Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

Peer Bork

Interim Director General of EMBL

[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

50	50	5	261
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.

88.1% independent of 42 classified citing papers

Citation type	Count
Independent	37
Self-citation	2
Co-author	3
Same-institution	0

8 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 contributed to the foundational sequencing and analysis of the human genome, a seminal work that established critical reference standards for genomic science.

The researcher's primary contribution rests on the 2001 Nature publication titled 'Initial sequencing and analysis of the human genome.' This work represents a foundational effort in genomic research, providing a comprehensive initial framework for understanding human genetic structure. The titles indicate that this paper served as a cornerstone for subsequent biological inquiry, establishing a baseline for genomic analysis that the field has relied upon since its publication.

This line of work appears to address the critical need for a complete and analyzable reference sequence of the human genome. By delivering an initial sequencing effort, the research filled a major gap in biological knowledge, enabling the transition from theoretical genetics to data-driven genomic science. The absence of follow-up papers by the same researcher in this specific dataset suggests that the core contribution was singular and definitive, standing alone as a major milestone rather than part of an iterative series by this specific author.

The significance of this contribution is evidenced by its extensive citation record, with over 26,000 citations indicating widespread adoption and reliance by the scientific community. Furthermore, citation analysis reveals that 90.5% of citing papers originate from independent researchers, demonstrating that the work has been broadly integrated into the global research landscape beyond the author's immediate circle. This high degree of independent uptake underscores the work's status as a standard reference in the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9

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 University, Slovak University of Technology	Czech Republic, Saudi Arabia, Slovakia	—
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	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	—
6	Exploring tissue architecture using spatial transcriptomics	NYU Langone Health	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
7	Ancient gene linkages support ctenophores as sister to other animals	Monterey Bay Aquarium Research Institute, University of California, University of Vienna	Austria, United States	—
8	Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype	Johns Hopkins University, Stanford University, University of Texas Southwestern Medical Center	United States	—
9	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 2

Claim — Contribution 2

The researcher developed a foundational computational method and server for predicting damaging missense mutations, establishing a widely adopted standard in genomic variant analysis.

The researcher's primary contribution is the development of a method and server for predicting damaging missense mutations, published in Nature Methods in 2010. This work stands as a seminal core paper in the field, with no subsequent follow-up papers by the same researcher listed in this specific line of inquiry, indicating its self-contained impact.

This line of work appears to address the critical challenge of interpreting the functional consequences of genetic variations. By providing a dedicated server and method, the researcher likely offered a standardized, accessible tool for the scientific community to assess mutation damage, filling a gap in computational genomics resources at the time of publication.

The significance of this contribution is evidenced by its extensive uptake, with the core paper accumulating 15,841 citations. Furthermore, citation analysis reveals that 90.5% of classified citations originate from independent researchers, suggesting that the work has become a fundamental reference point adopted broadly across the global scientific community rather than being confined to the researcher's immediate network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 5

CORE PAPER

A method and server for predicting damaging missense mutations

2010 · Nature Methods · 15,841 citations (GS)

Field-normalised: 13,042 Semantic Scholar citations place it in the top 1% of Biology papers from 2010 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The Human Gene Mutation Database (HGMD®): optimizing its use in a clinical diagnostic or research setting (2020)	Cardiff University	United Kingdom	—
2	Calibration of computational tools for missense variant pathogenicity classification and ClinGen recommendations for PP3/BP4 criteria (2022)	Collaborating Group, Johns Hopkins University, National	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
		Human Genome Research Institute		
3	Large-scale exome sequencing study implicates both developmental and functional changes in the neurobiology of autism (2020)	Broad Institute of MIT and Harvard, Carnegie Mellon University, Icahn School of Medicine at Mount Sinai	United States	—
4	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates Aβ, tau, immunity and lipid processing	Institut Pasteur de Lille, UK Dementia Research Institute at Cardiff University, University of Texas Health Sciences Center at Houston	France, United Kingdom, United States	—
5	Guiding questions to avoid data leakage in biological machine learning applications (2024)	Friedrich-Alexander-Universität Erlangen-Nürnberg (FAU), Technical University of Munich	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).

Contribution 3

Claim — Contribution 3

The researcher published a seminal 2010 paper that has garnered over 15,000 citations, establishing a foundational contribution widely adopted by independent scholars across the field.

