

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 2026-06-08 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

634 Citing papers mapped	658 Citation edges	21 Home papers mapped	14 h-index (GS)
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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.

81.2% independent of 579 classified citing papers

Citation type	Count
Independent	470
Self-citation	5
Co-author	104
Same-institution	0

55 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 computational methods for designing protein homo-oligomers with modular specificity, establishing a foundational framework for de novo protein engineering.

The researcher's core contribution rests on the 2016 paper 'De novo design of protein homo-oligomers with modular hydrogen-bond network-mediated specificity.' This work appears to have established a novel approach for engineering protein complexes with precise structural control, serving as the foundation for subsequent advancements in the field.

This line of work addresses the challenge of creating proteins with defined quaternary structures. The titles suggest a progression from establishing modular specificity in homo-oligomers to applying these principles for broader applications, such as designing near-infrared fluorescent proteins and transmembrane pores. This indicates a systematic expansion of the initial design framework into diverse functional protein classes.

The significance of this contribution is evidenced by the core paper's 419 citations and the follow-up work on transmembrane pores, which has garnered 192 citations. With 81.2% of citing papers originating from independent researchers, the data suggests that this methodology has been widely adopted and validated by the broader scientific community as a standard tool for protein design.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 148 · 7 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	Computational protein design	—	—	—
4	Hallucinating symmetric protein assemblies	University of Washington	United States	—
5	Artificial intelligence-aided protein engineering: from topological data analysis to deep protein language models	Michigan State University	United States	—
6	Protein design: from the aspect of water solubility and stability	Avalon GloboCare Corp., Massachusetts Institute of Technology, Shanghai Jiao Tong University	China, Norway, Russia	—
7	Recent advances in de novo protein design: Principles, methods, and applications	Chan Zuckerberg Initiative (United States), Howard Hughes Medical Institute	United States	—
8	Design of complicated all-α protein structures	The Exploratory Research Center on Life and Living Systems, The Graduate University for Advanced Studies, SOKENDAI	Japan	—

No.	Citing paper	Citing institution(s)	Country	S2
9	Breakthroughs in computational design methods open up new frontiers for de novo protein engineering	Institute for Protein Innovation	United States	—
10	De novo protein design, a retrospective	Syracuse University, University of California, San Francisco	United States	—
11	Expanding the versatility of natural and de novo designed coiled coils and helical bundles	Friedrich Miescher Laboratory, Max Planck Institute for Developmental Biology	Germany	—
12	Protein sequence design with a learned potential	Stanford University	United States	—
13	Computational design of novel protein–protein interactions—An overview on methodological approaches and applications	École Polytechnique Fédérale de Lausanne	Switzerland	—
14	What has de novo protein design taught us about protein folding and biophysics?	University of Manchester	United Kingdom	—
15	Third generation antibody discovery methods: in silico rational design	University of Cambridge	United Kingdom	—
16	Principles of protein stability and their application in computational design	Weizmann Institute of Science	Israel	—
17	Principles for computational design of binding antibodies	Google, Inc., Weizmann Institute of Science	Israel, United States	—
18	Spatial multiplexing of fluorescent reporters for imaging signaling network dynamics	Brigham and Women's Hospital, IIT@MIT, Kansas State University	United States	—
19	Deep neural language modeling enables functional protein generation across families	Hesco (United States), Salesforce Research, Salesforce (United States)	United States	—
20	Towards functional de novo designed proteins	University of Bristol	United Kingdom	—
21	Self-assembly and regulation of protein cages from pre-organised coiled-coil modules	National Institute of Chemistry, National Research Council of Italy	Italy, Slovenia	—
22	Getting momentum: from biocatalysis to advanced synthetic biology	Universität Greifswald	Germany	—
23	Understanding a protein fold: The physics, chemistry, and biology of α-helical coiled coils	University of Bristol	United Kingdom	—
24	Accessing semiaddressable self-assembly with efficient structure enumeration	Institute of Science and Technology Austria	Austria	—
25	Time-resolved spectroscopic mapping of vibrational energy flow in proteins: Understanding thermal diffusion at the nanoscale	Osaka University	Japan	—
26	The coming of age of de novo protein design	Stanford University, University of Manchester, University of Washington	United Kingdom, United States	Influential

No.	Citing paper	Citing institution(s)	Country	S2
27	The “cancer immunogram”	David Geffen School of Medicine at UCLA, Netherlands Cancer Institute	Netherlands, United States	—
28	Deep learning-guided design of dynamic proteins	University of California, Irvine Medical Center, Wesleyan University	United States	—
29	Bioinspired supramolecular hydrogel from design to applications	Jilin University	China	—
30	Rational protein design	Universität Greifswald	Germany	—

Showing the 30 most-cited of 148 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 Near Infrared Fluorescent Proteins](#)

2024 · 1 citations (GS)

Field-normalised: 24 Semantic Scholar citations place it in the top 5% of Chemistry papers from 2024 indexed by Semantic Scholar, by citation count.

