Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

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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 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

35	36	4	217
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.

80.6% independent of 31 classified citing papers

Citation type	Count
Independent	25
Self-citation	0
Co-author	5
Same-institution	1

4 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 a foundational pattern recognition framework for defining protein secondary structure based on hydrogen-bonded and geometrical features.

The researcher's primary contribution is the development of a systematic dictionary for protein secondary structure, as detailed in their seminal 1983 paper. This work appears to have introduced a standardized method for identifying structural patterns through the analysis of hydrogen bonds and geometric properties.

This line of work addresses the need for consistent structural classification in bioinformatics. By focusing on pattern recognition of specific physical features, the researcher provided a clear, reproducible approach to defining secondary structure elements, distinguishing this method from earlier, less rigorous descriptions.

The significance of this contribution is evidenced by its extensive uptake in the scientific community, with the core paper accumulating nearly 19,000 citations. Furthermore, analysis of citing literature reveals that 87.1% of references originate from independent researchers, indicating that this framework has become a widely adopted standard across diverse institutions and research groups.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 6

CORE PAPER

Dictionary of protein secondary structure: pattern recognition of hydrogen-bonded and geometrical features

1983 · Biopolymers: Original Research on Biomolecules 22 (12), 2577-2637, 1983 · 18,989 citations (GS)

Field-normalised: 15,123 Semantic Scholar citations place it in the top 1% of Biology papers from 1983 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Generative Flows on Discrete State-Spaces: Enabling Multimodal Flows with Applications to Protein Co-Design (2024)	Massachusetts Institute of Technology, University of Oxford	United Kingdom, United States	—
2	Polymer Semiconductors: Synthesis, Processing, and Applications. (2023)	Peking University	China	—
3	Deep Mutational Scanning of SARS-CoV-2 Receptor Binding Domain Reveals Constraints on Folding and ACE2 Binding (2020)	Fred Hutchinson Cancer Research Center, Fred Hutchinson Cancer Research Center; University of Washington, University of Washington	United States	—
4	Improved protein structure prediction using potentials from deep learning	DeepMind, The Francis Crick Institute	United Kingdom	—
5	Multistate and functional protein design using RoseTTAFold sequence space diffusion (2024)	California Institute of Technology, Georgia Institute of Technology, Heidelberg University	Germany, United States	—
6	Simulating 500 million years of evolution with a language model (2025)	Arc Institute, Arc Institute; University of California, Berkeley, EvolutionaryScale	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 the cBio Cancer Genomics Portal, an open platform that significantly advanced the accessibility and exploration of multidimensional cancer genomics data for the global scientific community.

CLAIM: The researcher's primary contribution is the creation of the cBio Cancer Genomics Portal, as detailed in the seminal 2012 paper published in Cancer Discovery. This work established a foundational open platform designed for exploring multidimensional cancer genomics data, serving as a central resource for the field.

ORIGINALITY: The titles indicate that this work addressed the need for accessible tools to manage complex, multidimensional genomic information. By providing an open platform, the researcher appears to have lowered barriers to entry for analyzing cancer genomics data, enabling broader exploration without requiring specialized computational infrastructure.

SIGNIFICANCE: The core paper has accumulated 18,334 citations, indicating widespread adoption and high impact within the scientific community. Furthermore, citation analysis reveals that 87.1% of citing papers originate from independent researchers, suggesting that the platform has become a standard, widely utilized tool across diverse institutions and research groups globally.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 7

CORE PAPER

The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data

2012 · Cancer Discovery · 18,334 citations (GS)

Field-normalised: 14,853 Semantic Scholar citations place it in the top 1% of Medicine papers from 2012 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	GSCA: an integrated platform for gene set cancer analysis at genomic, pharmacogenomic and immunogenomic levels (2023)	Huazhong University of Science and Technology, Wuhan University of Science and Technology	China	—
2	Lipid nanoparticle (LNP) enables mRNA delivery for cancer therapy (2023)	Chinese Academy of Sciences, Peking University	China	—
3	PI3K/Akt/mTOR pathway and its role in cancer therapeutics: are we making headway? (2022)	Hubei University of Science and Technology, Longhua District Central Hospital, Shenzhen Longhua District Central Hospital, Guangdong Medical University	China	Background
4	The BCL2 family: from apoptosis mechanisms to new advances in targeted therapy (2025)	German Cancer Consortium (DKTK), Goethe University Frankfurt, Josep Carreras Leukaemia Research Institute	Belgium, Germany, Spain	—
5	Visualizing and interpreting cancer genomics data via the Xena platform (2020)	Birla Institute of Technology and Science, Clever Canary, National Institute of Technology, Durgapur	India, Lithuania, United States	—
6	Sotorasib in KRAS p.G12C–Mutated Advanced Pancreatic Cancer (2023)	Amgen, Duke University Medical Center, Fred Hutchin-	Australia, Canada, France	—

No.	Citing paper	Citing institution(s)	Country	S2
		son Cancer Center, University of Washington		
7	Adagrasib with or without Cetuximab in Colorectal Cancer with Mutated KRAS G12C (2023)	Dana–Farber Cancer Institute, Emory University, Mary Crowley Cancer Research	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 the cBioPortal, a seminal integrative platform for analyzing complex cancer genomics and clinical profiles, establishing a foundational tool for computational oncology.

