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 2026-06-11 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

637	638	30	15
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.

84.0% independent of 563 classified citing papers

Citation type	Count
Independent	473
Self-citation	13
Co-author	77
Same-institution	0

74 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 pioneered the de novo design of protein homo-oligomers with modular specificity, subsequently extending this framework to engineer bioactive switches and logic gates.

The researcher established a foundational contribution in protein engineering through the 2016 publication on the de novo design of protein homo-oligomers with modular hydrogen-bond network–mediated specificity. This core work appears to have introduced a systematic approach for controlling protein assembly and interaction specificity at the molecular level.

This line of work addresses the challenge of creating precise, programmable protein interactions from scratch. The subsequent publications on bioactive protein switches (2019) and protein logic gates (2020) suggest that the researcher successfully expanded the initial oligomer design principles into functional devices capable of sensing and processing biological signals, indicating a progression from structural design to functional application.

The significance of this contribution is evidenced by substantial citation activity, with the core paper accumulating 419 citations and the follow-up works garnering 335 and 263 citations respectively. Furthermore, analysis indicates that 83.8% of citing papers originate from independent researchers, demonstrating that this framework has been widely adopted and utilized by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 161 · **5 flagged influential by Semantic Scholar**

CORE PAPER

De novo design of protein homo-oligomers with modular hydrogen-bond network–mediated specificity

2016 · 419 citations (GS)

Field-normalised: 293 Semantic Scholar citations place it in the top 1% of Chemistry papers from 2016 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Large language models generate functional protein sequences across diverse families	Salesforce Research	United States	—
2	Advances in protein structure prediction and design	University of North Carolina at Chapel Hill	United States	—
3	De novo designed phospho-switchable protein-protein interaction domains for synthetic biology applications	Sinovac Biotech, Tsinghua University	China	—
4	Artificial intelligence-aided protein engineering: from topological data analysis to deep protein language models	Michigan State University	United States	—
5	Protein design: from the aspect of water solubility and stability	Avalon GloboCare Corp., Massachusetts Institute of Technology, Shanghai Jiao Tong University	China, Norway, Russia	—
6	Recent advances in de novo protein design: Principles, methods, and applications	Chan Zuckerberg Initiative (United States), Howard Hughes Medical Institute	United States	—
7	Protein design via deep learning	Beijing Advanced Sciences and Innovation Center, The University of Tokyo, Tsinghua University	China, Japan	—

No.	Citing paper	Citing institution(s)	Country	S2
8	Exploration of the hierarchical assembly space of collagen-like peptides beyond the triple helix	University of Washington	United States	—
9	Structure-based protein design with deep learning	Google DeepMind, Seoul National University	South Korea, United Kingdom	—
10	Design of complicated all-α protein structures	The Exploratory Research Center on Life and Living Systems, The Graduate University for Advanced Studies, SOKENDAI	Japan	—
11	Breakthroughs in computational design methods open up new frontiers for de novo protein engineering	Institute for Protein Innovation	United States	—
12	De novo protein design, a retrospective	Syracuse University, University of California, San Francisco	United States	—
13	Expanding the versatility of natural and de novo designed coiled coils and helical bundles	Friedrich Miescher Laboratory, Max Planck Institute for Developmental Biology	Germany	—
14	Protein sequence design with a learned potential	Stanford University	United States	—
15	Computational design of novel protein–protein interactions–An overview on methodological approaches and applications	École Polytechnique Fédérale de Lausanne	Switzerland	—
16	What has de novo protein design taught us about protein folding and biophysics?	University of Manchester	United Kingdom	—
17	Third generation antibody discovery methods: in silico rational design	University of Cambridge	United Kingdom	—
18	Principles of protein stability and their application in computational design	Weizmann Institute of Science	Israel	—
19	Principles for computational design of binding antibodies	Google, Inc., Weizmann Institute of Science	Israel, United States	—
20	Spatial multiplexing of fluorescent reporters for imaging signaling network dynamics	Brigham and Women's Hospital, IIT@MIT, Kansas State University	United States	—
21	Deep neural language modeling enables functional protein generation across families	Hesco (United States), Salesforce Research, Salesforce (United States)	United States	—
22	Towards functional de novo designed proteins	University of Bristol	United Kingdom	—
23	Self-assembly and regulation of protein cages from pre-organised coiled-coil modules	National Institute of Chemistry, National Research Council of Italy	Italy, Slovenia	—
24	Getting momentum: from biocatalysis to advanced synthetic biology	Universität Greifswald	Germany	—
25	Dissecting the stability determinants of a challenging de novo protein fold using massively parallel design and experimentation	Northwestern Medicine, Princess Margaret Cancer Centre, University of Toronto	Canada, United States	—
26	Understanding a protein fold: The physics, chemistry, and biology of α-helical coiled coils	University of Bristol	United Kingdom	—
27	The advent of de novo proteins for cancer immunotherapy	Neoleukin Therapeutics (United States)	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
28	Accessing semiaddressable self-assembly with efficient structure enumeration	Institute of Science and Technology Austria	Austria	—
29	Time-resolved spectroscopic mapping of vibrational energy flow in proteins: Understanding thermal diffusion at the nanoscale	Osaka University	Japan	—
30	The “cancer immunogram”	David Geffen School of Medicine at UCLA, Netherlands Cancer Institute	Netherlands, United States	—

Showing the 30 most-cited of 161 independent citing papers.

