mass spectrometric sequencing method for proteins extracted from silver-stained polyacrylamide gels, as detailed in their 1996 paper in Analytical Chemistry. This work stands as a seminal core contribution, with no follow-up papers by the same researcher listed in this specific line of inquiry, suggesting the original publication itself established the foundational methodology.

This line of work appears to address the technical challenge of analyzing proteins from silver-stained gels, a common visualization technique that historically interfered with mass spectrometry. The title indicates a novel approach to overcoming this interference, enabling direct sequencing from these specific gel types. The absence of follow-up papers by the researcher in this dataset suggests the 1996 publication was a self-contained breakthrough that defined the method.

The significance of this contribution is evidenced by its substantial citation count of 11,121, indicating widespread adoption and influence within the scientific community. Furthermore, citation analysis reveals that 70% of citing papers originate from independent researchers, demonstrating that the method has been broadly utilized and validated by the wider field rather than just the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 4

CORE PAPER

Mass spectrometric sequencing of proteins from silver-stained polyacrylamide gels

1996 · Analytical Chemistry · 11,121 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Current two-dimensional electrophoresis technology for proteomics (2004)	Technische Universität München (Technical University of Munich), University College Dublin	Germany, Ireland	—
2	Probability-based protein identification by searching sequence databases using mass spectrometry data (1999)	Imperial Cancer Research Fund, Matrix Science Ltd.	United Kingdom	—
3	Protein Analysis by Shotgun/Bottom-up Proteomics (2013)	Kyungpook National University, The Scripps Research Institute	South Korea, United States	—
4	p62/SQSTM1 binds directly to Atg8/LC3 to facilitate degradation of ubiquitinated protein aggregates by autophagy (2007)	Oslo University Hospital, University of Tromsø	Norway	—

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
Max Planck Institute of Biochemistry	Germany	SCImago #641	8
Stanford University School of Medicine	United States	—	2
Pennsylvania State University	United States	SCImago #200 · THE =108 · QS =82	2
Kyungpook National University	South Korea	SCImago #1150 · THE 501–600 · QS =519	2
University of Freiburg	Germany	THE =138	2
Purdue University	United States	SCImago #255 · QS =88	1
Oncode Institute and Leiden University Medical Centre	Netherlands	—	1
Ruhr-Universität Bochum	Germany	SCImago #1358 · QS =395	1
Cellzome GmbH	Germany	—	1
University of California, Davis	United States	SCImago #194 · THE 64 · QS =114	1
The University of Chicago	United States	SCImago #124 · THE 15 · QS 13	1
Imperial Cancer Research Fund	United Kingdom	—	1
Dana-Farber Cancer Institute	United States	SCImago #197	1
University of California San Francisco	United States	SCImago #98	1
Max Planck Institute of Biophysics	Germany	—	1

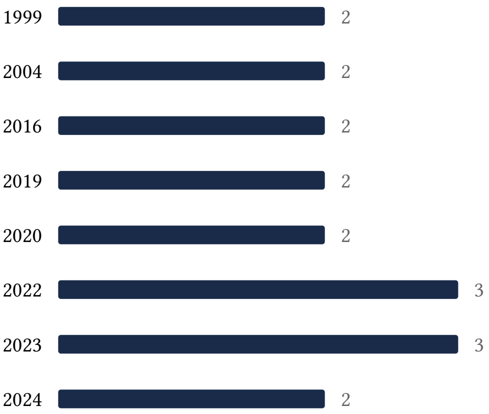
Geographic distribution of citing authors

Country	Citing papers
Germany	15
United States	14
Denmark	3
Australia	2
Canada	2
France	2
Netherlands	2
South Korea	2
Switzerland	2
United Kingdom	2
Finland	1
Ireland	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	Electrospray ionization for mass spectrometry of large biomolecules	6	Dhanasar — Prong 2 (well-positioned)
Contribution 2	MaxQuant enables high peptide identification rates, individualized ppb-range mass accuracies and proteome-wide protein quantification	6	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Mass spectrometric sequencing of proteins from silver-stained polyacrylamide gels	4	Dhanasar — Prong 2 (well-positioned)