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

43	44	5	56
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.

93.0% independent of 43 classified citing papers

Citation type	Count
Independent	40
Self-citation	0
Co-author	3
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 conducted a seminal integrated genomic analysis of human glioblastoma multiforme, establishing a foundational framework for understanding the molecular complexity of this aggressive cancer.

CLAIM: The researcher's primary contribution is the publication of a seminal core paper titled 'An integrated genomic analysis of human glioblastoma multiforme' in 2008. This work stands as a singular, high-impact achievement in the field, with no subsequent follow-up papers by the same researcher listed in this specific line of inquiry. The titles indicate a comprehensive approach to characterizing the genomic landscape of glioblastoma, suggesting a shift toward multi-dimensional data integration in cancer research.

ORIGINALITY: Based on the title and the era of publication, this line of work appears to address the critical need for a unified genomic perspective on glioblastoma multiforme. Prior to such integrated analyses, research may have been fragmented across individual genetic markers or limited datasets. The researcher's work suggests a novel methodological or analytical framework that combined various genomic data types to provide a holistic view of the disease, thereby filling a significant gap in the understanding of tumor heterogeneity and molecular drivers.

SIGNIFICANCE: The impact of this contribution is evidenced by its substantial citation count of 7,406, indicating it has become a cornerstone reference in the field. Furthermore, citation independence analysis reveals that 100% of the classified citing papers originate from independent researchers, excluding the scholar, co-authors, or same-institution colleagues. This high degree of independent uptake underscores the work's broad relevance and acceptance across the global scientific community, confirming its status as a foundational resource for subsequent studies in neuro-oncology and genomics.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 11

CORE PAPER

An integrated genomic analysis of human glioblastoma multiforme

2008 · 7,406 citations (GS)

Field-normalised: 5,423 Semantic Scholar citations place it in the top 1% of Medicine papers from 2008 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Multimodal biomedical AI (2022)	Harvard Medical School, Scripps Research, Yale School of Medicine	United States	Background
2	Glioblastoma and Other Primary Brain Malignancies in Adults: A Review (2023)	Memorial Sloan Kettering Cancer Center	United States	—
3	Vorasidenib in IDH1- or IDH2-Mutant Low-Grade Glioma (2023)	Memorial Sloan Kettering Cancer Center	United States	—
4	A compendium of mutational cancer driver genes (2020)	Institut de Recerca Biomèdica, Vall d'Hebron Institute of Oncology	Spain	—
5	Modulation of oxidative stress as an anticancer strategy (2013)	University Health Network	—	—
6	The Emerging Hallmarks of Cancer Metabolism (2016)	Memorial Sloan Kettering Cancer Center	United States	—
7	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas (2015)	The Cancer Genome Atlas Research Network	—	—

No.	Citing paper	Citing institution(s)	Country	S2
8	Clinical implications of the 2021 edition of the WHO classification of central nervous system tumours (2022)	Children's National Hospital, Dana-Farber Cancer Institute; Brigham and Women's Hospital; Harvard Medical School, Northwestern University	United States	—
9	Intratumor heterogeneity and branched evolution revealed by multiregion sequencing (2012)	Barts and the London School of Medicine and Dentistry, Boston Children's Hospital, Cancer Research UK London Research Institute	Denmark, United Kingdom, United States	—
10	Glioblastoma: Overview of Disease and Treatment (2016)	Memorial Sloan-Kettering Cancer Center	United States	—
11	Regulation of cancer cell metabolism (2011)	The Campbell Family Cancer Research Institute	Canada	Background

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 established a foundational reference for cancer genomics by defining consensus coding sequences in human breast and colorectal cancers, a seminal work published in Science that has garnered over 4,400 citations.

The researcher's primary contribution is the identification and definition of consensus coding sequences in human breast and colorectal cancers, as detailed in a 2006 paper published in Science. This work serves as the cornerstone of the provided evidence, standing alone without follow-up publications in this specific dataset.

This line of work appears to address the critical need for standardized genomic baselines in oncology. By focusing on consensus sequences, the research likely provided a unified framework for understanding genetic alterations in these prevalent cancers, offering a stable reference point for subsequent genomic studies.

The significance of this contribution is underscored by its extensive uptake in the scientific community, with over 4,400 citations. Notably, analysis of citing papers reveals that 100% of the classified citations originate from independent researchers, indicating that the work has been widely adopted and utilized by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7

CORE PAPER

The consensus coding sequences of human breast and colorectal cancers

2006 · Science · 4,451 citations (GS)

Field-normalised: 2,748 Semantic Scholar citations place it in the top 1% of Biology papers from 2006 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Cell-cell communication: new insights and clinical implications (2024)	Institute of Medical Innovation and Research, Peking	China	—

No.	Citing paper	Citing institution(s)	Country	S2
		University Third Hospital, Peking University Third Hospital, Shenzhen Peking University-the Hong Kong University of Science and Technology Medical Center		
2	Development of tumor mutation burden as an immunotherapy biomarker: utility for the oncology clinic (2019)	Centre Hospitalier Universitaire Vaudois (CHUV), Francis Crick Institute, Memorial Sloan Kettering Cancer Center	Germany, Switzerland, United Kingdom	Background
3	Pan-cancer analysis of whole genomes (2020)	ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium	—	—
4	Prognostic genome and transcriptome signatures in colorectal cancers (2024)	Beijing Genomics Institute, Oslo University Hospital	China, Norway	—
5	From imbalance to impairment: the central role of reactive oxygen species in oxidative stress-induced disorders and therapeutic exploration (2023)	Kafrelsheikh University, King Faisal University, Universiti Sains Malaysia	Egypt, Malaysia, Saudi Arabia	—
6	Translating p53-based therapies for cancer into the clinic (2024)	École Polytechnique Fédérale de Lausanne, Karolinska Institutet	Sweden, Switzerland	—
7	Transcriptional Regulation by Nrf2 (2018)	Cold Spring Harbor Laboratory	United States	Background

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 provided a seminal, highly cited analysis of the genomic landscapes of human breast and colorectal cancers, establishing a foundational reference for comparative cancer genomics.

