Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

Steven Salzberg

Bloomberg Distinguished Professor, Johns Hopkins University

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

14	**15**	**3**	**169**
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.

92.9% independent of 14 classified citing papers

Citation type	Count
Independent	13
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 developed Bowtie 2, a high-performance algorithm for fast gapped-read alignment, establishing a foundational tool for efficient genomic data analysis.

CLAIM: The researcher's primary contribution is the development of Bowtie 2, a software tool for fast gapped-read alignment, as detailed in the seminal 2012 Nature Methods paper. This work stands as a core achievement in computational genomics.

ORIGINALITY: The title suggests this work addressed the need for efficient alignment methods capable of handling gaps, a critical requirement for accurate genomic analysis. By focusing on speed and gapped alignment, the researcher appears to have provided a solution to computational bottlenecks in processing large-scale sequencing data.

SIGNIFICANCE: With over 60,000 citations, this paper is highly influential. Analysis of citing literature indicates that 100% of sampled citations come from independent researchers, demonstrating broad adoption and impact across the global scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 5 **· 2 flagged influential by Semantic Scholar**

CORE PAPER

Fast gapped-read alignment with Bowtie 2

2012 · Nature Methods · 60,681 citations (GS)

Field-normalised: 49,776 Semantic Scholar citations place it in the top 1% of Computer Science papers from 2012 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Next-Generation Sequencing Technology: Current Trends and Advancements	miBiome Therapeutics, UMass Chan Medical School	India, United States	**Methodology**
2	A distinct Fusobacterium nucleatum clade dominates the colorectal cancer niche (2024)	Chosun University, Dana-Farber Cancer Institute, Forsyth Institute	Italy, South Korea, United States	**Methodology**
3	Safety, efficacy and determinants of response of allogeneic CD19-specific CAR-NK cells in CD19+ B cell tumors: a phase 1/2 trial (2024)	The University of Texas MD Anderson Cancer Center	United States	**Methodology**
4	Chromatin accessibility profiling by ATAC-seq (2022)	Gladstone Institute of Neurological Disease, Gladstone Institutes; University of California San Francisco, University of California San Francisco	United States	—
5	Persistent complement dysregulation with signs of thromboinflammation in active Long Covid (2024)	Charles Bronfman Institute for Personalized Medicine, Icahn School of Medicine at Mount Sinai, ETH Zurich, ETH Zurich & Swiss Institute of Bioinformatics (SIB)	Sweden, Switzerland, United Kingdom	**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 Next-Generation Sequencing Technology: Current Trends and Advancements

*"MethylDackel * Differential methylation Metilene [138], BSsmooth [139], methylKit [140] Epigenomics-ChIP [147], MAnorm [148], MMDiff [149]"*

METHODOLOGY A distinct Fusobacterium nucleatum clade dominates the colorectal cancer niche

"Metagenomic samples were mapped against the Fna SB010 eut , pdu and gdar operons using Bowtie2 (version 2.4.5, --sensitive parameter) 77 ."

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

"4.2) 57 as the aligner and hg19 transcriptome as the reference."

METHODOLOGY Persistent complement dysregulation with signs of thromboinflammation in active Long Covid

"Epitope hit counts were obtained using SAMtools (84) upon mapping of reads to the epitope library using Bowtie2 (85)."

Contribution 2

Claim — Contribution 2

The researcher developed an ultrafast, memory-efficient algorithm for aligning short DNA sequences to the human genome, establishing a foundational standard for genomic data processing.

The researcher's primary contribution is the development of a highly efficient computational method for aligning short DNA sequences to the human genome, as detailed in their 2009 publication. This work addresses the critical need for speed and memory optimization in genomic analysis, enabling the processing of large-scale sequencing data that was previously computationally prohibitive. The titles suggest a focus on algorithmic efficiency, indicating a novel approach to handling the growing volume of biological data.

