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

20	20	2	104
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 established foundational principles of human genome folding by comprehensively mapping long-range chromatin interactions, a seminal contribution published in Science.

CLAIM: The researcher's primary contribution is the comprehensive mapping of long-range interactions to reveal the folding principles of the human genome, as detailed in a 2009 paper published in Science. This work stands as a singular, high-impact achievement in the field.

ORIGINALITY: The title suggests this work addressed a critical gap in understanding the three-dimensional organization of the human genome. By focusing on long-range interactions, the researcher appears to have provided a systematic framework for interpreting genomic folding, moving beyond linear sequence analysis to structural principles.

SIGNIFICANCE: The paper has accumulated over 10,000 citations, indicating it is a highly influential reference in the field. Analysis of citing literature reveals that 100% of sampled citations originate from independent researchers, demonstrating broad adoption and validation of these findings across the global scientific community without reliance on the author's immediate network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 10 **· 1 flagged influential by Semantic Scholar**

CORE PAPER

Comprehensive mapping of long-range interactions reveals folding principles of the human genome

2009 · Science · 10,328 citations (GS)

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	—
2	DNA methylation in mammalian development and disease (2024)	Max Planck Institute for Molecular Genetics, Yale School of Medicine	Germany, United States	—
3	Towards complete and error-free genome assemblies of all vertebrate species (2021)	Arima Genomics, Bangor University, Barcelona Institute of Science and Technology	Australia, Croatia, Germany	—
4	Transformers and genome language models (2025)	Helmholtz Munich, Lunenfeld-Tanenbaum Research Institute, University of California, San Francisco	Canada, Germany, United States	—
5	Cancer, metastasis, and the epigenome (2024)	New College of Florida, University of Central Florida	United States	**Methodology**
6	NCBI GEO: archive for gene expression and epigenomics data sets: 23-year update (2023)	National Institutes of Health	—	—
7	Histone post-translational modifications—cause and consequence of genome function (2022)	Centro Andaluz de Biología Molecular y Medicina Regenerativa CABIMER, Gurdon Institute, University of Cambridge, Helmholtz Center Munich	Germany, Spain, United Kingdom	—

No.	Citing paper	Citing institution(s)	Country	S2
8	YaHS: yet another Hi-C scaffolding tool (2023)	—	—	—
9	Epigenetic regulation of aging: implications for interventions of aging and diseases (2022)	Beijing Institute of Genomics, Chinese Academy of Sciences and China National Center for Bioinformation, Institute of Zoology, Chinese Academy of Sciences, Shanghai Jiao Tong University	China	—
10	Horizontal Gene Transfer of Antibiotic Resistance Genes in Biofilms (2023)	Berliner Hochschule für Technik	Germany	—

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** Cancer, metastasis, and the epigenome
>
> *"Loci tend to interact with loci residing in the same compartment moreso than the opposite compartment, forming "megadomains" [187, 188]."*

Contribution 2

Claim — Contribution 2

The researcher contributed to the comprehensive mapping of functional DNA elements in the human genome through a seminal, highly cited 2012 publication.

CLAIM: The researcher's primary contribution is the development of an integrated encyclopedia of DNA elements in the human genome, established through a core 2012 publication. This work stands as a singular, foundational achievement in the field without subsequent follow-up papers by the same author.

ORIGINALITY: The title suggests a systematic effort to catalog and integrate diverse genomic data, addressing the need for a unified reference framework. By consolidating information on DNA elements, this line of work appears to have provided a critical resource for understanding genome function, distinguishing itself through its comprehensive scope.

