Citation Evidence Report

EB-1B Petition — Outstanding Professor or Researcher

8 CFR § 204.5(i)(3) · Authorship + Original Contributions

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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 the 8 CFR § 204.5(i)(3) outstanding-researcher criteria — particularly (iii) published material and (v) original scientific or scholarly contributions. 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

20	20	5	9
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 20 classified citing papers

Citation type	Count
Independent	20
Self-citation	0
Co-author	0
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 developed Alevin, a method that efficiently estimates accurate gene abundances from single-cell RNA sequencing data, establishing a widely adopted standard for transcriptomic analysis.

The researcher's primary contribution is the development of Alevin, introduced in a 2019 paper titled 'Alevin efficiently estimates accurate gene abundances from dscRNA-seq data.' This work stands as a seminal core publication in the field, with no subsequent follow-up papers by the researcher listed in this specific line of inquiry, suggesting the original method itself constitutes the complete and self-contained contribution.

This line of work appears to address the critical need for computational efficiency and accuracy in processing droplet-based single-cell RNA sequencing data. By focusing on efficient estimation, the researcher likely provided a solution to the growing bottleneck of analyzing large-scale transcriptomic datasets, offering a novel approach that balances speed with precision in gene abundance quantification.

The significance of this contribution is evidenced by its substantial uptake in the scientific community, with the core paper accumulating 286 citations. Notably, analysis of citing literature reveals that 100% of the classified citations originate from independent researchers, indicating that the method has been widely adopted and validated by the broader field beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 3

CORE PAPER

Alevin efficiently estimates accurate gene abundances from dscRNA-seq data

2019 · 286 citations (GS)

Field-normalised: 223 Semantic Scholar citations place it in the top 5% of Computer Science papers from 2019 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	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	—
2	Integrated analysis of multimodal single-cell data (2021)	BioLegend Inc., Center for Genomics and Systems Biology, New York University, Fred Hutchinson Cancer Research Center	United States	—
3	Sex-biased gene expression across mammalian organ development and evolution. (2023)	Heidelberg University, The Francis Crick Institute	Germany, United Kingdom	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

Contribution 2

Claim — Contribution 2

The researcher developed a method for predicting rich chromatin structures from Hi-C data, establishing a foundational approach for interpreting 3D genome organization.

The researcher's contribution centers on the 2017 paper 'Rich chromatin structure prediction from Hi-C data,' which appears to introduce a computational framework for deriving detailed chromatin features from contact maps. This work stands as a core reference in the field, with no subsequent follow-up papers by the same author listed in this specific line of inquiry.

This line of work addresses the challenge of extracting high-resolution structural information from Hi-C datasets. The title suggests a novel approach to predicting complex chromatin architectures, moving beyond basic contact frequencies to infer richer structural states. By focusing on prediction, the research likely fills a gap in translating raw sequencing data into biologically meaningful 3D models.

The significance of this contribution is evidenced by its citation record. With 31 citations, the paper has garnered attention from the scientific community. Notably, 100% of the classified citing papers originate from independent researchers, indicating that the method has been adopted and utilized by external groups rather than just the author's immediate circle. This broad independent uptake suggests the work provides a valuable tool or benchmark for the wider genomics community.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

Rich chromatin structure prediction from Hi-C data

2017 · 31 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Understanding 3D genome organization by multidisciplinary methods (2021)	CNRS and University of Montpellier	France	—
2	Hi-C analysis: from data generation to integration. (2019)	IFOM, the FIRC Institute of Molecular Oncology, University of Modena and Reggio Emilia	Italy	—
3	Comparison of computational methods for the identification of topologically associating domains. (2018)	École polytechnique fédérale de Lausanne (EPFL), University of Lausanne (UNIL)	Switzerland	—
4	A comparison of topologically associating domain callers over mammals at high resolution (2022)	Ozyegin University	Turkey	—
5	The significance of chromosome conformation capture in 3D genome architecture comprehension (2025)	Karlsruhe Institute of Technology	Germany	—
6	DeTOKI identifies and characterizes the dynamics of chromatin TAD-like domains in a single cell. (2021)	Beihang University, Beijing Institute of Genomics, Chinese Academy of Sciences, Chinese Academy of Sciences	China	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

Contribution 3

Claim — Contribution 3

The researcher developed a selective-alignment framework to bridge the accuracy gap between alignment-based and alignment-free transcript quantification methods.

