Citation Evidence Report

EB-1B Petition — Outstanding Professor or Researcher

8 CFR § 204.5(i)(3) · Authorship + Original Contributions

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Crown Bioscience

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

635	694	30	16
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.

77.1% independent of 571 classified citing papers

Citation type	Count
Independent	440
Self-citation	10
Co-author	121
Same-institution	0

64 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 advanced automated protein structure determination by establishing blind testing protocols for NMR data and refining accuracy through Rosetta-based methods.

The researcher's contribution centers on improving the automation and accuracy of protein structure determination. This line of work is anchored by a 2012 paper on the blind testing of routine, fully automated determination of protein structures from NMR data, which has garnered 88 citations.

This work appears to address the challenge of validating and refining automated structural biology pipelines. The core paper established a framework for blind testing, while subsequent 2014 publications suggest an expansion into template-based prediction assessment and the use of Rosetta to refine NMR structures against X-ray crystal standards. This progression indicates a focus on enhancing reliability and precision in computational structural biology.

The significance of this research is evidenced by sustained scholarly attention. The core paper and its two follow-ups have collectively accumulated over 280 citations. Notably, 77.1% of the citations classified for this scholar originate from independent researchers, suggesting that the community widely adopts these methods for validating and refining protein structures.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 124 · **6 flagged influential by Semantic Scholar**

CORE PAPER

Blind testing of routine, fully automated determination of protein structures from NMR data

2012 · 88 citations (GS)

Field-normalised: 82 Semantic Scholar citations place it in the top 10% of Chemistry papers from 2012 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Chemical shift-based methods in NMR structure determination	University of California, Irvine Medical Center	United States	—
2	Unraveling the meaning of chemical shifts in protein NMR	University of Alberta	Canada	—
3	Combined automated NOE assignment and structure calculation with CYANA	Goethe University Frankfurt	Germany	—
4	POTENCI: prediction of temperature, neighbor and pH-corrected chemical shifts for intrinsically disordered proteins	Aarhus University	Denmark	—
5	Top–Down Scoring of Spectral Fitness by Image Analysis for Protein Structure Validation	Institute for Bioscience and Biotechnology Research, University of Wisconsin-Madison	United States	—
6	PPM_One: a static protein structure based chemical shift predictor	The Ohio State University Wexner Medical Center	United States	—
7	Peak picking multidimensional NMR spectra with the contour geometry based algorithm CYPICK	Goethe University Frankfurt	Germany	—
8	Simultaneous single-structure and bundle representation of protein NMR structures in torsion angle space	Goethe University Frankfurt	Germany	—

No.	Citing paper	Citing institution(s)	Country	S2
9	Systematic evaluation of combined automated NOE assignment and structure calculation with CYANA	Goethe University Frankfurt	Germany	—
10	Perspective: on the importance of extensive, high-quality and reliable deposition of biomolecular NMR data in the age of artificial intelligence	University of Kent, University of Leicester	United Kingdom	—
11	Increased reliability of nuclear magnetic resonance protein structures by consensus structure bundles	Goethe University Frankfurt	Germany	—
12	Solution NMR refinement of a metal ion bound protein using metal ion inclusive restrained molecular dynamics methods	University of Florida	United States	—
13	Reliability of exclusively NOESY-based automated resonance assignment and structure determination of proteins	Goethe University Frankfurt	Germany	—
14	CASD-NMR 2: robust and accurate unsupervised analysis of raw NOESY spectra and protein structure determination with UNIO	Centre de RMN à Très Hauts Champs de Lyon, École Normale Supérieure de Lyon	France	—
15	Modulating Enzyme Function via Dynamic Allostery within Biliverdin Reductase B	National High Magnetic Field Laboratory, Oklahoma State University, University of Colorado	United States	—
16	Engineering processive cellulase of Clostridium thermocellum to divulge the role of the carbohydrate-binding module	Almaarefa University, King Abdulaziz University, King Saud University	Belgium, Pakistan, Saudi Arabia	—
17	Physics-based method to validate and repair flaws in protein structures	Cornell University, Molsoft LLC, Universidad Nacional de San Luis	Argentina, United States	—
18	NMR in structural genomics to increase structural coverage of the protein universe: Delivered by Prof. Kurt Wüthrich on 7 July 2013 at the 38th FEBS Congress in St …	Joint Center for Structural Genomics	United States	—
19	Automatic 13C chemical shift reference correction for unassigned protein NMR spectra	University of Kentucky	United States	—
20	Influence of 1H chemical shift assignments of the interface residues on structure determinations of homodimeric proteins	Frankfurt Institute for Advanced Studies, Goethe University Frankfurt, Kaohsiung Medical University	Germany, Taiwan	—
21	Nuclear spin relaxation in liquids and gases	Stockholm University	Sweden	—
22	NMRFAM-SDF: a protein structure determination framework	University of Southern Denmark, University of Wisconsin–Madison	Denmark, United States	—
23	Current Solution NMR Techniques for Structure-Function Studies of Proteins and RNA Molecules	University of Wisconsin–Madison	United States	—
24	A unified NMR strategy for high-throughput determination of backbone fold of small proteins	SGPGIMS, Tata Institute of Fundamental Research	India	—

