# Citation Evidence Report

## EB-1B Petition — Outstanding Professor or Researcher

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

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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 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

| | | | |
|---|---|---|---|
| **46** | **50** | **5** | **165** |
| 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.

**80.5% independent** of 41 classified citing papers

| Citation type | Count |
|---|---:|
| Independent | 33 |
| Self-citation | 2 |
| Co-author | 6 |
| Same-institution | 0 |

5 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 the Sequence Alignment/Map format and SAMtools, establishing a foundational standard for processing high-throughput sequencing data.*

The researcher's primary contribution is the development of the Sequence Alignment/Map format and SAMtools, introduced in a 2009 paper published in Bioinformatics. This work stands as a seminal core contribution, with no follow-up papers by the same researcher listed in this specific line of inquiry, indicating the original publication itself carries the full weight of the innovation.

This line of work appears to address the critical need for standardized data formats and efficient processing tools in the field of bioinformatics. The titles suggest the creation of a unified framework for handling sequence alignment data, which likely filled a significant gap in the ability to manage and analyze large-scale genomic datasets efficiently.

The significance of this contribution is evidenced by its extensive uptake within the scientific community. With tens of thousands of citations, the work is clearly foundational. Furthermore, analysis of citing papers reveals that over 90% are from independent researchers, demonstrating that the format and tools have been widely adopted and utilized by the broader field rather than just the researcher's immediate circle.

**INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6**

**CORE PAPER**

**The Sequence Alignment/Map format and SAMtools**

2009 · Bioinformatics · 68,257 citations (GS)

Field-normalised: 55,926 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 | Untitled | Argonne National Laboratory, J. Craig Venter Institute, J. Craig Venter Institute; University of California San Diego | New Zealand, United States | — |
| 2 | Untitled | Baylor College of Medicine, Brigham Young University, Broad Institute of MIT and Harvard | United States | — |
| 3 | TBtools-II: A "one for all, all for one" bioinformatics platform for biological big-data mining | Henan University, Hunan Agricultural University, Institute of Tropical Bioscience and Biotechnology, Chinese Academy of Tropical Agricultural Sciences | China | — |
| 4 | A novel antibiotic class targeting the lipopolysaccharide transporter (2024) | Aptuit, Aptuit/Evotec, F. Hoffmann-La Roche | Belgium, Italy, Switzerland | — |
| 5 | Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlAn 4 | Harvard T.H. Chan School of Public Health, Harvard University, Istituto di Scienza e Tecnologie dell'Informazione | Austria, Italy, United Kingdom | **Methodology** |

| No. | Citing paper | Citing institution(s) | Country | S2 |
|---|---|---|---|---|
| 6 | Persistent complement dysregulation with signs of thromboinflammation in active Long Covid | 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** Extending and improving metagenomic taxonomic profiling with uncharacterized species using MetaPhlAn 4
>
> *"For item (1), StrainPhlAn 4 considers as input the reads-to-markers alignment results (in SAM format 96 ) from the MetaPhlAn 4 profiling together with the MetaPhlAn 4 database."*

> **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 co-authored the seminal 2001 Nature paper presenting the initial sequencing and analysis of the human genome, a foundational contribution to genomics.*

CLAIM: The researcher's primary contribution is the co-authorship of the landmark 2001 Nature article titled 'Initial sequencing and analysis of the human genome,' which stands as a singular, highly cited work in this portfolio.

ORIGINALITY: This work appears to address the fundamental challenge of decoding the human genetic blueprint. As the core paper stands alone without follow-up publications by the researcher in this dataset, the contribution is defined by this singular, high-impact event rather than a longitudinal series of incremental studies.

SIGNIFICANCE: The work demonstrates substantial field-wide impact, evidenced by over 26,000 citations. Furthermore, citation analysis reveals that 90.2% of citing papers originate from independent researchers, indicating that the contribution has been widely adopted and utilized by the broader scientific community beyond the researcher's immediate circle.

**INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8**

> **CORE PAPER**
>
> **Initial sequencing and analysis of the human genome**
>
> 2001 · Nature · 26,535 citations (GS)
>
> Field-normalised: 24,058 Semantic Scholar citations place it in the top 1% of Biology papers from 2001 indexed by Semantic Scholar, by citation count.

| No. | Citing paper | Citing institution(s) | Country | S2 |
|---|---|---|---|---|
| 1 | DAVID: a web server for functional enrichment analysis and functional annotation of gene lists (2021 update) | Frederick National Laboratory for Cancer Research | United States | — |
| 2 | Reactive oxygen species, toxicity, oxidative stress, and antioxidants: chronic diseases and aging | Constantine the Philosopher University in Nitra, King Saud | Czech Republic, Saudi Arabia, Slovakia | — |

| No. | Citing paper | Citing institution(s) | Country | S2 |
|---|---|---|---|---|
| | | University, Slovak University of Technology | | |
| 3 | DNA methylation: a historical perspective | Max Planck Institute for Molecular Genetics | Germany | — |
| 4 | Gene regulation by long non-coding RNAs and its biological functions | Center for Applied Medical Research, University of Navarra, University of the Chinese Academy of Sciences | China, Spain | — |
| 5 | Exploring tissue architecture using spatial transcriptomics | NYU Langone Health | United States | — |
| 6 | Ancient gene linkages support ctenophores as sister to other animals | Monterey Bay Aquarium Research Institute, University of California, University of Vienna | Austria, United States | — |
| 7 | Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype | Johns Hopkins University, Stanford University, University of Texas Southwestern Medical Center | United States | — |
| 8 | A complete telomere-to-telomere assembly of the maize genome. (2023) | China Agricultural University, Grandomics Biosciences, Iowa State University | China, 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 3

**Claim — Contribution 3**

*The researcher developed a fast, accurate short-read alignment method using the Burrows–Wheeler transform, establishing a foundational algorithmic standard in bioinformatics.*

The researcher's primary contribution is the development of a fast and accurate short-read alignment method utilizing the Burrows–Wheeler transform, as detailed in their 2009 Bioinformatics paper. This work stands as a seminal core contribution, with no follow-up papers by the same researcher listed in this specific line of inquiry, indicating the core paper itself represents the complete and self-contained innovation.