The significance of this contribution is evidenced by its extensive adoption within the scientific community, with the core paper accumulating over 25,000 citations. Analysis of citing literature reveals that 100% of the classified citations originate from independent researchers, demonstrating that the work has become a widely accepted standard tool used across diverse institutions and research groups rather than being confined to the researcher's immediate circle. This broad, independent uptake underscores the method's utility and impact on the field of bioinformatics.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 4

CORE PAPER

Ultrafast and memory-efficient alignment of short DNA sequences to the human genome

2009 · 25,902 citations (GS)

Field-normalised: 22,039 Semantic Scholar citations place it in the top 1% of Computer Science papers from 2009 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Single-cell and spatial transcriptomics: deciphering brain complexity in health and disease (2023)	Berlin Institute for Medical Systems Biology (BIMSB), Max Delbrueck Center for Molecular Medicine, Institute of Bioorganic Chemistry, Polish Academy of Sciences, Max Delbrück Center for Molecular Medicine in the Helmholtz Association	Germany, Poland	—
2	Metabolic regulation of gene expression by histone lactylation	Jingjie PTM Biolab (Hangzhou) Co. Ltd., Kyungpook National University, Ludwig Institute for Cancer Research, University of California, San Diego	China, South Korea, United States	—

No.	Citing paper	Citing institution(s)	Country	S2
3	Dictionary learning for integrative, multimodal and scalable single-cell analysis	New York Genome Center, New York University	United States	—
4	Circular RNA discovery with emerging sequencing and deep learning technologies (2025)	Chinese Academy of Sciences, Institute of Zoology, Chinese Academy of Sciences	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 developed HISAT, a fast spliced aligner with low memory requirements, published in Nature Methods in 2015, which has garnered over 23,000 citations.

The researcher's primary contribution is the development of HISAT, a fast spliced aligner with low memory requirements, as detailed in a 2015 paper published in Nature Methods. This work stands as a seminal core paper in the field, with no follow-up papers by the same researcher listed in this specific line of inquiry.

This line of work appears to address the computational challenges associated with spliced alignment, specifically targeting the need for speed and reduced memory usage. The title suggests a novel approach to balancing performance efficiency with resource constraints, a critical gap in genomic data analysis tools at the time of publication.

The significance of this contribution is evidenced by its extensive uptake, with the core paper accumulating 23,463 citations. Furthermore, analysis of citing papers indicates that 100% of the classified citations originate from independent researchers, suggesting broad adoption and impact across the scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 4

CORE PAPER

HISAT: a fast spliced aligner with low memory requirements

2015 · Nature Methods · 23,463 citations (GS)

Field-normalised: 19,648 Semantic Scholar citations place it in the top 1% of Computer Science papers from 2015 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Using SPAdes De Novo Assembler (2020)	Saint Petersburg State University	Russia	**Methodology**
2	Ferroptosis surveillance independent of GPX4 and differentially regulated by sex hormones	Memorial Sloan Kettering Cancer Center	United States	—
3	Single-cell RNA-seq technologies and related computational data analysis (2019)	East China Normal University, National Center for Toxicological Research, United States Food and Drug Administration, United States Food and Drug Administration	China, United States	—

No.	Citing paper	Citing institution(s)	Country	S2
4	RNA sequencing: the teenage years	AstraZeneca, Cancer Research UK Cambridge Institute, University of Cambridge	United Kingdom	—

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
The University of Chicago	United States	SCImago #124 · THE 15 · QS 13	1
Chinese Academy of Sciences	China	SCImago #2	1
Fred Hutchinson Cancer Center	United States	SCImago #397	1
Dana-Farber Cancer Institute	United States	SCImago #197	1
AstraZeneca	United Kingdom	SCImago #244	1
University of California San Francisco	United States	SCImago #98	1
University of Washington	United States	SCImago #45 · THE 25 · QS 81	1
Imperial College London	United Kingdom	SCImago #69 · THE 8 · QS 2	1
University of Georgia	United States	SCImago #597 · THE 351–400 · QS 525	1
Gladstone Institutes; University of California San Francisco	United States	—	1
The Rockefeller University	United States	SCImago #365	1
Shanghai Institute of Materia Medica, Chinese Academy of Sciences	China	—	1
University of Texas Southwestern Medical Center	United States	SCImago #562	1
UMass Chan Medical School	United States	SCImago #1179	1
University of Zurich & University Hospital Zurich	Switzerland	—	1

Geographic distribution of citing authors

Country	Citing papers
United States	10
China	3
United Kingdom	2
South Korea	2
Poland	1
Russia	1
Sweden	1

Country	Citing papers
Switzerland	1
India	1
Germany	1
Italy	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	Fast gapped-read alignment with Bowtie 2	5	Dhanasar — Prong 2 (well-positioned)
Contribution 2	Ultrafast and memory-efficient alignment of short DNA sequences to the human genome	4	Dhanasar — Prong 2 (well-positioned)
Contribution 3	HISAT: a fast spliced aligner with low memory requirements	4	Dhanasar — Prong 2 (well-positioned)