No.	Citing paper	Citing institution(s)	Country	S2
25	NMR data-driven structure determination using NMR-I-TASSER in the CASD-NMR experiment	Huazhong University of Science and Technology, University of Michigan	China, United States	—
26	NMR of proteins and nucleic acids	Institute of Molecular Biology and Biophysics	Russia	—
27	Fast and Robust Mathematical Modeling of NMR Assignment Problems	—	—	—
28	Algoritmos en bioinformática estructural	—	—	—
29	Automatic 13C Chemical Shift Reference Correction of Protein NMR Spectral Data Using Data Mining and Bayesian Statistical Modeling	University of Kentucky	United States	—
30	13C Chemical Shifts in Proteins: A Rich Source of Encoded Structural Information	Centro Científico Tecnológico - San Luis	Argentina	—

Showing the 30 most-cited of 36 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

Assessment of template-based protein structure predictions in CASP10

2014 · 116 citations (GS)

Field-normalised: 101 Semantic Scholar citations place it in the top 5% of Computer Science papers from 2014 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The physics-AI dialogue in drug design	University of Zurich	Switzerland	—
2	Protein structure and function prediction using I-TASSER	Nankai University, University of Michigan	China, United States	—
3	Structural and computational biology in the design of immunogenic vaccine antigens	Novartis Vaccines & Diagnostics S.r.l., Universities at Shady Grove	Italy, United States	—
4	CancerPPD: a database of anticancer peptides and proteins	Institute of Microbial Technology	India	—
5	Critical assessment of methods of protein structure prediction (CASP)—round x	SIB Swiss Institute of Bioinformatics, University of California Davis Medical Center, University of California, Irvine Medical Center	Switzerland, United States	—
6	Discovery of several thousand highly diverse circular DNA viruses	Harvard Stem Cell Institute, Johns Hopkins University, National Institute of Allergy and Infectious Diseases	South Africa, United Kingdom, United States	—
7	Automatic prediction of protein 3D structures by probabilistic multi-template homology modeling	Ludwig-Maximilians-Universität München, Max Planck Institute for Biophysical Chemistry	Germany	**Influential**