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

De novo design of bioactive protein switches

2019 · 335 citations (GS)

Field-normalised: 235 Semantic Scholar citations place it in the top 1% of Chemistry papers from 2019 indexed by Semantic Scholar, by citation count.

No independent citing papers resolved for this paper in the current crawl.

FOLLOW-UP WORK

De novo design of protein logic gates

2020 · 263 citations (GS)

Field-normalised: 183 Semantic Scholar citations place it in the top 1% of Chemistry papers from 2020 indexed by Semantic Scholar, by citation count.

No independent citing papers resolved for this paper in the current crawl.

Contribution 2

Claim — Contribution 2

The researcher pioneered cargo-sorting DNA robots and extended this framework to protein-based base pairing, establishing a foundational approach for molecular-scale autonomous systems.

The researcher’s core contribution centers on the development of a cargo-sorting DNA robot, introduced in a 2017 paper that has garnered 639 citations. This work appears to establish a functional prototype for molecular-scale automation, serving as the foundation for subsequent investigations into biomolecular engineering.

This line of work addresses the challenge of creating autonomous molecular machines capable of specific sorting tasks. The progression from DNA-based robots to a 2019 study on creating protein versions of DNA base pairing suggests an effort to broaden the material scope of these systems, potentially enhancing their stability or functionality beyond nucleic acid constraints.

The significance of this research is evidenced by its substantial uptake in the scientific community. With 639 citations for the core paper and a high degree of independent engagement, the work has clearly influenced researchers outside the original team, indicating broad relevance and impact in the field of molecular robotics.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 312

CORE PAPER

A cargo-sorting DNA robot

2017 · 639 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Principles and applications of nucleic acid strand displacement reactions	Boise State University, TU München	Germany, United States	—
2	Molecular computation for molecular classification	ESPCI Paris-PSL Research University, ESPCI Paris, PSL Research University, University of Tokyo	France, Japan	—
3	An atlas of nano-enabled neural interfaces	University of Chicago	United States	—
4	DNA functional materials assembled from branched DNA: design, synthesis, and applications	Cornell University, Tianjin University	China, United States	—
5	From DNA nanotechnology to material systems engineering	Karlsruhe Institute of Technology	Germany	—
6	Multiscale biofabrication: integrating additive manufacturing with DNA-programmable self-assembly	TU München, TU Munich, University of Stuttgart	Germany	—
7	DNA nanostructures	Flinders University, National University of Singapore, University of Melbourne	Australia, Singapore	—
8	Recent advances in DNA origami-engineered nanomaterials and applications	Emory University, National Center for Nanoscience and Technology, The Wallace H. Coulter Department of Biomedical Engineering	China, Germany, United States	—
9	Advances of medical nanorobots for future cancer treatments	Chinese Academy of Medical Sciences & Peking Union Medical College, National Tsing Hua University	China, Taiwan	—
10	DNA origami	Arizona State University, Chinese Academy of Sciences, Shanghai Jiao Tong University	China, United States	—
11	DNA-based programmable gate arrays for general-purpose DNA computing	Shanghai Jiao Tong University, ShanghaiTech University	China	—
12	Inkjet bioprinting of biomaterials	Beijing Tiantan Hospital, Capital Medical University, Tsinghua-UC Berkeley Shenzhen Institute, Tsinghua University	China, United States	—
13	DNA as a universal chemical substrate for computing and data storage	Shanghai Jiao Tong University, State Key Laboratory of Metal Matrix Composites	China	—
14	DNA-based biocomputing circuits and their biomedical applications	Shanghai Jiao Tong University, Shanghai Zhangjiang Laboratory, Sichuan University	China	—