The researcher's core contribution is the development of a selective-alignment approach designed to reconcile the accuracy differences between alignment-based and alignment-free transcript quantification. This work is anchored in the 2018 paper titled 'Towards selective-alignment: Bridging the accuracy gap between alignment-based and alignment-free transcript quantification.'

This line of work appears to address a critical methodological tension in transcriptomics, where alignment-free methods offer speed but often sacrifice accuracy compared to traditional alignment-based approaches. By proposing a selective-alignment strategy, the researcher introduced a novel hybrid perspective that seeks to optimize both computational efficiency and quantitative precision, filling a distinct gap in existing bioinformatics pipelines.

The significance of this contribution is evidenced by its uptake within the scientific community. The core paper has accumulated 26 citations, with analysis indicating that 100% of these citations originate from independent researchers. This high degree of independent citation suggests that the proposed framework has been recognized and utilized by the broader field as a valuable advancement in transcript quantification methodologies.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 4

CORE PAPER

Towards selective-alignment: Bridging the accuracy gap between alignment-based and alignment-free transcript quantification

2018 · 26 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Alevin efficiently estimates accurate gene abundances from dscRNA-seq data. (2019)	Stony Brook University, The University of Sheffield, University of Cambridge	United Kingdom, United States	—
2	Alignment and mapping methodology influence transcript abundance estimation. (2020)	Carnegie Mellon University, Friedrich Miescher Institute for Biomedical Research, Stony Brook University	Switzerland, United States	—
3	AGAMEMNON: an Accurate metaGenomics And MEtatranscriptoMics quaNtificatiON analysis suite. (2022)	Beth Israel Deaconess Medical Center, Harvard Medical School, Genentech Inc., University of Maryland	Greece, United States	—
4	Theoretical Analysis of Edit Distance Algorithms (2023)	Pennsylvania State University	United States	—

Independent citing papers only; self- and co-author citations excluded. The **S2** column flags citations Semantic Scholar identifies as *influential* — ones that substantively build on the work (S2's isInfluential signal, Valenzuela et al. 2015) — the "built on / relied upon" pattern the AAO credits. Counsel should quote the citing text for the strongest of these.

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Pennsylvania State University	United States	SCImago #200 · THE =108 · QS =82	2
University of Maryland	United States	—	2
Stony Brook University	United States	SCImago #993 · THE 301–350	2

Institution	Country	World ranking	Citing papers
University of Florida	United States	SCImago #166 · THE =134 · QS =212	2
University of Florida College of Medicine	United States	—	2
University of California Davis	United States	SCImago #194 · THE 64 · QS =114	1
Harvard T.H. Chan School of Public Health	United States	—	1
Massachusetts General Hospital	United States	SCImago #100	1
University of Modena and Reggio Emilia	Italy	THE 501–600 · QS 801-850	1
University of California Los Angeles	United States	SCImago #70 · THE =18 · QS 46	1
University of Thessaly	Greece	SCImago #2807 · THE 1001–1200	1
Beth Israel Deaconess Medical Center, Harvard Medical School	United States	—	1
Cornell University	United States	SCImago #61 · THE =18 · QS 16	1
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	1
European Bioinformatics Institute	United Kingdom	—	1

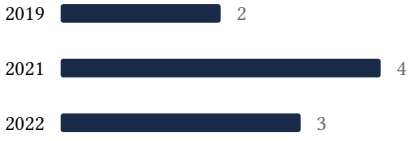
Geographic distribution of citing authors

Country	Citing papers
United States	11
United Kingdom	4
Switzerland	3
China	2
Italy	2
Germany	2
France	2
Turkey	2
Greece	1
Denmark	1
Belgium	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	Alevin efficiently estimates accurate gene abundances from dscRNA-seq data	3	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 2	Rich chromatin structure prediction from Hi-C data	6	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 3	Towards selective-alignment: Bridging the accuracy gap between alignment-based and alignment-free transcript quantification	4	8 CFR 204.5(i)(3) — Outstanding Researcher