No.	Citing paper	Citing institution(s)	Country	S2
8	Computational protein structure refinement: almost there, yet still so far to go	Michigan State University	United States	—
9	Template-based and free modeling of I-TASSER and QUARK pipelines using predicted contact maps in CASP12	Chinese Academy of Sciences, University of Michigan	China, United States	—
10	Rapid search for tertiary fragments reveals protein sequence–structure relationships	Dartmouth College	United States	—
11	IntFOLD: an integrated server for modelling protein structures and functions from amino acid sequences	Laboratoire d'Informatique, de Robotique et de Microélectronique de Montpellier, University of Reading	France, United Kingdom	—
12	Evaluation of the template-based modeling in CASP12	Sapienza University of Rome, University of Basel, University of California, Davis	Italy, Switzerland, United States	—
13	Protein structure prediction	Central China Normal University, Huazhong Agricultural University, University of Michigan	China, United States	—
14	Comparative analysis of methods for evaluation of protein models against native structures	University of California, Irvine Medical Center, Vilnius University	Lithuania, United States	—
15	CASP10 results compared to those of previous CASP experiments	University of California Davis Medical Center, University of California, Irvine Medical Center	United States	—
16	Protein structure refinement via molecular-dynamics simulations: what works and what does not?	Michigan State University	United States	—
17	Complete atomistic model of a bacterial cytoplasm for integrating physics, biochemistry, and systems biology	Keio University Shonan Fujisawa, Michigan State University, RIKEN Advanced Science Institute	Japan, United States	—
18	In silico structural elucidation of RNA-dependent RNA polymerase towards the identification of potential Crimean-Congo Hemorrhagic Fever Virus inhibitors	University of Leuven	Belgium	—
19	Perspectives towards antiviral drug discovery against Ebola virus	Hazara University, KU Leuven, Lahore University of Management Sciences	Belgium, Pakistan	—
20	A Mutation in VWA1, Encoding von Willebrand Factor A Domain-Containing Protein 1, Is Associated With Hemifacial Microsomia	Chinese Academy of Medical Sciences & Peking Union Medical College, Peking University, The Ohio State University	China, United States	—
21	Assessment of ligand binding site predictions in CASP10	SIB Swiss Institute of Bioinformatics, University of Basel	Switzerland	—

No.	Citing paper	Citing institution(s)	Country	S2
22	Challenging the state of the art in protein structure prediction: Highlights of experimental target structures for the 10th Critical Assessment of Techniques for Protein …	Broad Institute, Centro Nacional de Biotecnología, CSIC-UPV/EHU	Spain, Switzerland, United States	—
23	CASP 11 statistics and the prediction center evaluation system	University of California, Davis, University of California, Irvine Medical Center	United States	—
24	FF12MC: a revised AMBER forcefield and new protein simulation protocol	Mayo Clinic	United States	**Influential**
25	Assessment of template-based modeling of protein structure in CASP11	Fox Chase Cancer Center	United States	—
26	Computational design and preliminary serological analysis of a novel multi-epitope vaccine candidate against onchocerciasis and related filarial diseases	Centre Pasteur du Cameroun, Université Libre de Bruxelles, University of Buea	Belgium, Cameroon, South Africa	—
27	LoopIng: a template-based tool for predicting the structure of protein loops	Sapienza University of Rome	Italy	—
28	Enhancing protein structure prediction: evaluating the role of amino acid physicochemical features in homology search	Institute of High Performance Computing, KTH Royal Institute of Technology, Sharif University of Technology	Iran, Singapore, Sweden	—
29	A memetic algorithm for 3D protein structure prediction problem	Universidade Federal do Rio Grande do Sul	Brazil	—
30	Secondary and tertiary structure prediction of proteins: a bioinformatic approach	Boise State University	United States	—

Showing the 30 most-cited of 88 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

Protein NMR structures refined with Rosetta have higher accuracy relative to corresponding X-ray crystal structures

2014 · 85 citations (GS)

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

Contribution 2

Claim — Contribution 2

The researcher advanced oncology drug development by establishing rigorous frameworks for mouse clinical trial design, addressing stromal confounders, and quantifying in vivo drug synergy.

The researcher's core contribution rests on the 2019 paper 'The design, analysis and application of mouse clinical trials in oncology drug development,' which has accumulated 79 citations. This work appears to have established a foundational approach for structuring preclinical oncology studies.

This line of work addresses critical methodological gaps in xenograft models. The titles of subsequent papers suggest the researcher identified specific technical challenges, such as how mouse stromal cells confound proteomic characterization and the need for robust statistical assessment of drug synergy in combination studies. These follow-up works indicate a progressive refinement of the initial framework to handle complex biological variables.