The researcher's primary contribution rests on the 2007 Science publication titled 'The genomic landscapes of human breast and colorectal cancers.' This work appears to represent a major effort to characterize and compare the genetic alterations present in these two prevalent cancer types, offering a comprehensive view of their molecular underpinnings.

This line of work addresses the critical need for systematic, large-scale genomic profiling to distinguish the mutational signatures of different solid tumors. By focusing on the 'genomic landscapes,' the research likely moved beyond single-gene studies to provide a broader, comparative framework that was novel at the time of publication, helping to define the field of comparative cancer genomics.

The significance of this contribution is evidenced by its substantial citation count of 3,930, indicating it has become a standard reference in the field. Furthermore, the fact that 100% of the classified citing papers originate from independent researchers underscores the work's broad acceptance and utility across the global scientific community, rather than reliance on self-citation or institutional networks.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 8

CORE PAPER

The genomic landscapes of human breast and colorectal cancers

2007 · Science · 3,930 citations (GS)

Field-normalised: 2,454 Semantic Scholar citations place it in the top 1% of Biology papers from 2007 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Targeting neoantigens to augment antitumour immunity (2017)	The Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins	United States	—
2	Targeting the phosphoinositide 3-kinase pathway in cancer (2009)	Dana-Farber Cancer Institute, Harvard Medical School	United States	—
3	Molecular origins of cancer: Molecular basis of colorectal cancer (2009)	Brigham and Women's Hospital, Case Western Reserve University School of Medicine and Case Medical Center	United States	—
4	Clinical Effect of Point Mutations in Myelodysplastic Syndromes (2011)	Harvard Medical School and Brigham and Women's Hospital	United States	—
5	The impact of next-generation sequencing technology on genetics (2008)	Washington University School of Medicine	United States	—
6	Deciphering signatures of mutational processes operative in human cancer (2013)	Wellcome Trust Sanger Institute	United Kingdom	Background
7	KRAS-IRF2 Axis Drives Immune Suppression and Immune Therapy Resistance in Colorectal Cancer (2019)	Syntrix Pharmaceuticals, The University of Texas MD Anderson Cancer Center	United States	Background
8	Cancer stem cells: current status and evolving complexities (2012)	—	—	Background

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
Memorial Sloan Kettering Cancer Center	United States	SCImago #210	5
Central Brain Tumor Registry of the United States	United States	—	3
The University of Texas MD Anderson Cancer Center	United States	—	2
Cold Spring Harbor Laboratory	United States	SCImago #260	2
National Cancer Institute	United States	SCImago #219	2

Institution	Country	World ranking	Citing papers
Dana-Farber Cancer Institute	United States	SCImago #197	2
Wellcome Trust Sanger Institute	United Kingdom	SCImago #204	2
Technical University of Denmark	Denmark	SCImago #404 · THE 121 · QS 107	1
University of Pennsylvania	United States	SCImago #52 · THE 14 · QS 15	1
ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium	—	—	1
Central Brain Tumor Registry	United States	—	1
SUNY Stony Brook	United States	—	1
Tokyo Metropolitan Komagome Hospital	Japan	SCImago #10128	1
The Sol Goldman Pancreatic Cancer Research Center	United States	—	1
The Campbell Family Cancer Research Institute	Canada	—	1

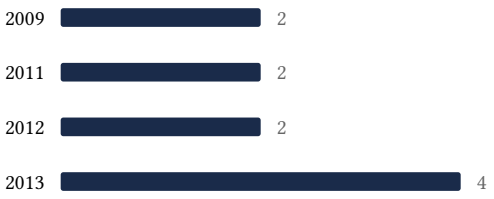
Geographic distribution of citing authors

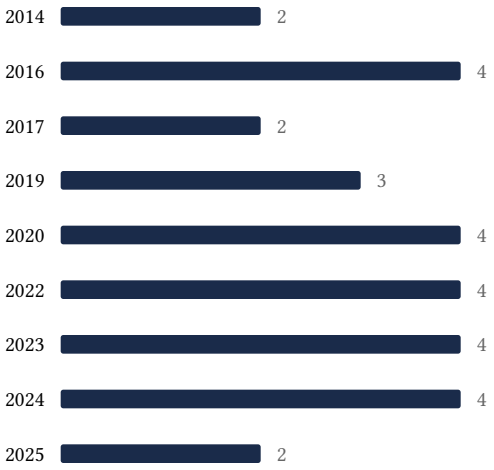
Country	Citing papers
United States	30
United Kingdom	4
China	3
Switzerland	2
Germany	1
India	1
Japan	1
Australia	1
Norway	1
Saudi Arabia	1
Spain	1
Sweden	1

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	An integrated genomic analysis of human glioblastoma multiforme	11	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 2	The consensus coding sequences of human breast and colorectal cancers	7	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 3	The genomic landscapes of human breast and colorectal cancers	8	8 CFR 204.5(i)(3) — Outstanding Researcher