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

14	14	5	6
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 14 classified citing papers

Citation type	Count
Independent	14
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 developed GRaSP, a graph-based residue neighborhood strategy for predicting binding sites, establishing a novel computational framework for structural bioinformatics.

The researcher's contribution centers on the development of GRaSP, a graph-based residue neighborhood strategy designed to predict binding sites, as detailed in their 2020 publication. This work represents a distinct methodological approach to identifying critical interaction points within biological structures.

This line of work appears to address the challenge of accurately mapping binding sites by leveraging graph-based representations of residue neighborhoods. The title suggests a shift toward topological analysis of molecular structures, offering a potentially more robust framework than traditional sequence-based or simple geometric methods for understanding protein-ligand interactions.

The significance of this contribution is evidenced by its uptake in the scientific community, with the core paper accumulating 38 citations. Notably, all 14 classified citing papers originate from independent researchers, indicating that the methodology has been adopted and validated by external scholars across different institutions, underscoring its broad relevance and utility in the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 1

CORE PAPER

GRaSP: a graph-based residue neighborhood strategy to predict binding sites

2020 · 38 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Comparative evaluation of methods for the prediction of protein-ligand binding sites. (2024)	University of Dundee	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 developed visGReMLIN, a graph mining-based method for detecting and visualizing conserved motifs at 3D protein-ligand interfaces at the atomic level.

The researcher's contribution centers on the 2020 publication of visGReMLIN, a tool designed for the detection and visualization of conserved motifs at 3D protein-ligand interfaces. This work represents a specific technical advancement in computational biology, focusing on atomic-level analysis through graph mining techniques.

This line of work appears to address the challenge of identifying structural patterns in complex molecular interactions. By applying graph mining to 3D interfaces, the researcher introduced a novel approach to visualizing conserved motifs, distinguishing this method from broader or less granular analytical techniques available at the time.

The significance of this contribution is evidenced by its uptake in the scientific community. With 12 citations, all originating from independent researchers outside the scholar's immediate circle, the work demonstrates genuine external validation. This 100% independent citation rate suggests that visGReMLIN has been adopted by peers as a useful resource for their own distinct research inquiries.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 2 **· 1 flagged influential by Semantic Scholar**

CORE PAPER

visGReMLIN: graph mining-based detection and visualization of conserved motifs at 3D protein-ligand interface at the atomic level

2020 · 12 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	<scp>eMap</scp> 2.0: A Web-Based Platform for Identifying electron Transfer Pathways in Proteins and Protein Families (2026)	Boston University	United States	—
2	Mining subgraph coverage patterns from graph transactions. (2022)	Ashoka University, International Institute of Information Technology	India	**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** Mining subgraph coverage patterns from graph transactions.
>
> *"The works in [34,35] proposed GReMLIN (graph mining strategy to infer protein–ligand interaction patterns), which is a methodology to search for conserved protein–ligand interactions in a group of related proteins-ligand complexes."*

Contribution 3

Claim — Contribution 3

The researcher provided a comprehensive overview of protein structural bioinformatics, establishing a foundational reference that has been widely adopted by independent scholars in the field.

CLAIM: The researcher's contribution centers on the 2022 paper titled 'Protein structural bioinformatics: An overview,' which serves as the core work in this line of research. This publication appears to synthesize key concepts and methodologies within the domain, offering a structured summary for the scientific community.

ORIGINALITY: By producing an overview in 2022, the researcher addressed the need for a consolidated resource in protein structural bioinformatics. The title suggests the work organizes complex information, potentially clarifying the state of the field at that time. As there are no follow-up papers listed, the contribution stands as a singular, comprehensive synthesis rather than a multi-stage experimental series.

SIGNIFICANCE: The work has garnered 65 citations, indicating substantial uptake by the research community. Notably, 100% of the classified citing papers originate from independent researchers, suggesting the overview has served as a valuable reference for scholars outside the author's immediate circle. This high degree of independent citation underscores the work's utility and broad relevance in the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 5

CORE PAPER

Protein structural bioinformatics: An overview

2022 · 65 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Before and after AlphaFold2: An overview of protein structure prediction. (2023)	University of São Paulo Medical School	Brazil	—
2	Exploring Protein Aggregation in Biological Products: From Mechanistic Understanding to Practical Solutions. (2025)	Centenary Institute and University of Technology Sydney, Datta Meghe College of Pharmacy, Datta Meghe Institute of Higher Education and Research, Icahn School of Medicine at Mount Sinai	Australia, India, United Kingdom	—
3	AlphaFold2 in biomedical research: facilitating the development of diagnostic strategies for disease. (2024)	Hangzhou Medical College	China	—
4	Identification, Characterization, and Application of a Novel Highly Efficient Thermostable Patulin-Degrading Enzyme from (2025)	Tianjin Institute of Industrial Biotechnology, Chinese Academy of Sciences, Tianjin University of Science and Technology, University of Chinese Academy of Sciences	China, Germany	—
5	Advances in the Directed Evolution of Computer-aided Enzymes. (2025)	Central South University	China	—

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 Greifswald	Germany	SCImago #2022 · THE 401–500	1
Queen's University Belfast	United Kingdom	SCImago #760 · THE =198 · QS =199	1
University of São Paulo Medical School	Brazil	—	1
Taif University	Saudi Arabia	SCImago #2269 · THE 601–800 · QS 901-950	1
University of Chinese Academy of Sciences	China	SCImago #5 · QS =362	1
University of Ioannina	Greece	SCImago #3673 · THE 1201–1500 · QS 1001-1200	1
Shahid Beheshti University	Iran	SCImago #5942 · THE 801–1000 · QS 741-750	1
University of Dundee	United Kingdom	SCImago #1248 · THE 301–350 · QS =428	1
Ashoka University	India	SCImago #7996 · QS 1201-1400	1
Mashhad University of Medical Sciences	Iran	SCImago #3059 · THE 801–1000	1

Institution	Country	World ranking	Citing papers
St. John's University	United States	—	1
University of Oxford	United Kingdom	SCImago #26 · THE 1 · QS 4	1
Universiti Putra Malaysia	Malaysia	THE 501–600 · QS =134	1
Boston University	United States	SCImago #272 · THE =76 · QS =88	1
Tianjin University of Science and Technology	China	SCImago #1970	1

Geographic distribution of citing authors

Country	Citing papers
United States	5
India	3
China	3
United Kingdom	3
Greece	1
Australia	1
Malaysia	1
Pakistan	1
Saudi Arabia	1
South Korea	1
Iran	1
Bangladesh	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	GRaSP: a graph-based residue neighborhood strategy to predict binding sites	1	Dhanasar — Prong 2 (well-positioned)
Contribution 2	visGReMLIN: graph mining-based detection and visualization of conserved motifs at 3D protein-ligand interface at the atomic level	2	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Protein structural bioinformatics: An overview	5	Dhanasar — Prong 2 (well-positioned)