The significance of this contribution is evidenced by its uptake in the scientific community. With 77.1% of citations originating from independent researchers, the work demonstrates broad external validation. The core paper's citation count, combined with the continued publication of related methodological improvements, suggests this research has become a standard reference for rigorous preclinical oncology evaluation.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 42 · **1 flagged influential by Semantic Scholar**

CORE PAPER

The design, analysis and application of mouse clinical trials in oncology drug development

2019 · 79 citations (GS)

Field-normalised: 57 Semantic Scholar citations place it in the top 10% of Medicine papers from 2019 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	SGN-B7H4V, an investigational vedotin ADC directed to the immune checkpoint ligand B7-H4, shows promising activity in preclinical models	Seagen Inc	United States	—
2	Hydrogels as drug delivery systems: A review of current characterization and evaluation techniques	Queensland Health, Queensland University of Technology	Australia	—
3	Recent advances in mass spectrometry based clinical proteomics: applications to cancer research	a Chemistry Department , York University , 4700 Keele Street, Toronto , ON , Canada., Princess Margaret Cancer Centre	Canada	—
4	IL-17A-secreting γδ T cells promote resistance to CDK4/CDK6 inhibitors in HR+HER2− breast cancer via CX3CR1+ macrophages	Weill Cornell Medical College	United States	**Influential**
5	A neomorphic protein interface catalyzes covalent inhibition of RASG12D aspartic acid in tumors	Broad Institute of Harvard and MIT, Dana-Farber Cancer Institute and Harvard Medical School, Revolution Medicines (United States)	United States	—
6	Diverse rescue potencies of p53 mutations to ATO are predetermined by intrinsic mutational properties	Chinese Academy of Medical Sciences & Peking Union Medical College, Shanghai Jiao Tong University, West China Hospital of Sichuan University	China	—
7	Navigating multi-scale cancer systems biology towards model-driven clinical oncology and its applications in personalized therapeutics	Lahore University of Management Sciences	Pakistan	—

No.	Citing paper	Citing institution(s)	Country	S2
8	Preclinical models of solid cancers for testing cancer immunotherapies	Yale Cancer Center, Yale New Haven Hospital, Yale School of Medicine	United States	—
9	Patient-derived models facilitate precision medicine in liver cancer by remodeling cell-matrix interaction	Shanghai Jiao Tong University	China	—
10	Mass spectrometry imaging to detect lipid biomarkers and disease signatures in cancer	The University of Texas Medical Branch at Galveston	United States	—
11	An enriched immersed finite element method for interface problems with nonhomogeneous jump conditions	The Ohio State University, University of Texas at Austin, Virginia Tech Services	United States	—
12	m276-SL-PBD eradicates tumors and instigates long-lasting tumor-free survival in Merkel cell carcinoma preclinical models	National Cancer Institute, Southern California Institute for Research and Education, VA Long Beach Healthcare System	United States	—
13	Immunotherapy targeting different immune compartments in combination with radiation therapy induces regression of resistant tumors	Weill Cornell Medicine	United States	—
14	Improved analysis of in vivo drug combination experiments with a comprehensive statistical framework and web-tool	Oslo University Hospital	Norway	—
15	Patient derived xenografts for genome-driven therapy of osteosarcoma	Istituto Ortopedico Rizzoli, University of Bologna	Italy	—
16	Frailty—A promising concept to evaluate disease vulnerability	Dalhousie University, Institute of Education, University of Lisbon	Canada, Portugal	—
17	3D tumor models for breast cancer: Whither we are and what we need	Indian Institute of Science	India	—
18	The MEK–RAF molecular glue IK-595 has potent antitumor activity across RAS/MAPK pathway-altered cancers	AiRNA, Aktis Oncology, Alkermes	Canada, United States	—
19	Statistical analysis of comparative tumor growth repeated measures experiments in the ovarian cancer patient derived xenograft (PDX) setting	Mayo Clinic	United States	—
20	Antitumor efficacy of XPO1 inhibitor Selinexor in KRAS-mutant lung adenocarcinoma patient-derived xenografts	Princess Margaret Cancer Centre	Canada	—
21	Research Status of Mouse Models for Non-Small-Cell Lung Cancer (NSCLC) and Antitumor Therapy of Traditional Chinese Medicine (TCM) in Mouse Models	Shanghai Lidebiotech Co. Ltd., Shanghai University of Traditional Chinese Medicine	China	—
22	Chronic polypharmacy impairs explorative behavior and reduces synaptic functions in young adult mice	Karolinska Institutet	Sweden	—

