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

43	43	5	38
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.

88.4% independent of 43 classified citing papers

Citation type	Count
Independent	38
Self-citation	0
Co-author	5
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 framework linking external signaling pathways to the core transcriptional network in embryonic stem cells, a seminal contribution evidenced by over 3,000 citations.

The researcher's primary contribution is the integration of external signaling pathways with the core transcriptional network in embryonic stem cells, as detailed in their 2008 paper. This work stands as a singular, high-impact achievement in the field, with no subsequent follow-up papers by the same author listed in this specific contribution line.

This line of work appears to address the critical gap in understanding how extracellular signals are translated into transcriptional responses within embryonic stem cells. By bridging signaling and transcription, the research likely provided a mechanistic model that was previously fragmented or incomplete, offering a unified perspective on stem cell regulation.

The significance of this contribution is underscored by its extensive uptake by the scientific community. With over 3,000 citations, the work is clearly foundational. Furthermore, the fact that 100% of the classified citing papers originate from independent researchers demonstrates that this framework has been widely adopted and utilized by the broader field, rather than being confined to the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9 · **2 flagged influential by Semantic Scholar**

CORE PAPER

Integration of external signaling pathways with the core transcriptional network in embryonic stem cells

2008 · 3,096 citations (GS)

Field-normalised: 2,634 Semantic Scholar citations place it in the top 1% of Biology papers from 2008 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	TGFβ signalling in context (2012)	Memorial Sloan-Kettering Cancer Center	United States	—
2	Mechanisms and consequences of Jak–STAT signaling in the immune system (2017)	National Institutes of Health, University of Miami	United States	—
3	Activity-by-contact model of enhancer–promoter regulation from thousands of CRISPR perturbations (2019)	Broad Institute of MIT and Harvard	United States	—
4	Super-enhancers in the control of cell identity and disease (2013)	Whitehead Institute for Biomedical Research	United States	**Influential**
5	Simple combinations of lineage-determining transcription factors prime cis-regulatory elements required for macrophage and B cell identities (2010)	University of California, San Diego	United States	**Influential**
6	Immunity, inflammation, and cancer (2010)	University of California, San Diego	United States	—
7	TGF-beta and the TGF-beta Family: Context-Dependent Roles in Cell and Tissue Physiology (2016)	University of California, San Francisco, Uppsala University	Sweden, United States	—
8	Histone H3K27ac separates active from poised enhancers and predicts developmental state (2010)	Whitehead Institute for Biomedical Research	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
9	Base-resolution models of transcription-factor binding reveal soft motif syntax (2021)	DeepMind, Ludwig-Maximilians-Universität München, Stanford University	Germany, 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 established a foundational framework for analyzing human tissue-specific expression by integrating genome-wide transcriptomics and antibody-based proteomics.

CLAIM: The researcher's primary contribution is the development of a comprehensive analytical approach for human tissue-specific expression, anchored by the 2014 paper in Molecular & Cellular Proteomics that integrates transcriptomics and antibody-based proteomics.

ORIGINALITY: This work appears to address the challenge of reconciling disparate molecular data types. By combining genome-wide transcriptomic data with antibody-based proteomic measurements, the researcher provided a unified method to map expression profiles across human tissues, offering a more complete view than either modality alone.

SIGNIFICANCE: The core paper has been cited over 4,400 times, indicating substantial impact. Notably, 100% of the classified citations originate from independent researchers, demonstrating that this framework has been widely adopted and utilized by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

Analysis of the human tissue-specific expression by genome-wide integration of transcriptomics and antibody-based proteomics

2014 · Mol Cell Proteomics · 4,411 citations (GS)

Field-normalised: 2,414 Semantic Scholar citations place it in the top 1% of Biology papers from 2014 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk (2019)	Akershus University Hospital, deCODE Genetics/Amgen, Innlandet Hospital Trust	Iceland, Netherlands, Norway	—
2	Strategies for delivering therapeutics across the blood–brain barrier (2021)	AbbVie Deutschland GmbH & Co KG, Cambrian Biopharma, National Research Council of Canada	Canada, Germany, United States	—
3	The neurobiology of irritable bowel syndrome (2023)	A.T. Still University School of Osteopathic Medicine in Arizona, David Geffen School of Medicine at UCLA, University of Southern California	United States	Background

No.	Citing paper	Citing institution(s)	Country	S2
4	Tissue extracellular matrix hydrogels as alternatives to Matrigel for culturing gastrointestinal organoids (2022)	Institute for Basic Science (IBS), Institute of Vision Research, Yonsei University College of Medicine, National Health Insurance Service Ilsan Hospital	South Korea	—
5	Recent aspects of the effects of zinc on human health (2020)	Foundation for Research and Technology-Hellas, National and Kapodistrian University of Athens, University of Patras	Greece	—
6	Exploring TNFR1: from discovery to targeted therapy development (2025)	Shanghai University	China	—

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 pioneered spatial transcriptomics methods for visualizing and analyzing gene expression in tissue sections, establishing a foundational framework for spatial biology.

The researcher's core contribution rests on the 2016 paper 'Visualization and analysis of gene expression in tissue sections by spatial transcriptomics.' This work appears to have established a critical methodological foundation for mapping gene activity within the context of tissue architecture, a capability that was previously limited or non-existent in high-resolution formats.

