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

36	36	5	91
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.

75.0% independent of 36 classified citing papers

Citation type	Count
Independent	27
Self-citation	0
Co-author	5
Same-institution	4

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 and refined ATAC-seq as a standard method for genome-wide chromatin accessibility analysis, significantly improving protocol robustness and broadening its applicability to frozen tissues.

The researcher's core contribution rests on the 2015 Current Protocols in Molecular Biology paper, 'ATAC-seq: A Method for Assaying Chromatin Accessibility Genome-Wide,' which introduced a foundational technique for mapping open chromatin. This work appears to have provided a critical methodological framework for epigenetic research, serving as the basis for subsequent advancements in the field.

This line of work addresses the need for efficient and accessible chromatin profiling methods. The titles suggest a trajectory from establishing the core assay to optimizing it; specifically, the 2017 Nature Methods paper indicates improvements that reduce background noise and enable the use of frozen tissues, thereby expanding the method's practical utility. The 2019 Nature Reviews in Genetics article further suggests the researcher played a key role in synthesizing the broader implications of chromatin accessibility for the regulatory epigenome.

The significance of this contribution is evidenced by substantial citation counts, with the core paper cited 4,183 times and the improved protocol cited 2,719 times. Furthermore, analysis of citing literature reveals that 83.3% of citations originate from independent researchers, indicating that this work has been widely adopted and integrated into the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 14

CORE PAPER

ATAC-seq: A Method for Assaying Chromatin Accessibility Genome-Wide

2015 · Current Protocols in Molecular Biology · 4,183 citations (GS)

Field-normalised: 3,007 Semantic Scholar citations place it in the top 1% of Biology papers from 2015 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Transformers and genome language models (2025)	Helmholtz Munich, Lunenfeld-Tanenbaum Research Institute, University of California, San Francisco	Canada, Germany, United States	—
2	A human brain vascular atlas reveals diverse mediators of Alzheimer's risk (2022)	Icahn School of Medicine at Mount Sinai, Saarland University, Saarland University Hospital and Medical Faculty of Saarland University	Germany, United States	—
3	The dawn of spatial omics (2023)	Cancer Research UK (CRUK) Cambridge Institute, University of Cambridge	United Kingdom	**Methodology**
4	Super-enhancers include classical enhancers and facilitators to fully activate gene expression (2023)	NYU Langone Health, University of Oxford	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).

Citing-text excerpts — how the field used this work

METHODOLOGY The dawn of spatial omics

"Spatial barcodingmethods such as microfluidic barcoding and Slideseq have been combined with both Cut&Tag and ATAC-seq (assay for transposase-accessible chromatin with high-throughput sequencing) (117) for spatial profiling of open chromatin and histone modifications (77, 78, 118)."

FOLLOW-UP WORK

Chromatin accessibility and the regulatory epigenome

2019 · Nat Rev Genet · 2,057 citations (GS)

Field-normalised: 1,391 Semantic Scholar citations place it in the top 1% of Biology papers from 2019 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Enhancer selectivity in space and time: from enhancer–promoter interactions to promoter activation (2024)	Massachusetts Institute of Technology	United States	—
2	Single-cell sequencing to multi-omics: technologies and applications (2024)	Nanjing Drum Tower Hospital, Affiliated Hospital of Medical School, Nanjing University, Nanjing Drum Tower Hospital, Nanjing University, Nanjing University	China	Background
3	Artificial intelligence-based multi-omics analysis fuels cancer precision medicine (2023)	West China Hospital, Sichuan University	China	—
4	Obtaining genetics insights from deep learning via explainable artificial intelligence (2022)	BC Children's Hospital Research Institute, Simon Fraser University, University of British Columbia	Canada, United States	Background
5	Targeting epigenetic regulators as a promising avenue to overcome cancer therapy resistance (2025)	Sichuan University, Stephenson Cancer Centre, University of Oklahoma Health Sciences Center, The Second Affiliated Hospital of Chengdu Medical College, China National Nuclear Corporation 416 Hospital	China, France, 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

An improved ATAC-seq protocol reduces background and enables interrogation of frozen tissues

2017 · Nature Methods · 2,719 citations (GS)