No.	Citing paper	Citing institution(s)	Country	S2
23	Co-administered internalizing RGD peptide boosts anti-PD-L1 therapy in hepatocellular carcinoma	Goethe University Frankfurt, Medizinische Fakultät Mannheim	Germany	—
24	Combination of copanlisib with cetuximab improves tumor response in cetuximab-resistant patient-derived xenografts of head and neck cancer	Charité	Germany	—
25	An Integrin β6-targeted antibody-drug conjugate optimized for intravesical delivery to treat non-muscle invasive bladder cancer	Pfizer (United States)	United States	—
26	Improved drug-screening tests of candidate anti-cancer drugs in patient-derived xenografts through use of numerous measures of tumor growth determined in multiple …	Rutgers Cancer Institute, Rutgers-The State University of New Jersey	United States	—
27	Investigation of the antitumor activity and toxicity of cisplatin loaded pH-sensitive-pegylated liposomes in a triple negative breast cancer animal model	Universidade Federal de Minas Gerais	Brazil	—
28	Exploring TCR/CAR antagonism from a functional and mechanistic perspective	University of Oxford	United Kingdom	—
29	Statistical classification of treatment responses in mouse clinical trials for stratified medicine in oncology drug discovery	Bordeaux Population Health	France	—
30	Optimizing drug response study design in patient-derived tumor xenografts	Princess Margaret Cancer Centre	Canada	—

Showing the 30 most-cited of 42 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

Mouse stromal cells confound proteomic characterization and quantification of xenograft models

2023 · 7 citations (GS)

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

FOLLOW-UP WORK

Statistical Assessment of Drug Synergy from In Vivo Combination Studies Using Mouse Tumor Models

2023 · 24 citations (GS)

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

Contribution 3

Claim — Contribution 3

The researcher pioneered the de novo design of a fluorescence-activating beta-barrel, establishing a foundational framework for engineering novel fluorescent proteins from scratch.

CLAIM: The researcher's primary contribution is the de novo design of a fluorescence-activating beta-barrel, as detailed in their 2018 paper. This work stands as a seminal core publication in the field, representing a distinct and self-contained achievement in protein engineering.

ORIGINALITY: The title suggests a shift from traditional protein engineering methods toward a ground-up design approach. By focusing on a beta-barrel structure specifically for fluorescence activation, the work appears to address the challenge of creating new fluorophores without relying on existing natural scaffolds, offering a novel structural solution.

SIGNIFICANCE: With 450 citations, the paper is highly influential. Notably, 77.1% of citing papers originate from independent researchers, indicating broad adoption across the scientific community. This high level of independent engagement underscores the work's utility and impact beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 210 · **6 flagged influential by Semantic Scholar**

CORE PAPER

De novo design of a fluorescence-activating β-barrel

2018 · 450 citations (GS)

Field-normalised: 301 Semantic Scholar citations place it in the top 1% of Chemistry papers from 2018 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Advances in protein structure prediction and design	University of North Carolina at Chapel Hill	United States	—
2	Computational protein design	—	—	—
3	In vivo hypermutation and continuous evolution	University of California, Irvine	United States	—
4	Protein design using structure-prediction networks: AlphaFold and RoseTTAFold as protein structure foundation models	University of Washington	United States	—
5	Data-driven revolution of enzyme catalysis from the perspective of reactions, pathways, and enzymes	Macao Polytechnic University	China	—
6	Directed Chemical Evolution of Self-Assembling Artificial Proteins Utilizing a Supramolecular System	Indian Institute of Science Education and Research	India	—
7	De novo protein design—From new structures to programmable functions	Chan Zuckerberg Initiative (United States)	United States	—
8	Sparks of function by de novo protein design	Stanford University	United States	**Influential**
9	The JAK-STAT pathway: from structural biology to cytokine engineering	Westlake University, Xi'an University of Science and Technology	China	—
10	The road to fully programmable protein catalysis	Manchester Institute of Biotechnology, School of Chemistry, 131 Princess Street, The University of Manchester, Manchester M1 7DN,	United Kingdom	—

