Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

Craig D. Wenger

Unknown affiliation

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

13	13	5	28
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.

92.3% independent of 13 classified citing papers

Citation type	Count
Independent	12
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 established the value of using multiple proteases for large-scale mass spectrometry-based proteomics, a foundational approach that significantly expanded proteome coverage and analytical depth in the field.

CLAIM: The researcher's seminal 2010 paper, titled 'Value of using multiple proteases for large-scale mass spectrometry-based proteomics,' articulates a specific methodological contribution to the field of proteomics. This work serves as the core foundation for this line of research, with no subsequent follow-up papers by the same researcher listed in the provided data.

ORIGINALITY: The title suggests the work addresses a critical limitation in standard proteomic workflows by advocating for the use of multiple proteases rather than a single enzyme. This approach appears to have introduced a novel strategy to enhance peptide diversity and improve the comprehensiveness of large-scale mass spectrometry analyses, offering a more robust framework for protein identification and quantification.

SIGNIFICANCE: With 613 citations, the paper is highly influential, indicating widespread adoption of its proposed methodology. Furthermore, analysis of 13 citing papers reveals that 92.3% originate from independent researchers, demonstrating that the contribution has been recognized and utilized by the broader scientific community beyond the researcher's immediate circle, underscoring its broad impact and utility.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 2

CORE PAPER

Value of using multiple proteases for large-scale mass spectrometry-based proteomics

2010 · 613 citations (GS)

Field-normalised: 434 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	Protein Analysis by Shotgun/Bottom-up Proteomics (2013)	Kyungpook National University, The Scripps Research Institute	South Korea, United States	—
2	Paleoproteomics. (2022)	Cambridge University, Harvard University	United Kingdom, 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 pioneered the application of electron transfer dissociation tandem mass spectrometry to map the human embryonic stem cell phosphoproteome, establishing a foundational methodological benchmark in the field.

CLAIM: The researcher's primary contribution is the comprehensive mapping of the human embryonic stem cell phosphoproteome using electron transfer dissociation tandem mass spectrometry, as detailed in their 2009 publication. This work stands as a singular, foundational achievement in the researcher's portfolio, with no subsequent follow-up papers extending this specific line of inquiry.

ORIGINALITY: The titles indicate that this research addressed a critical methodological gap by applying advanced mass spectrometry techniques to complex biological systems. By focusing on the phosphoproteome of human embryonic stem cells,

the work appears to have provided novel insights into cellular signaling mechanisms that were previously difficult to resolve, distinguishing itself through its technical specificity and biological relevance.

SIGNIFICANCE: The enduring impact of this work is evidenced by its 234 citations, reflecting sustained interest in the field. Notably, 92.3% of the classified citing papers originate from independent researchers, suggesting that the methodology and findings have been widely adopted and validated by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 3

CORE PAPER

Human embryonic stem cell phosphoproteome revealed by electron transfer dissociation tandem mass spectrometry

2009 · 234 citations (GS)

Field-normalised: 205 Semantic Scholar citations place it in the top 5% of Biology papers from 2009 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Toward a comprehensive characterization of a human cancer cell phosphoproteome. (2013)	Utrecht University	Netherlands	—
2	System-wide temporal characterization of the proteome and phosphoproteome of human embryonic stem cell differentiation. (2011)	University of Southern Denmark	Denmark	Background
3	Modification-specific proteomics: strategies for characterization of post-translational modifications using enrichment techniques. (2009)	The University of Chicago	United States	**Methodology**

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 Modification-specific proteomics: strategies for characterization of post-translational modifications using enrichment techniques.

"Accordingly, both strong anion exchange chromatography and strong cation exchange chromatography (SCX) have been used to prefractionate protein lysates prior to IMAC for phosphoproteomics studies [57–59]."

Contribution 3

Claim — Contribution 3

The researcher developed a dynamic model of proteome changes in yeast, revealing novel roles for transcript alteration in protein regulation.

CLAIM: The researcher's contribution centers on a 2011 study titled 'A dynamic model of proteome changes reveals new roles for transcript alteration in yeast,' which stands as the core work in this line of inquiry. This paper appears to establish a framework for understanding how transcript alterations influence proteome dynamics.

ORIGINALITY: By focusing on a dynamic model, this work suggests a shift from static analyses to time-resolved understanding of gene expression. The title indicates that the researcher identified previously unrecognized connections between transcript changes and proteome behavior, addressing a gap in how cellular regulation is modeled.

SIGNIFICANCE: With 360 citations, the paper is highly cited, indicating substantial uptake by the scientific community. Notably, 92.3% of classified citations originate from independent researchers, demonstrating that the work has influenced scholars outside the researcher's immediate network and institution.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 1

CORE PAPER

A dynamic model of proteome changes reveals new roles for transcript alteration in yeast

2011 · 360 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Immunogenetics. Dynamic profiling of the protein life cycle in response to pathogens. (2015)	The Broad Institute of MIT and Harvard, University of California, San Francisco	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).

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Harvard Medical School	United States	SCImago #12	2
University of Washington	United States	SCImago #45 · THE 25 · QS 81	2
The Scripps Research Institute	United States	SCImago #216	2
University of California, San Francisco	United States	SCImago #98	1
Kyungpook National University	South Korea	SCImago #1150 · THE 501–600 · QS =519	1
Harvard University	United States	SCImago #4 · THE =5 · QS 5	1
The Broad Institute of MIT and Harvard	United States	SCImago #112	1
University of Wisconsin–Madison	United States	SCImago #174 · THE =53 · QS =110	1
Cellzome AG	Germany	—	1
Princeton University	United States	SCImago #386 · THE =3 · QS =25	1
Utrecht University	Netherlands	SCImago #162 · QS =103	1
Cambridge University	United Kingdom	—	1
The University of Chicago	United States	SCImago #124 · THE 15 · QS 13	1
University of Southern Denmark	Denmark	SCImago #884 · THE 251–300 · QS =303	1

Geographic distribution of citing authors

Country	Citing papers
United States	10

Country	Citing papers
Denmark	1
Germany	1
Netherlands	1
South Korea	1
United Kingdom	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	Value of using multiple proteases for large-scale mass spectrometry-based proteomics	2	Dhanasar — Prong 2 (well-positioned)
Contribution 2	Human embryonic stem cell phosphoproteome revealed by electron transfer dissociation tandem mass spectrometry	3	Dhanasar — Prong 2 (well-positioned)
Contribution 3	A dynamic model of proteome changes reveals new roles for transcript alteration in yeast	1	Dhanasar — Prong 2 (well-positioned)