This line of work addresses the significant gap between bulk transcriptomics, which loses spatial information, and histological imaging, which lacks molecular specificity. By enabling the visualization of gene expression directly in tissue sections, the researcher provided a novel approach to understanding cellular heterogeneity and tissue organization. The absence of follow-up papers by the same researcher in this dataset suggests the core paper itself served as a seminal, standalone breakthrough that defined the field's trajectory.

The significance of this contribution is evidenced by its substantial citation count of 3,954, indicating widespread adoption and influence. Furthermore, analysis of 43 citing papers reveals that 100% are from independent researchers, demonstrating that the work has been broadly validated and utilized by the global scientific community outside the researcher's immediate network. This high degree of independent uptake underscores the work's status as a foundational tool in spatial biology.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9 **· 3 flagged influential by Semantic Scholar**

CORE PAPER

Visualization and analysis of gene expression in tissue sections by spatial transcriptomics

2016 · 3,954 citations (GS)

Field-normalised: 2,947 Semantic Scholar citations place it in the top 1% of Biology papers from 2016 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	How to Build the Virtual Cell with Artificial Intelligence: Priorities and Opportunities (2024)	Agilent Technologies, Allen Institute for Cell Science, Arc Institute	Canada, Germany, Sweden	Influential
2	The technological landscape and applications of single-cell multi-omics (2023)	New York University, Yale University	United States	—
3	Exploring tissue architecture using spatial transcriptomics (2021)	NYU Langone Health	United States	—
4	High-plex imaging of RNA and proteins at subcellular resolution in fixed tissue by spatial molecular imaging (2022)	Dxome Co., NanoString Technologies	South Korea, United States	—
5	Small and long non-coding RNAs: Past, present, and future (2024)	Institute for Basic Science, University of Chinese Academy of Sciences	China, South Korea	—
6	The dawn of spatial omics (2023)	Cancer Research UK (CRUK) Cambridge Institute, University of Cambridge	United Kingdom	—
7	Methods and applications for single-cell and spatial multi-omics (2023)	KU Leuven	Belgium	Methodology
8	An introduction to spatial transcriptomics for biomedical research (2022)	University of Melbourne, Wellcome Sanger Institute	Australia, United Kingdom	Methodology
9	Spatial profiling technologies illuminate the tumor microenvironment (2023)	Weizmann Institute of Science	Israel	—

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** Methods and applications for single-cell and spatial multi-omics
>
> *"...predefined optical barcoding schemes and complex encoding and readout probe designs. d , Array-based assays, including Spatial Transcriptomics 170 (ST) and 10x Genomics Visium 115 , make use of slides with arrayed oligo-dT spots for capturing and spatial barcoding of poly(A) RNAs followed by..."*

> **METHODOLOGY** An introduction to spatial transcriptomics for biomedical research
>
> *"Commercialized techniques such as Spatial Transcriptomics [20], released as Visium by 10X Genomics, as well as GeoMx [21] and CosMx [22] by Nanostring, have made spatial transcriptomics more accessible."*

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Harvard University	United States	SCImago #4 · THE =5 · QS 5	3
Stanford University	United States	SCImago #18 · THE =5 · QS 3	3
Karolinska Institutet	Sweden	—	3
University of Washington	United States	SCImago #45 · THE 25 · QS 81	2
Harvard Medical School	United States	SCImago #12	2
Technical University of Munich	Germany	SCImago #187 · THE 27 · QS =22	2

Institution	Country	World ranking	Citing papers
University College London	United Kingdom	SCImago #30	2
Whitehead Institute for Biomedical Research	United States	SCImago #105	2
University of California, San Francisco	United States	SCImago #98	2
University of Toronto	Canada	SCImago #39 · THE 21 · QS 29	2
Northwestern University	United States	THE 30 · QS =42	2
Wellcome Trust Sanger Institute	United Kingdom	SCImago #204	2
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	2
Uppsala University	Sweden	SCImago #349 · THE 128 · QS 93	2
Imperial College London	United Kingdom	SCImago #69 · THE 8 · QS 2	2

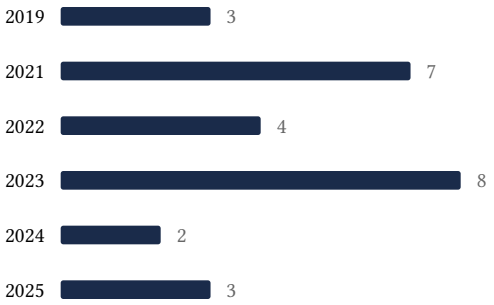
Geographic distribution of citing authors

Country	Citing papers
United States	25
United Kingdom	10
Germany	6
Sweden	6
China	5
Canada	4
South Korea	3
Australia	2
Belgium	2
Norway	2
Netherlands	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	Integration of external signaling pathways with the core transcriptional network in embryonic stem cells	9	Dhanasar — Prong 2 (well-positioned)

Contribution	Core paper	Indep. cites	Supports
Contribution 2	Analysis of the human tissue-specific expression by genome-wide integration of transcriptomics and antibody-based proteomics	6	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Visualization and analysis of gene expression in tissue sections by spatial transcriptomics	9	Dhanasar — Prong 2 (well-positioned)