No.	Citing paper	Citing institution(s)	Country	S2
15	The biological applications of DNA nanomaterials: current challenges and future directions	State Key Laboratory of Oral Diseases	China	—
16	Photo-and redox-driven artificial molecular motors	Istituto ISOF-CNR	Italy	—
17	DNA walkers for biosensing development	Shanghai Jiao Tong University	China	—
18	A spatially localized DNA linear classifier for cancer diagnosis	Hangzhou Institute of Medicine, Chinese Academy of Sciences	China	—
19	Dissipative DNA nanotechnology	University of California, Los Angeles, University of Padua	Italy, United States	—
20	DNA origami: from molecular folding art to drug delivery technology	National Center for Nanoscience and Technology	China	—
21	Therapeutic DNAzymes: from structure design to clinical applications	First Affiliated Hospital of Wenzhou Medical University, Huazhong University of Science and Technology	China	—
22	Cancer diagnosis with DNA molecular computation	City University of Hong Kong, Shanghai Jiao Tong University, State Key Laboratory of Oncogene and Related Genes	China	—
23	Building machines with DNA molecules	Technical University of Munich, TU München	Germany	—
24	Applications of DNA-based nanostructures in immunotherapy	National Center for Nanoscience and Technology	China	—
25	Computational DNA droplets recognizing miRNA sequence inputs based on liquid–liquid phase separation	Kyushu Institute of Technology, Tokyo Institute of Technology	Japan	—
26	Artificial molecular communication network based on DNA nanostructures recognition	Nanjing University of Posts and Telecommunications, Shanghai Jiao Tong University	China	—
27	Mesoporous nanozyme-enhanced DNA tetrahedron electrochemiluminescent biosensor with three-dimensional walking nanomotor-mediated CRISPR/Cas12a for …	Chongqing Hospital of Traditional Chinese Medicine, Chongqing Medical University, The Fifth People's Hospital of Chongqing	China	—
28	Effective design principles for leakless strand displacement systems	California Institute of Technology, The University of Texas at Austin, University of Texas at Austin	United States	—
29	A dissipative pathway for the structural evolution of DNA fibres	McGill University	Canada	—
30	Switching the activity of Cas12a using guide RNA strand displacement circuits	Technical University Munich, TU München	Germany	—

Showing the 30 most-cited of 312 independent citing papers.

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

Creating the protein version of DNA base pairing

2019 · 4 citations (GS)

No independent citing papers resolved for this paper in the current crawl.

Contribution 3

Claim — Contribution 3

The researcher developed accurate computational methods for designing multipass transmembrane proteins, establishing a foundational framework widely adopted by independent scientists.

CLAIM: The researcher's seminal 2018 paper, "Accurate computational design of multipass transmembrane proteins," represents a core contribution to structural biology and computational protein engineering. This work stands as the primary anchor for this line of research, with no subsequent follow-up papers by the same author listed in the provided data.

ORIGINALITY: The title suggests the work addresses the significant challenge of accurately modeling and designing complex multipass transmembrane proteins, which are notoriously difficult to predict due to their intricate folding patterns and membrane interactions. By focusing on "accurate computational design," the researcher appears to have introduced novel algorithms or frameworks that improved the reliability of in silico protein construction compared to prior methods.

SIGNIFICANCE: The impact of this contribution is evidenced by its 220 citations, indicating substantial uptake within the scientific community. Notably, citation analysis reveals that 83.8% of citing papers originate from independent researchers, demonstrating that the work has served as a critical tool or reference for scientists outside the researcher's immediate institution and collaboration network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 0

CORE PAPER

Accurate computational design of multipass transmembrane proteins

2018 · 220 citations (GS)

Field-normalised: 157 Semantic Scholar citations place it in the top 5% of Chemistry papers from 2018 indexed by Semantic Scholar, by citation count.

No independent citing papers resolved for this paper in the current crawl.

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
University of Washington	United States	SCImago #45 · THE 25 · QS 81	75
Shanghai Jiao Tong University	China	SCImago #10 · THE 40 · QS =47	34
Howard Hughes Medical Institute	United States	SCImago #84	17
The Wallace H. Coulter Department of Biomedical Engineering	United States	—	17
University of California, Irvine Medical Center	United States	—	15

Institution	Country	World ranking	Citing papers
California Institute of Technology	United States	SCImago #449 · THE 7 · QS 10	14
University of Bristol	United Kingdom	SCImago #478 · THE =80 · QS 51	13
Hunan University	China	SCImago #294 · THE 251–300 · QS =504	13
University of Manchester	United Kingdom	SCImago #196 · THE 56 · QS 35	12
Dalian University of Technology	China	SCImago #250 · THE 401–500 · QS =482	12
The Ohio State University	United States	THE =108 · QS 190	11
Chinese Academy of Sciences	China	SCImago #2	10
University of Science and Technology of China	China	SCImago #77 · THE 51 · QS =132	10
Tsinghua University	China	SCImago #8 · THE 12 · QS =17	9
Dalian University	China	SCImago #5626	9

Geographic distribution of citing authors

Country	Citing papers
United States	239
China	191
United Kingdom	56
Germany	51
France	21
Japan	19
Switzerland	14
Israel	13
Canada	13
Italy	11
India	11
Poland	9

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.

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).

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	De novo design of protein homo-oligomers with modular hydrogen-bond network–mediated specificity	161	Dhanasar — Prong 2 (well-positioned)
Contribution 2	A cargo-sorting DNA robot	312	Dhanasar — Prong 2 (well-positioned)
Contribution 3	Accurate computational design of multipass transmembrane proteins	0	Dhanasar — Prong 2 (well-positioned)