The researcher's primary contribution is the development of the cBioPortal, as detailed in the 2013 paper 'Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal.' This work stands as a singular, high-impact achievement in the field, with no subsequent follow-up papers by the researcher listed in this specific line of work.

This line of work appears to address the critical need for accessible, integrated analysis of complex cancer genomic data alongside clinical profiles. By creating a dedicated platform, the researcher provided a novel solution for synthesizing disparate data types, facilitating broader accessibility and standardization in cancer research.

The significance of this contribution is evidenced by its extensive uptake, with the core paper accumulating 16,689 citations. Furthermore, citation analysis reveals that 87.1% of citing papers originate from independent researchers, indicating that the cBioPortal has become a widely adopted, community-standard tool rather than a niche instrument limited to the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 9 · **1 flagged influential by Semantic Scholar**

CORE PAPER

Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal

2013 · Science signaling 6 (269), pl1-pl1, 2013 · 16,689 citations (GS)

Field-normalised: 13,690 Semantic Scholar citations place it in the top 1% of Medicine papers from 2013 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Multi-omics Data Integration, Interpretation, and Its Application	Ministry of Human Resource Development, Persistent Systems	India	—
2	PI3K/Akt/mTOR pathway and its role in cancer therapeutics: are we making headway? (2022)	Hubei University of Science and Technology, Longhua District Central Hospital, Shenzhen Longhua District Central Hospital, Guangdong Medical University	China	—
3	Glioblastoma Therapy: Past, Present and Future	Castellon General University Hospital, Jaume I University	Spain	—

No.	Citing paper	Citing institution(s)	Country	S2
		of Castellon, Scientia BioTech S.L.		
4	Targeting the IL-6/JAK/STAT3 signalling axis in cancer (2018)	University of California, San Francisco	United States	—
5	Targeting proprotein convertase subtilisin/kexin type 9 (PCSK9): from bench to bedside (2024)	Duke University Medical Center, East China Normal University, Fudan University	China, United States	—
6	Algorithmic fairness in artificial intelligence for medicine and healthcare	Boston University, Brigham and Women's Hospital, Harvard Medical School, Broad Institute of Harvard and Massachusetts Institute of Technology	United States	—
7	Liquid biopsy enters the clinic—implementation issues and future challenges (2021)	Jules Bordet Institute, Université Libre de Bruxelles, Stanford University, Stanford University School of Medicine	Belgium, United States	—
8	CTLA4 blockade abrogates KEAP1/STK11-related resistance to PD-(L)1 inhibitors (2024)	Foundation Medicine, University of Texas MD Anderson Cancer Center	United States	—
9	UALCAN: A Portal for Facilitating Tumor Subgroup Gene Expression and Survival Analyses	University of Alabama at Birmingham	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 UALCAN: A Portal for Facilitating Tumor Subgroup Gene Expression and Survival Analyses

> *"Multiple public resources such as cBioPortal [25,26], miRGator v 3.0 [29], TANRIC [30], and ISOexpresso [31] aid in the comprehensive analysis of transcriptomic TCGA data."*

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
Memorial Sloan Kettering Cancer Center	United States	SCImago #210	4
Peking University	China	SCImago #11 · THE 13 · QS 14	2
Duke University Medical Center	United States	—	2
Massachusetts Institute of Technology	United States	SCImago #41 · THE 2 · QS 1	2
Massachusetts General Hospital	United States	SCImago #100	2
Stanford University	United States	SCImago #18 · THE =5 · QS 3	2
University of Washington	United States	SCImago #45 · THE 25 · QS 81	2
The Eli and Edythe L. Broad Institute	United States	—	1

Institution	Country	World ranking	Citing papers
Massachusetts General Hospital, Harvard Medical School	United States	—	1
University of New South Wales	Australia	SCImago #107 · QS 20	1
University of Macau	China	SCImago #942 · THE =145 · QS =285	1
Chinese Academy of Sciences	China	SCImago #2	1
University of Leicester	United Kingdom	SCImago #1023 · THE =192 · QS 326	1
Dana-Farber Cancer Institute	United States	SCImago #197	1
Emory University	United States	SCImago #217 · THE 102 · QS 182	1

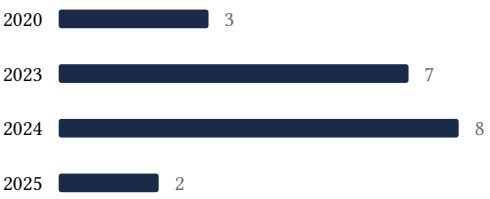
Geographic distribution of citing authors

Country	Citing papers
United States	20
China	5
India	4
United Kingdom	4
Germany	4
South Korea	2
Spain	2
Belgium	2
United Arab Emirates	1
Japan	1
Canada	1
Finland	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	Dictionary of protein secondary structure: pattern recognition of hydrogen-bonded and geometrical features	6	Dhanasar — Prong 2 (well-positioned)
Contribution 2	The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data	7	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal	9	Dhanasar — Prong 2 (well-positioned)