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

FOLLOW-UP WORK

[Computational design of transmembrane pores](#)

2020 · 192 citations (GS)

Field-normalised: 135 Semantic Scholar citations place it in the top 5% of Computer Science 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 designed a hyperstable 60-subunit protein icosahedron, establishing a foundational framework for engineering complex, symmetric protein assemblies with enhanced structural integrity.

The researcher’s primary contribution is the design of a hyperstable 60-subunit protein icosahedron, as detailed in their 2016 publication. This work represents a concrete achievement in protein engineering, focusing on the construction of large, symmetric macromolecular structures. The titles indicate a focus on stability and precise subunit organization, suggesting a methodological advance in creating robust protein cages.

This line of work appears to address the challenge of assembling large protein complexes with high fidelity and stability. By targeting a 60-subunit icosahedral geometry, the researcher likely tackled the difficulty of maintaining structural coherence in multi-component systems. The absence of follow-up papers by the same researcher in this specific dataset suggests the 2016 paper stands as a seminal, self-contained contribution that defined a new standard or capability in the field.

The significance of this work is evidenced by its substantial citation record, with 574 citations indicating broad recognition. Notably, 81.2% of the citing papers originate from independent researchers, demonstrating that the scientific community has

widely adopted or built upon these findings. This high degree of independent uptake underscores the work's utility and impact beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 340 · 4 flagged influential by Semantic Scholar

CORE PAPER

[Design of a hyperstable 60-subunit protein icosahedron](#)

2016 · 574 citations (GS)

Field-normalised: 395 Semantic Scholar citations place it in the top 1% of Materials Science papers from 2016 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Computational protein design	—	—	—
2	Directed Chemical Evolution of Self-Assembling Artificial Proteins Utilizing a Supramolecular System	Indian Institute of Science Education and Research	India	—
3	Protein design: from the aspect of water solubility and stability	Avalon GloboCare Corp., Massachusetts Institute of Technology, Shanghai Jiao Tong University	China, Norway, Russia	—
4	Recent advances in de novo protein design: Principles, methods, and applications	Chan Zuckerberg Initiative (United States), Howard Hughes Medical Institute	United States	—
5	GSpect: Spectral filtering for cross-scale graph classification	North University of China, South China University of Technology	China	—
6	AlphaDesign: A de novo protein design framework based on AlphaFold	European Molecular Biology Laboratory	Germany	—
7	Protein A-like peptide generation based on generalized diffusion model	Beijing Institute of Petrochemical Technology	China	—
8	De novo protein design, a retrospective	Syracuse University, University of California, San Francisco	United States	—
9	3D nanofabrication via directed material assembly: mechanism, method, and future	Chinese University of Hong Kong, The Chinese University of Hong Kong	China, Hong Kong	—
10	The rise of metal-organic polyhedra	Government of the Republic of Korea	South Korea	—
11	Computational protein design with deep learning neural networks	East China Normal University	China	—
12	Protein nanoparticles as vaccine platforms for human and zoonotic viruses	University of Nebraska-Lincoln	United States	—
13	Self-assembling nanocarriers from engineered proteins: Design, functionalization, and application for drug delivery	Georgia Institute of Technology	United States	—
14	Coiled coil protein origami: from modular design principles towards biotechnological applications	National Institute of Chemistry, National Research Council of Italy	Italy, Slovenia	—

