Citation Evidence Report

EB-1A Petition — Original Contributions of Major Significance

8 CFR § 204.5(h)(3)(v) · Criterion 5

Jennifer Doudna

Professor of Molecular and Cell Biology and Chemistry, UC Berkeley

Google Scholar profile

Generated 2026-05-31 by CiteMap. This report organises Google Scholar citation data into the structure USCIS adjudicators apply to Criterion 5 (original contributions of major significance). 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

2,630	3,052	3	169
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.

96.8% independent of 1,761 classified citing papers

Citation type	Count
Independent	1,705
Self-citation	17
Co-author	38
Same-institution	1

869 citing papers could not be classified (no author data) and are excluded from the percentages above.

C. Significant Contributions & Their Citation Evidence

Each contribution below is presented as the AAO expects: a specific claim, followed by the **independent** citation evidence for the paper(s) that carry it. Citation counts are stated **per article**, never as a body-of-work total — the AAO holds aggregate totals to be a final-merits signal, not Criterion-5 evidence.

Where the data allows, a paper also shows its **field-normalised** standing — how its citation count ranks against Semantic Scholar papers in the same field and publication year. The comparison field is named explicitly; counsel should confirm it is the appropriate one, as the AAO scrutinises a petitioner's choice of comparison field.

Contribution 1

Claim — Contribution 1

The researcher established the foundational framework for programmable RNA-guided DNA endonuclease activity in adaptive bacterial immunity, subsequently expanding this platform for sequence-specific gene expression control.

The researcher's contribution centers on the seminal 2012 Science paper describing a programmable dual-RNA–guided DNA endonuclease in adaptive bacterial immunity. This work is followed by a 2013 publication that repurposes CRISPR as an RNA-guided platform for sequence-specific control of gene expression, indicating a progression from mechanistic discovery to functional application.

This line of work appears to address the challenge of achieving precise, programmable genetic manipulation. The chronological shift from characterizing the endonuclease mechanism to repurposing it for gene expression control suggests the researcher identified and exploited the system's versatility, moving beyond natural immunity to broader biotechnological utility.

The significance of this contribution is evidenced by the core paper's 23,743 citations and the follow-up's 6,776 citations. With 99.0% of classified citations originating from independent researchers, the work demonstrates widespread adoption and validation across the global scientific community, confirming its status as a foundational advance in the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 1,188 **· 81 flagged influential by Semantic Scholar**

CORE PAPER

A programmable dual-RNA–guided DNA endonuclease in adaptive bacterial immunity

2012 · Science · 23,743 citations (GS)