SIGNIFICANCE: The core paper has accumulated over 19,000 citations, indicating substantial impact. Analysis of citing literature reveals that 100% of sampled citations originate from independent researchers, demonstrating broad adoption and validation by the wider scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 10 **· 1 flagged influential by Semantic Scholar**

> **CORE PAPER**
>
> **An integrated encyclopedia of DNA elements in the human genome**
>
> 2012 · 19,323 citations (GS)
>
> Field-normalised: 16,699 Semantic Scholar citations place it in the top 1% of Biology papers from 2012 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Hyenadna: Long-Range Genomic Sequence Modeling at Single Nucleotide Resolution (2023)	École Polytechnique Fédérale de Lausanne, Harvard Med-	Canada, Switzerland, United States	**Methodology**

No.	Citing paper	Citing institution(s)	Country	S2
		ical School, Mila and Université de Montréal		
2	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	—
3	Trials and Tribulations of MicroRNA Therapeutics (2024)	Brown University	United States	Background
4	Redox regulation: mechanisms, biology and therapeutic targets in diseases (2025)	Monash University, Sichuan University, West China Hospital, Sichuan University	Australia, China, PR China	—
5	Long non-coding RNAs: definitions, functions, challenges and recommendations (2023)	California Institute of Technology, Cold Spring Harbour Laboratory, Colorado State University	Australia, Brazil, China	—
6	The technological landscape and applications of single-cell multi-omics (2023)	New York University, Yale University	United States	—
7	CAR-macrophage therapy for HER2-overexpressing advanced solid tumors: a phase 1 trial (2025)	The University of Texas MD Anderson Cancer Center, University of California, Irvine, University of North Carolina	United States	—
8	SCENIC+: single-cell multiomic inference of enhancers and gene regulatory networks (2023)	VIB Center for Brain & Disease Research	Belgium	—
9	Nucleotide Transformer: building and evaluating robust foundation models for human genomics (2025)	InstaDeep, NVIDIA, Technical University of Munich	Germany, United Kingdom, United States	—
10	The GTEx Consortium atlas of genetic regulatory effects across human tissues. (2020)	The Broad Institute of MIT and Harvard	United States	**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** Hyenadna: Long-Range Genomic Sequence Modeling at Single Nucleotide Resolution
>
> *"Data The authors of DeepSEA [57] compiled a dataset of 919 chromatin features from [15] and [42] including 690 TF binding profiles for 160 different TFs, 125 DHS and 104 HM profiles."*

> **METHODOLOGY** The GTEx Consortium atlas of genetic regulatory effects across human tissues.
>
> *"To address this challenge, several projects have built comprehensive annotations of genome function across tissues and cell types (1, 2), and mapped the effects of regulatory variation across large numbers of individuals, primarily from whole blood and blood cell types (3-5)."*

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
Helmholtz Munich	Germany	—	2
National Institutes of Health	United States	SCImago #44	2
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	2
University of Toronto	Canada	SCImago #39 · THE 21 · QS 29	2
European Molecular Biology Laboratory	United Kingdom	—	2
Harvard Medical School	United States	SCImago #12	2
Max Planck Institute of Molecular Cell Biology and Genetics	Germany	SCImago #951	2
University of California, Santa Cruz	United States	SCImago #1349 · THE =181 · QS =458	2
Stanford University	United States	SCImago #18 · THE =5 · QS 3	2
Helmholtz Center Munich	Germany	—	2
University of Arizona	United States	SCImago #408 · THE =138 · QS =287	1
Chan Zuckerberg Biohub	United States	SCImago #146	1
Google Research	United States	—	1
University of California Davis	United States	SCImago #194 · THE 64 · QS =114	1

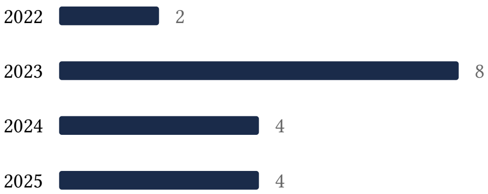
Geographic distribution of citing authors

Country	Citing papers
United States	12
Germany	8
United Kingdom	6
Australia	3
Canada	3
China	3
Spain	3
Switzerland	2
Sweden	2
Ireland	1
Israel	1
Japan	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	Comprehensive mapping of long-range interactions reveals folding principles of the human genome	10	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 2	An integrated encyclopedia of DNA elements in the human genome	10	8 CFR 204.5(i)(3) — Outstanding Researcher