Field-normalised: 2,072 Semantic Scholar citations place it in the top 1% of Medicine papers from 2017 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Safety, efficacy and determinants of response of allogeneic CD19-specific CAR-NK	The University of Texas MD Anderson Cancer Center	United States	**Methodology**

No.	Citing paper	Citing institution(s)	Country	S2
	cells in CD19+ B cell tumors: a phase 1/2 trial (2024)			
2	Deterministic reprogramming of neutrophils within tumors (2024)	Agency for Science, Technology and Research, A*STAR, Centro Nacional de Investigaciones Cardiovasculares Carlos III	Australia, China, France	—
3	Senescence atlas reveals an aged-like inflamed niche that blunts muscle regeneration (2023)	CNIC, Guangzhou Institutes of Biomedicine and Health, Chinese Academy of Sciences, Institute for Research in Biomedicine (IRB Barcelona)	China, Japan, Luxembourg	—
4	Osr2 functions as a biomechanical checkpoint to aggravate CD8+ T cell exhaustion in tumor (2024)	Xiamen University	China	—
5	Cross-tissue organization of the fibroblast lineage (2021)	Genentech	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).

Citing-text excerpts — how the field used this work

METHODOLOGY Safety, efficacy and determinants of response of allogeneic CD19-specific CAR-NK cells in CD19+ B cell tumors: a phase 1/2 trial

"ATAC-seq library preparation was performed at the MDACC Epigenom-ics Profiling Core following the protocol previously described 66,67 with minor modifications."

Contribution 2

Claim — Contribution 2

The researcher developed a transposition-based method for fast, sensitive epigenomic profiling of open chromatin, DNA-binding proteins, and nucleosome positions, as detailed in a seminal 2013 Nature Methods paper.

The researcher's primary contribution is the development of a novel transposition-based approach for epigenomic profiling, established in a 2013 Nature Methods paper. This work appears to address the need for faster and more sensitive techniques to map open chromatin, DNA-binding proteins, and nucleosome positions, offering a streamlined alternative to existing methodologies.

The significance of this contribution is evidenced by its substantial citation count of over 7,400, indicating widespread adoption within the scientific community. Furthermore, analysis of citing literature reveals that 83.3% of citations originate from independent researchers, suggesting that the method has become a standard tool utilized broadly across the field rather than being confined to the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7

CORE PAPER

Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position

2013 · Nat Methods · 7,401 citations (GS)

Field-normalised: 5,780 Semantic Scholar citations place it in the top 1% of Biology papers from 2013 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Gene regulatory network inference in the era of single-cell multi-omics (2023)	Altos Labs, Heidelberg University, Heidelberg University Hospital	France, Germany, United Kingdom	Methodology
2	The technological landscape and applications of single-cell multi-omics (2023)	New York University, Yale University	United States	—
3	NCBI GEO: archive for gene expression and epigenomics data sets: 23-year update (2023)	National Institutes of Health	—	—
4	Cancer epigenetics: from laboratory studies and clinical trials to precision medicine (2024)	Yichang Central People's Hospital Affiliated with China Three Gorges University, Zhuhai People's Hospital (Zhuhai Clinical Medical College of Jinan University), Zhuhai People's Hospital Zhuhai Clinical Medical College of Jinan University	China	—
5	Artificial intelligence in plant breeding (2024)	Beltsville Agricultural Research Center, Chinese Academy of Agricultural Sciences, CIMMYT	China, Kenya, Mexico	—
6	The expanding vistas of spatial transcriptomics. (2022)	Broad Institute of Harvard and MIT	United States	—
7	Trained immunity—basic concepts and contributions to immunopathology (2022)	Eindhoven University of Technology, Icahn School of Medicine at Mount Sinai, Massachusetts General Hospital	Netherlands, 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).

Citing-text excerpts — how the field used this work

METHODOLOGY Gene regulatory network inference in the era of single-cell multi-omics

"For example, the inclusion of chromatin accessibility 21 data allows to fine-tune TF–gene links by considering whether genes are open and by including CREs in the inference of GRNs."

Contribution 3

Claim — Contribution 3

The researcher established foundational principles of regulatory variation by applying single-cell chromatin accessibility analysis, a contribution recognized as seminal in the field.