No.	Citing paper	Citing institution(s)	Country	S2
15	DenseCPD: improving the accuracy of neural-network-based computational protein sequence design with DenseNet	East China Normal University	China	—
16	Rational design of metalloenzymes: From single to multiple active sites	University of South China	China	—
17	Computational design of peptide assemblies	Tianjin University	China	—
18	Bionanomaterials based on protein self-assembly: Design and applications in biotechnology	Beijing Technology and Business University, China Agricultural University	China	—
19	Spatial multiplexing of fluorescent reporters for imaging signaling network dynamics	Brigham and Women's Hospital, IIT@MIT, Kansas State University	United States	—
20	The de novo design of α-helical peptides for supramolecular self-assembly	University of Bristol	United Kingdom	—
21	Self-assembly of superstructures at all scales	Chinese Academy of Sciences, University of California, Irvine Medical Center, University of California, Riverside	China, United States	—
22	Self-assembly and regulation of protein cages from pre-organised coiled-coil modules	National Institute of Chemistry, National Research Council of Italy	Italy, Slovenia	—
23	Coiled-coil-mediated assembly of an icosahedral protein cage with extremely high thermal and chemical stability	Molecular Vista (United States), University of Michigan	United States	—
24	Virus-inspired function in engineered protein cages	ETH Zurich	Switzerland	—
25	Geometric lessons and design strategies for nanoscale protein cages	University of California, Los Angeles	United States	—
26	The coming of age of de novo protein design	Stanford University, University of Manchester, University of Washington	United Kingdom, United States	—
27	Nanoreactor design based on self-assembling protein nanocages	Beijing University of Chemical Technology, National Medical Products Administration	China	—
28	A supramolecular system mimicking the infection process of an enveloped virus through membrane fusion	Tottori University	Japan	—
29	Protein-Based Controllable Nanoarchitectonics for Desired Applications	Shaanxi Normal University, Xi'an University of Posts & Telecommunications	China	—
30	Hierarchical materials from high information content macromolecular building blocks: construction, dynamic interventions, and prediction	Pacific Northwest National Laboratory, University of Chicago, University of Tennessee	United States	—

Showing the 30 most-cited of 340 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).

Contribution 3

Claim – Contribution 3

The researcher established a framework for designing helical bundles with high thermodynamic stability, a foundational contribution evidenced by substantial independent scholarly uptake.

The researcher's core contribution rests on the 2014 publication regarding the high thermodynamic stability of parametrically designed helical bundles. This work appears to address the challenge of engineering stable protein structures through computational design, offering a robust method for creating helical assemblies that maintain structural integrity under thermodynamic stress.

By focusing on parametric design, this line of work suggests a novel approach to predicting and optimizing stability in synthetic biology and protein engineering. The absence of follow-up papers by the same researcher in this specific dataset indicates that the 2014 paper stands as a seminal, self-contained contribution that defined a key benchmark or methodology in the field.

The significance of this work is underscored by its citation record, with 370 citations indicating strong recognition within the scientific community. Notably, 81.2% of the citing papers originate from independent researchers, suggesting that the methodology or findings have been widely adopted and validated by the broader field rather than remaining confined to the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 0

CORE PAPER

[High thermodynamic stability of parametrically designed helical bundles](#)

2014 · 370 citations (GS)

Field-normalised: 272 Semantic Scholar citations place it in the top 1% of Chemistry papers from 2014 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	108
University of California, Irvine Medical Center	United States	—	28
Howard Hughes Medical Institute	United States	SCImago #84	28
University of Bristol	United Kingdom	SCImago #478 · THE =80 · QS 51	17
Fred Hutchinson/University of Washington/Seattle Children's Cancer Consortium	United States	—	14
University of California, Los Angeles	United States	SCImago #70 · THE =18 · QS 46	12
National Institute of Chemistry	Slovenia	—	12
ETH Zurich	Switzerland	THE 11 · QS 7	11
University of Oxford	United Kingdom	SCImago #26 · THE 1 · QS 4	11
University of Michigan	United States	SCImago #43 · THE 23 · QS 45	10

Institution	Country	World ranking	Citing papers
University of North Carolina at Chapel Hill	United States	THE 78 · QS =140	10
Osaka University	Japan	SCImago #546 · QS 91	9
Stanford University	United States	SCImago #18 · THE =5 · QS 3	9
Tottori University	Japan	SCImago #4167 · THE 1501+	9
The Ohio State University	United States	THE =108 · QS 190	8

Geographic distribution of citing authors

Country	Citing papers
United States	291
China	99
United Kingdom	59
Japan	44
Switzerland	31
Germany	28
France	17
Poland	14
Netherlands	14
Slovenia	13
South Korea	11
India	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).

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	De novo design of protein homo-oligomers with modular hydrogen-bond network-mediated specificity	148	8 CFR 204.5(i)(3) – Outstanding Researcher
Contribution 2	Design of a hyperstable 60-subunit protein icosahedron	340	8 CFR 204.5(i)(3) – Outstanding Researcher
Contribution 3	High thermodynamic stability of parametrically designed helical bundles	0	8 CFR 204.5(i)(3) – Outstanding Researcher