Field-normalised: 14,992 Semantic Scholar citations place it in the top 1% of Biology papers from 2012 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Advances in genomic tools for plant breeding: harnessing DNA molecular markers, genomic selection, and genome editing (2024)	G.B.P.U.A.&T., ICAR-Central Soil Salinity Research Institute, ICAR -Krishi Vigyan Kendra	India	—
2	Translational Applications of Hydrogels. (2021)	Stanford University	United States	—
3	DNA methylation: a historical perspective (2022)	Max Planck Institute for Molecular Genetics	Germany	—
4	Glioblastoma Therapy: Past, Present and Future (2024)	Castellon General University Hospital, Jaume I University of Castellon, Scientia BioTech S.L.	Spain	—
5	mRNA-based cancer therapeutics (2023)	Brigham and Women's Hospital, Harvard Medical School, Zhejiang University Medical Center	China, United States	—
6	The present and future of the Cancer Dependency Map	Broad Institute of MIT and Harvard, Dana-Farber Cancer Institute and Harvard Medical School	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
7	Breeding crops to feed 10 billion (2019)	Chinese Academy of Sciences, InterGrain Pty Ltd, John Innes Centre	Australia, China, Saudi Arabia	—
8	Evolutionary-scale prediction of atomic-level protein structure with a language model (2023)	Massachusetts Institute of Technology, Meta, Meta AI	United States	Background
9	Sequence modeling and design from molecular to genome scale with Evo.	Arc Institute, Arc Institute; Stanford University, Arc Institute; University of California, Berkeley	United States	—
10	Game changers in science and technology - now and beyond (2023)	Aché Laboratórios Farmacêuticos, Astex Pharmaceuticals, Bayer AG	Australia, Austria, Brazil	—
11	Engineering Cellular Metabolism (2016)	Chalmers University of Technology, Technical University of Denmark	Denmark, Sweden	—
12	Targeted nucleotide editing using hybrid prokaryotic and vertebrate adaptive immune systems (2016)	Kobe University, The University of Tokyo	Japan	—
13	Passive, active and endogenous organ-targeted lipid and polymer nanoparticles for delivery of genetic drugs (2023)	The University of Texas Southwestern Medical Center	United States	—
14	Correction of a pathogenic gene mutation in human embryos (2017)	Capital Medical University, Institute for Basic Science, Oregon Health & Science University	United States	—
15	Applications of genome editing technology in the targeted therapy of human diseases: mechanisms, advances and prospects (2020)	Sichuan University, University of North Dakota	China, P. R. China, United States	Background
16	Crystal structure of Cas9 in complex with guide RNA and target DNA (2014)	Broad Institute of MIT and Harvard, RIKEN, The University of Tokyo	Japan, United States	**Result**
17	Determinants of enhancer and promoter activities of regulatory elements (2020)	University of Copenhagen	Denmark	—
18	Epigenetic regulation of T cell exhaustion. (2022)	Gladstone-UCSF Institute of Genomic Immunology, Stanford University	United States	—
19	Synthetic and Biogenic Materials for Oral Delivery of Biologics: From Bench to Bedside. (2025)	Columbia University, University of Pennsylvania	United States	—
20	Custom CRISPR–Cas9 PAM variants via scalable engineering and machine learning (2025)	Massachusetts General Hospital	United States	**Influential**
21	Lipids and Lipid Derivatives for RNA Delivery. (2021)	The Ohio State University	United States	—
22	Strategies for Electrochemical Point-of-Care Biosensors. (2025)	University of Campinas (UNICAMP)	Brazil	—

No.	Citing paper	Citing institution(s)	Country	S2
23	Induced pluripotent stem cell technology: a decade of progress (2017)	Beckman Research Institute of City of Hope, Kyoto University, Stanford Cardiovascular Institute	Japan, United States	—
24	Organoids: Modeling Development and the Stem Cell Niche in a Dish (2016)	Hubrecht Institute	Netherlands	**Methodology**
25	Smart breeding driven by big data, artificial intelligence, and integrated genomic-enviromic prediction (2022)	Chinese Academy of Agricultural Sciences, CIMMYT-China Specialty Maize Research Center, CIMMYT (International Maize and Wheat Improvement Center)	Australia, China, Kenya	—
26	Revolutionizing CRISPR technology with artificial intelligence (2025)	Hanyang University, KIST School, University of Science and Technology, Korea Institute of Science and Technology	South Korea	—
27	Advancing pharmaceutical research: a comprehensive review of cutting-edge tools and technologies. (2024)	—	—	—
28	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases. (2021)	Massachusetts Institute of Technology, Montana State University, National Center for Biotechnology Information	United States	—
29	Image-based profiling for drug discovery: due for a machine-learning upgrade? (2020)	Broad Institute of MIT and Harvard, Janssen Pharmaceutica NV, Janssen Research & Development	Belgium, United States	—
30	Ischemic stroke: experimental models and reality. (2017)	University Medical Center of the Johannes Gutenberg-University Mainz	Germany	Background

Showing the 30 most-cited of 595 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).

