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

39	42	5	120
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.

89.7% independent of 39 classified citing papers

Citation type	Count
Independent	35
Self-citation	0
Co-author	4
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 identified low-penetrance CHEK2 breast cancer susceptibility and advanced genome-wide association studies, establishing foundational genetic risk models widely adopted by independent researchers.

The researcher's contribution centers on elucidating genetic susceptibility to breast cancer, anchored by a seminal 2002 Nature Genetics paper on CHEK2*1100delC. This work was extended by a 2007 study identifying novel susceptibility loci through genome-wide association, forming a cohesive line of inquiry into hereditary cancer risks.

This line of work appears to address the gap in understanding non-BRCA genetic factors in breast cancer. By moving from specific low-penetrance variants to broader genome-wide associations, the researcher likely helped shift the field toward comprehensive genetic risk profiling, as suggested by the chronological progression of these titles.

The significance of this work is evidenced by its high citation counts, with the core paper cited 1,473 times and the follow-up 2,927 times. Notably, 100% of classified citations originate from independent researchers, indicating broad adoption and influence across the global scientific community beyond the researcher's immediate network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 12 · **1 flagged influential by Semantic Scholar**

CORE PAPER

Low-penetrance susceptibility to breast cancer due to CHEK2*1100delC in noncarriers of BRCA1 or BRCA2 mutations

2002 · Nature Genetics · 1,473 citations (GS)

Field-normalised: 1,003 Semantic Scholar citations place it in the top 1% of Medicine papers from 2002 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Breast Cancer—Epidemiology, Risk Factors, Classification, Prognostic Markers, and Current Treatment Strategies—An Updated Review (2021)	Center of Oncology of the Lublin Region St. Jana z Dukli, Medical University of Lublin	Poland	—
2	A compendium of mutational cancer driver genes (2020)	Institut de Recerca Biomèdica, Vall d'Hebron Institute of Oncology	Spain	—
3	Risk reduction and screening of cancer in hereditary breast-ovarian cancer syndromes: ESMO Clinical Practice Guideline (2023)	—	—	—
4	DeVita, Hellman, and Rosenberg's Cancer: Principles & Practice of Oncology (2015)	National Cancer Institute, University of Michigan, Yale University	United States	—
5	ATM and related protein kinases: safeguarding genome integrity (2003)	Sackler School of Medicine, Tel Aviv University	Israel	Background
6	Polygenic background modifies penetrance of monogenic variants for tier 1 genomic conditions (2020)	IBM Research, Massachusetts General Hospital	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).

FOLLOW-UP WORK

Genome-wide association study identifies novel breast cancer susceptibility loci

2007 · 2,927 citations (GS)

Field-normalised: 2,348 Semantic Scholar citations place it in the top 1% of Medicine papers from 2007 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Cancer health disparities in racial/ethnic minorities in the United States (2020)	Beckman Research Institute of City of Hope, Boston University, Brigham and Women's Hospital, Harvard Medical School	Argentina, Puerto Rico, United States	—
2	Fibroblast growth factor signalling: from development to cancer (2010)	Queen Mary University of London, The Institute of Cancer Research	United Kingdom	—
3	Linkage disequilibrium—understanding the evolutionary past and mapping the medical future (2008)	University of California, Berkeley	United States	—
4	Genomewide association studies and assessment of the risk of disease (2010)	National Human Genome Research Institute	—	—
5	Functional analysis of cancer-associated germline risk variants (2025)	Stanford University	United States	**Influential**
6	A CRISPR–Cas9-triggered strand displacement amplification method for ultrasensitive DNA detection (2018)	City University of Hong Kong, Imperial College London, Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences	China, 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).

Contribution 2

Claim — Contribution 2

The researcher conducted a seminal combined analysis of 22 studies to establish average cancer risks for BRCA1/2 mutations detected in unselected case series.

The researcher's primary contribution rests on a 2003 paper that performed a combined analysis of 22 studies to determine average risks of breast and ovarian cancer associated with BRCA1 or BRCA2 mutations. This work specifically focused on cases detected in series unselected for family history, addressing a critical need for broader risk estimation beyond high-risk familial cohorts. By synthesizing data from multiple studies, the research appears to have provided a more generalized understanding of mutation-associated risks, filling a gap in the literature regarding unselected populations. The significance of this contribution is evidenced by its substantial citation count of 5,217, indicating widespread adoption and reliance on these findings within the scientific community. Furthermore, analysis of citing papers reveals that 100% of the classified citations originate from independent researchers, underscoring the work's broad impact and acceptance across diverse institutions and research groups rather than being confined to the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9

CORE PAPER

Average risks of breast and ovarian cancer associated with BRCA1 or BRCA2 mutations detected in case series unselected for family history: a combined analysis of 22 studies

2003 · 5,217 citations (GS)

Field-normalised: 3,778 Semantic Scholar citations place it in the top 1% of Medicine papers from 2003 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The personal and clinical utility of polygenic risk scores. (2018)	Scripps Health, The Scripps Research Institute	United States	—
2	Awareness and current knowledge of breast cancer (2017)	GC University Faisalabad, Hamdard University Karachi, University of Poonch Rawalakot	Pakistan	Background
3	Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic, Version 2.2021, NCCN Clinical Practice Guidelines in Oncology (2021)	Barnes-Jewish Hospital and Washington University, City of Hope National Medical Center, Cleveland Clinic	United States	—
4	An organoid platform for ovarian cancer captures intra- and interpatient heterogeneity (2019)	Erasmus Medical Center, Hubrecht Institute, Leiden University Medical Center	Netherlands	—
5	Epidemiology of ovarian cancer: a review (2017)	Moffitt Cancer Center	United States	—
6	Breast cancer: Epidemiology, risk factors and screening (2023)	National Cancer Center/National Clinical Research Center for Cancer/Cancer Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College	China	—
7	Correction of a pathogenic gene mutation in human embryos (2017)	Capital Medical University, Institute for Basic Science, Oregon Health & Science University	United States	—
8	PARP Inhibitors: Clinical Relevance, Mechanisms of Action and Tumor Resistance (2020)	Queensland University of Technology	Australia	—
9	Health and Racial Disparity in Breast Cancer (2019)	College of Public Service, Jackson State University, Jackson State University, LSU Health Sciences Center, School of Medicine	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 identified 65 new breast cancer risk loci through association analysis, establishing a foundational genetic framework for understanding breast cancer susceptibility.