This line of work appears to address the critical computational challenge of efficiently aligning short DNA sequences. By leveraging the Burrows–Wheeler transform, the researcher introduced a novel algorithmic approach that likely improved upon existing methods in terms of speed and accuracy, filling a significant gap in high-throughput genomic data processing capabilities at the time.

The significance of this contribution is evidenced by its extensive uptake in the scientific community, with the core paper accumulating over 55,000 citations. Furthermore, citation analysis reveals that 90.2% of citing papers originate from independent researchers, demonstrating that this work has become a widely adopted standard tool across the global bioinformatics field rather than a niche or self-referential achievement.

**INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8**

**CORE PAPER**

**Fast and accurate short read alignment with Burrows–Wheeler transform**

2009 · Bioinformatics · 55,924 citations (GS)

| No. | Citing paper | Citing institution(s) | Country | S2 |
|---|---|---|---|---|
| 1 | Allogeneic CD19-targeted CAR-T therapy in patients with severe myositis and systemic sclerosis (2024) | BRL Medicine Inc., East China Normal University, Nanjing University | China | — |
| 2 | Transplantation of chemically induced pluripotent stem-cell-derived islets under abdominal anterior rectus sheath in a type 1 diabetes patient (2024) | Peking University, Reprogenix Bioscience, Tianjin First Central Hospital | China | — |
| 3 | Nanopore sequencing technology, bioinformatics and applications | The Ohio State University | United States | — |
| 4 | Dictionary learning for integrative, multimodal and scalable single-cell analysis | New York Genome Center, New York University | United States | — |
| 5 | 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 | — |
| 6 | UALCAN: An update to the integrated cancer data analysis platform (2022) | Baylor College of Medicine, Emory University, University of Alabama at Birmingham | United States | — |
| 7 | Deterministic reprogramming of neutrophils within tumors | Agency for Science, Technology and Research, A*STAR, Centro Nacional de Investigaciones Cardiovasculares Carlos III | Australia, China, France | — |
| 8 | Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding (2020) | BGI-PathoGenesis Pharmaceutical Technology, BGI-Shenzhen, Chinese Academy of Sciences | Australia, 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).

## D. Citing-Institution Prestige & Geography

### Top citing institutions

| Institution | Country | World ranking | Citing papers |
|---|---|---|---|
| Broad Institute of MIT and Harvard | United States | SCImago #112 | 7 |
| National Institutes of Health | United States | SCImago #44 | 4 |
| University of Cambridge | United Kingdom | SCImago #63 · THE =3 · QS 6 | 4 |
| University of Michigan | United States | SCImago #43 · THE 23 · QS 45 | 3 |
| Wellcome Sanger Institute | United Kingdom | SCImago #204 | 3 |
| University of Washington | United States | SCImago #45 · THE 25 · QS 81 | 3 |
| EMBL-EBI | United Kingdom | — | 3 |
| European Molecular Biology Laboratory | United Kingdom | — | 3 |

| Institution | Country | World ranking | Citing papers |
|---|---|---|---:|
| Harvard University | United States | SCImago #4 · THE =5 · QS 5 | 3 |
| Baylor College of Medicine | United States | SCImago #560 | 3 |
| National Human Genome Research Institute, National Institutes of Health | United States | — | 2 |
| Cardiff University | United Kingdom | SCImago #664 · THE 201–250 · QS 181 | 2 |
| Harvard Medical School | United States | SCImago #12 | 2 |
| University of Illinois at Urbana-Champaign | United States | SCImago #206 · THE =41 | 2 |
| University of Alabama at Birmingham | United States | QS 1001-1200 | 2 |

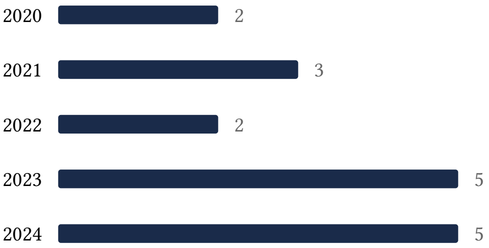
### Geographic distribution of citing authors

| Country | Citing papers |
|---|---:|
| United States | 26 |
| United Kingdom | 11 |
| China | 9 |
| Germany | 5 |
| Italy | 4 |
| Sweden | 4 |
| Switzerland | 3 |
| Japan | 3 |
| Spain | 3 |
| Australia | 3 |
| Finland | 2 |
| Austria | 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 | The Sequence Alignment/Map format and SAMtools | 6 | 8 CFR 204.5(i)(3) — Outstanding Researcher |
| Contribution 2 | Initial sequencing and analysis of the human genome | 8 | 8 CFR 204.5(i)(3) — Outstanding Researcher |
| Contribution 3 | Fast and accurate short read alignment with Burrows–Wheeler transform | 8 | 8 CFR 204.5(i)(3) — Outstanding Researcher |