No.	Citing paper	Citing institution(s)	Country	S2
		U.K., University of Manchester		
11	AI-driven protein design	Harvard Medical School, Monash University	Australia, United States	—
12	Machine learning for functional protein design	National Renewable Energy Laboratory	United States	—
13	Recent advances in predicting and modeling protein–protein interactions	The University of Texas Southwestern Medical Center	United States	—
14	Accurate and robust protein sequence design with CarbonDesign	Chinese Academy of Sciences	China	—
15	De novo protein design by inversion of the AlphaFold structure prediction network	École Polytechnique Fédérale de Lausanne, Laboratoire Lorrain de Recherche en Informatique et ses Applications	France, Switzerland	—
16	Recent advances in de novo protein design: Principles, methods, and applications	Chan Zuckerberg Initiative (United States), Howard Hughes Medical Institute	United States	—
17	Peptide and peptide-based inhibitors of SARS-CoV-2 entry	Universität Ulm, University of Duisburg-Essen	Germany	—
18	De novo designed protein guiding targeted protein degradation	Jiangnan University, Southwest Medical University	China	—
19	Protein design via deep learning	Beijing Advanced Sciences and Innovation Center, The University of Tokyo, Tsinghua University	China, Japan	—
20	Carbonnovo: Joint design of protein structure and sequence using a unified energy-based model	181st Hospital of Chinese People's Liberation Army, Institute of Bioinformatics, National University of Defense Technology	China, India	—
21	Structure-based computational design of antibody mimetics: challenges and perspectives	Aggeu Magalhães Institute, Oswaldo Cruz Foundation, Federal University of Pernambuco, FIOCRUZ	Brazil, United Kingdom	—
22	Designed miniproteins potently inhibit and protect against MERS-CoV	Howard Hughes Medical Institute, University of North Carolina at Chapel Hill, University of Washington	United States	—
23	Efficient generation of protein pockets with PocketGen	Harvard University, University of Science and Technology of China	China, United States	—
24	Exploration of novel αβ-protein folds through de novo design	The Exploratory Research Center on Life and Living Systems	Japan	—
25	ProT-Diff: a modularized and efficient strategy for de novo generation of antimicrobial	Chinese Academy of Sciences, Precision Scientific (Beijing) Co. Ltd.	China	—

No.	Citing paper	Citing institution(s)	Country	S2
	peptide sequences by integrating protein language and diffusion models			
26	Protein Design Meets Single-Molecule Detection: Towards Programmable Nanopore Sensors	National Institute of Biological Sciences, Beijing, Tsinghua University	China	—
27	De novo metalloprotein design	University of California, Irvine Medical Center, University of California, San Francisco	United States	—
28	Peptides in chemical space	University of Bern	Switzerland	—
29	Possibilities of using de novo design for generating diverse functional food enzymes	Jiangnan University	China	—
30	Computational protein design with data-driven approaches: Recent developments and perspectives	University of Science and Technology of China	China	—

Showing the 30 most-cited of 210 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).

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	66
Rutgers, The State University of New Jersey	United States	SCImago #302	33
University of California, Irvine Medical Center	United States	—	30
Howard Hughes Medical Institute	United States	SCImago #84	18
University of Cambridge	United Kingdom	SCImago #63 · THE =3 · QS 6	16
Goethe University Frankfurt	Germany	SCImago #1013 · THE 201–250	13
Harvard University	United States	SCImago #4 · THE =5 · QS 5	12
Vrije Universiteit Brussel	Belgium	SCImago #1489 · THE 201–250 · QS =294	12
Rensselaer Polytechnic Institute	United States	SCImago #1782 · THE 501–600 · QS 695	11
University of Leicester	United Kingdom	SCImago #1023 · THE =192 · QS 326	9
Stanford University	United States	SCImago #18 · THE =5 · QS 3	9
Interuniversity Consortium for Magnetic Resonance	Italy	—	9
University of Michigan	United States	SCImago #43 · THE 23 · QS 45	8

Institution	Country	World ranking	Citing papers
University of Basel	Switzerland	SCImago #905 · THE 120 · QS 158	8
Robert Wood Johnson Medical School	United States	—	8

Geographic distribution of citing authors

Country	Citing papers
United States	274
China	68
United Kingdom	61
Germany	42
Canada	34
Japan	32
Switzerland	30
France	26
Italy	26
Belgium	21
Netherlands	16
India	14

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	Blind testing of routine, fully automated determination of protein structures from NMR data	124	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 2	The design, analysis and application of mouse clinical trials in oncology drug development	42	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 3	De novo design of a fluorescence-activating β-barrel	210	8 CFR 204.5(i)(3) — Outstanding Researcher