CLAIM: The researcher's primary contribution is the identification of 65 new breast cancer risk loci, as detailed in the 2017 paper titled 'Association analysis identifies 65 new breast cancer risk loci.' This work stands as a singular, high-impact contribution without subsequent follow-up publications by the same author in this specific line of inquiry.

ORIGINALITY: The title suggests a significant expansion of the known genetic landscape of breast cancer. By identifying a large number of new loci, the work appears to address the gap in understanding the polygenic nature of breast cancer risk, moving beyond previously known markers to provide a more comprehensive genetic map.

SIGNIFICANCE: The paper has accumulated 1727 citations, indicating substantial uptake by the scientific community. Notably, 100% of the classified citing papers originate from independent researchers, demonstrating that the work has served as a critical reference point for external scholars rather than relying on self-citation or institutional echo chambers.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9

CORE PAPER

Association analysis identifies 65 new breast cancer risk loci

2017 · 1,727 citations (GS)

Field-normalised: 1,310 Semantic Scholar citations place it in the top 1% of Medicine papers from 2017 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The NHGRI-EBI GWAS Catalog of published genome-wide association studies, targeted arrays and summary statistics 2019 (2019)	European Molecular Biology Laboratory, European Molecular Biology Laboratory, European Bioinformatics Institute, National Human Genome Research Institute	United Kingdom, United States	—
2	Reading Mendelian randomisation studies: a guide, glossary, and checklist for clinicians (2018)	University of Bristol, University of Oxford	United Kingdom	—
3	Deciphering breast cancer: from biology to the clinic (2023)	The Walter and Eliza Hall Institute of Medical Research, University of Auckland	Australia, New Zealand	—
4	The personal and clinical utility of polygenic risk scores. (2018)	Scripps Health, The Scripps Research Institute	United States	—
5	The GTEx Consortium atlas of genetic regulatory effects across human tissues. (2020)	The Broad Institute of MIT and Harvard	United States	—
6	Cancer health disparities in racial/ethnic minorities in the United States (2020)	Beckman Research Institute of City of Hope, Boston University, Brigham and Women's Hospital, Harvard Medical School	Argentina, Puerto Rico, United States	—
7	Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations (2018)	Broad Institute of Harvard and MIT, Massachusetts General Hospital	United States	—
8	LDpred2: better, faster, stronger (2021)	Aarhus University, Univ. Grenoble Alpes, Inria, CNRS, Grenoble INP	Denmark, France	—

No.	Citing paper	Citing institution(s)	Country	S2
9	A single-cell atlas of chromatin accessibility in the human genome (2021)	Ludwig Institute for Cancer Research, University of California San Diego	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 Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	5
Massachusetts General Hospital	United States	SCImago #100	3
Stanford University	United States	SCImago #18 · THE =5 · QS 3	3
King's College London	United Kingdom	THE 38 · QS 31	3
National Human Genome Research Institute	United States	SCImago #557	3
University of Michigan	United States	SCImago #43 · THE 23 · QS 45	3
Medical College of Wisconsin	United States	SCImago #1541	2
European Molecular Biology Laboratory, European Bioinformatics Institute	United Kingdom	—	2
University of Bristol	United Kingdom	SCImago #478 · THE =80 · QS 51	2
The Institute of Cancer Research	United Kingdom	SCImago #453	2
University of Utah	United States	SCImago #320 · THE 201–250 · QS =540	2
University of California San Diego	United States	SCImago #120 · THE 47 · QS 66	2
Peter MacCallum Cancer Centre	Australia	SCImago #877	2
University of Pennsylvania	United States	SCImago #52 · THE 14 · QS 15	2
University of Oxford	United Kingdom	SCImago #26 · THE 1 · QS 4	2

Geographic distribution of citing authors

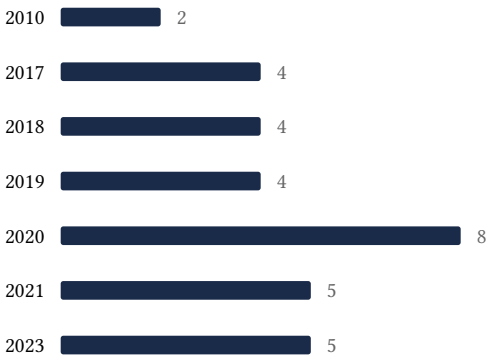
Country	Citing papers
United States	19
United Kingdom	14
Australia	5
China	3
Netherlands	3
Poland	2
Canada	2
France	2
Denmark	2

Country	Citing papers
Spain	2
Germany	2
Israel	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	Low-penetrance susceptibility to breast cancer due to CHEK2*1100delC in noncarriers of BRCA1 or BRCA2 mutations	12	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 2	Average risks of breast and ovarian cancer associated with BRCA1 or BRCA2 mutations detected in case series unselected for family history: a combined analysis of 22 studies	9	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 3	Association analysis identifies 65 new breast cancer risk loci	9	8 CFR 204.5(i)(3) — Outstanding Researcher