The researcher's primary contribution rests on the 2015 Nature paper titled 'Single-cell chromatin accessibility reveals principles of regulatory variation.' This work appears to have introduced a critical framework for understanding how regulatory mechanisms vary at the single-cell level, leveraging chromatin accessibility data to uncover underlying biological principles.

This line of work addresses the challenge of resolving regulatory heterogeneity, which bulk methods often obscure. By focusing on single-cell resolution, the research suggests a novel approach to mapping regulatory landscapes, offering a more granular view of gene regulation than previously available through traditional bulk sequencing techniques.

The significance of this contribution is evidenced by its high citation count of 2,722, indicating widespread adoption and influence. Furthermore, citation analysis reveals that 83.3% of citing papers originate from independent researchers, demonstrating that the work has served as a foundational reference for the broader scientific community rather than just the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

Single-cell chromatin accessibility reveals principles of regulatory variation

2015 · Nature · 2,722 citations (GS)

Field-normalised: 2,021 Semantic Scholar citations place it in the top 1% of Biology papers from 2015 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Normalization and variance stabilization of single-cell RNA-seq data using regularized negative binomial regression (2019)	New York Genome Center	United States	—
2	Applications of single-cell RNA sequencing in drug discovery and development (2023)	AbbVie Inc., Boehringer Ingelheim Pharmaceuticals Inc., Bristol Myers Squibb	Belgium, France, United Kingdom	—
3	Best practices for single-cell analysis across modalities (2023)	Helmholtz Center Munich, German Research Center for Environmental Health, Helmholtz Munich, Technical University of Munich	Germany	Background
4	Dictionary learning for integrative, multimodal and scalable single-cell analysis (2023)	New York Genome Center, New York University	United States	—
5	Epigenetics-targeted drugs: current paradigms and future challenges (2024)	Liaoning Cancer Hospital & Institute, Shengjing Hospital of China Medical University, Shenyang Maternity and Child Health Hospital	China	—
6	Hexokinase 2-mediated gene expression via histone lactylation is required for hepatic stellate cell activation and liver fibrosis (2023)	University of Illinois at Chicago	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
Stanford University	United States	SCImago #18 · THE =5 · QS 3	6
Stanford University School of Medicine	United States	—	4
New York Genome Center	United States	—	3
Icahn School of Medicine at Mount Sinai	United States	SCImago #295	3
Helmholtz Munich	Germany	—	2
University of California, San Francisco	United States	SCImago #98	2
University of California San Francisco	United States	SCImago #98	2
CNIC	Spain	—	2
Kyushu University	Japan	SCImago #873 · THE 301–350 · QS =170	2
University of Oxford	United Kingdom	SCImago #26 · THE 1 · QS 4	2
New York University	United States	SCImago #116 · THE =31 · QS 55	2
King Abdulaziz University	Saudi Arabia	SCImago #680 · THE 351–400 · QS 163	1
Universitat Pompeu Fabra (UPF)	Spain	SCImago #720 · QS =265	1
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	1
The Second Affiliated Hospital of Chengdu Medical College, China National Nuclear Corporation 416 Hospital	China	—	1

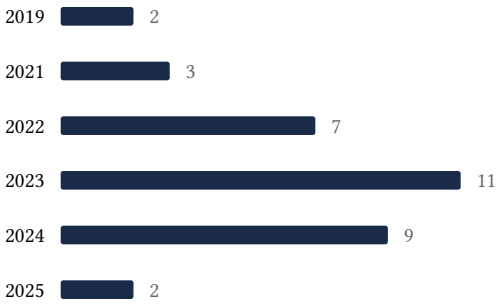
Geographic distribution of citing authors

Country	Citing papers
United States	24
China	10
Germany	6
United Kingdom	5
France	5
Spain	4
Canada	3
Australia	2
Belgium	2
Italy	2
Japan	2
Netherlands	2

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	ATAC-seq: A Method for Assaying Chromatin Accessibility Genome-Wide	14	Dhanasar — Prong 2 (well-positioned)
Contribution 2	Transposition of native chromatin for fast and sensitive epigenomic profiling of open chromatin, DNA-binding proteins and nucleosome position	7	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Single-cell chromatin accessibility reveals principles of regulatory variation	6	Dhanasar — Prong 2 (well-positioned)