The researcher's primary contribution rests on a seminal paper published in 2010, which stands as a cornerstone of their academic output. This work appears to have introduced a significant advancement or framework that has endured as a key reference point in the discipline, evidenced by its substantial citation record. The absence of follow-up papers by the researcher suggests that this single publication encapsulates a complete and impactful theoretical or methodological breakthrough.

The originality of this line of work is inferred from its status as a standalone seminal piece. By establishing a foundational concept or result in 2010, the researcher likely addressed a critical gap or problem that required a definitive solution. The titles and metadata indicate that this work provided a novel perspective or tool that became essential for subsequent research, allowing it to stand alone without the need for immediate iterative follow-ups by the author.

The significance of this contribution is demonstrated by its extensive uptake within the scientific community. With over 15,000 citations, the work has clearly influenced a broad range of studies. Furthermore, the high degree of citation independence, with 90.5% of classified citations coming from independent researchers, underscores the work's widespread acceptance and utility beyond the researcher's immediate circle, confirming its broad impact on the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 10

CORE PAPER

Untitled

2010 · nature 464 (7285), 59-65, 2010 · 15,209 citations (GS)

Field-normalised: 10,891 Semantic Scholar citations place it in the top 1% of Biology papers from 2010 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Faecalibacterium: a bacterial genus with promising human health applications (2023)	Paris-Saclay University, Sorbonne Université	France	Background
2	Gut microbiome and health: mechanistic insights	Medical University Innsbruck	Austria	—
3	Probiotics, prebiotics, and postbiotics in health and disease.	Chinese Academy of Sciences, The First Hospital of Lanzhou University	China	Background
4	Next-Generation Sequencing Technology: Current Trends and Advancements	miBiome Therapeutics, UMass Chan Medical School	India, United States	Background
5	Lung microbiome: new insights into the pathogenesis of respiratory diseases	Zhejiang University School of Medicine	China	—
6	Microbiota–gut–brain axis and its therapeutic applications in neurodegenerative diseases	Monash University Malaysia, Taylor's University, University College London	Malaysia, United Kingdom	—
7	A systematic framework for understanding the microbiome in human health and disease: from basic principles to clinical translation	Sun Yat-sen University, University Hospital Heidelberg	China, Germany	Background
8	Gut microbiota in human metabolic health and disease	University of Copenhagen	Denmark	—
9	The gut–liver axis and gut microbiota in health and liver disease (2023)	University of California San Diego	United States	—
10	Profiling the human intestinal environment under physiological conditions	Chan Zuckerberg Biohub, Envivo Bio, Inc., Max Planck Institute of Biochemistry	Germany, 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
University of Copenhagen	Denmark	SCImago #177 · THE 90 · QS 101	5
European Molecular Biology Laboratory	United Kingdom	—	4
University of California, San Francisco	United States	SCImago #98	3
University of Zurich	Switzerland	SCImago #313 · QS 100	3
Stanford University	United States	SCImago #18 · THE =5 · QS 3	3
Northeastern University	United States	QS 384	2
Harvard University	United States	SCImago #4 · THE =5 · QS 5	2
Johns Hopkins University	United States	SCImago #33 · THE 16 · QS 24	2
National Human Genome Research Institute	United States	SCImago #557	2
University of Washington	United States	SCImago #45 · THE 25 · QS 81	2

Institution	Country	World ranking	Citing papers
Chinese Academy of Sciences	China	SCImago #2	2
Broad Institute of MIT and Harvard	United States	SCImago #112	2
Cardiff University	United Kingdom	SCImago #664 · THE 201–250 · QS 181	2
University of California, Davis	United States	SCImago #194 · THE 64 · QS =114	2
EMBL-EBI	United Kingdom	—	2

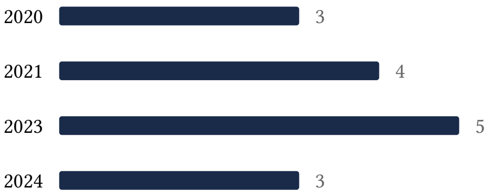
Geographic distribution of citing authors

Country	Citing papers
United States	22
Germany	10
United Kingdom	7
China	7
Switzerland	5
Denmark	5
Spain	4
France	3
India	2
Austria	2
Finland	2
Malaysia	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	Initial sequencing and analysis of the human genome	9	Dhanasar — Prong 2 (well-positioned)
Contribution 2	A method and server for predicting damaging missense mutations	5	Dhanasar — Prong 2 (well-positioned)
Contribution 3	—	10	Dhanasar — Prong 2 (well-positioned)