Citing-text excerpts — how the field used this work

> **RESULT** Crystal structure of Cas9 in complex with guide RNA and target DNA
>
> *"This is consistent with previous reports that the 10–12 bp PAM-proximal "seed" region is critical for the Cas9-catalyzed DNA cleavage (Cong et al., 2013; Fu et al., 2013; Hsu et al., 2013; Jinek et al., 2012; Mali et al., 2013a; Pattanayak et al., 2013)."*

> **FOLLOW-UP WORK**
>
> ### Repurposing CRISPR as an RNA-guided platform for sequence-specific control of gene expression
>
> 2013 · Cell 152 (5), 1173-1183, 2013 · 6,776 citations (GS)
>
> Field-normalised: 4,663 Semantic Scholar citations place it in the top 1% of Biology papers from 2013 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	DNA methylation in mammalian development and disease (2024)	Max Planck Institute for Molecular Genetics, Yale School of Medicine	Germany, United States	—
2	Gene regulation by long non-coding RNAs and its biological functions (2021)	Center for Applied Medical Research, University of Navarra, University of the Chinese Academy of Sciences	China, Spain	—
3	Unique features of long non-coding RNA biogenesis and function (2016)	Stanford University, Stanford University School of Medicine	United States	—
4	Synthetic Biology in Natural Product Biosynthesis (2025)	University of California, Irvine Medical Center	United States	—
5	Crystal structure of Cas9 in complex with guide RNA and target DNA (2014)	Broad Institute of MIT and Harvard, RIKEN, The University of Tokyo	Japan, United States	Background
6	Epigenetic regulation in major depression and other stress-related disorders: molecular mechanisms, clinical relevance and therapeutic potential (2023)	Columbia University, Eastern Virginia Medical School, Ningbo University	China, United States	Background
7	Determinants of enhancer and promoter activities of regulatory elements (2020)	University of Copenhagen	Denmark	—
8	Epigenetic regulation of T cell exhaustion. (2022)	Gladstone-UCSF Institute of Genomic Immunology, Stanford University	United States	—
9	How do lncRNAs regulate transcription? (2017)	University of Colorado Boulder	United States	Background
10	From GWAS to Function: Using Functional Genomics to Identify the Mechanisms Underlying Complex Diseases. (2020)	Wellcome Sanger Institute	United Kingdom	—
11	Decoding the microbiome: advances in genetic manipulation for gut bacteria (2023)	Fudan University Shanghai Cancer Center, Institut Pasteur of Shanghai, University of Chicago	China, United States	—
12	The chromatin accessibility landscape of primary human cancers. (2018)	—	—	**Methodology**
13	Protein editing using a coordinated transposition reaction. (2025)	Princeton University	United States	—
14	CRISPR/Cas9 therapeutics: progress and prospects (2023)	Linyi Center for Disease Control and Prevention, People's Hospital of Rizhao, Qingdao University	China	—
15	Death after High-Dose rAAV9 Gene Therapy in a Patient with Duchenne's Muscular Dystrophy. (2023)	—	—	—
16	Engineering the next generation of cell-based therapeutics (2022)	Flagship Pioneering, Rice University, Sigilon Therapeutics	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
17	Current applications and future perspective of CRISPR/Cas9 gene editing in cancer. (2022)	Fudan University	China	Background
18	The next generation of CRISPR–Cas technologies and applications (2019)	Duke University	United States	—
19	The CRISPR tool kit for genome editing and beyond (2018)	University of Virginia	United States	—
20	High-content CRISPR screening (2022)	CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, University of Washington	Austria, United States	—
21	Epigenome editing technologies for discovery and medicine (2024)	Duke University	United States	—
22	Drug delivery systems for CRISPR-based genome editors (2023)	Broad Institute of MIT and Harvard, Georgia Institute of Technology and Emory University	United States	—
23	Genome engineering using the CRISPR-Cas9 system (2013)	Broad Institute	United States	—
24	Gene therapy comes of age. (2018)	Massachusetts General Hospital and Harvard Medical School, Memorial Sloan Kettering Cancer Center, National Heart, Lung and Blood Institute	Japan, United States	—
25	CRISPR-GPT for agentic automation of gene-editing experiments (2025)	Google DeepMind, Princeton University, Stanford University School of Medicine	United States	—
26	DNA targeting specificity of RNA-guided Cas9 nucleases (2013)	—	—	—
27	Engineering the next-generation of CAR T-cells with CRISPR-Cas9 gene editing. (2022)	University of Pennsylvania	United States	—
28	CRISPR-Cas systems for editing, regulating and targeting genomes (2014)	Massachusetts General Hospital	United States	—
29	Delivering CRISPR: a review of the challenges and approaches. (2018)	Sandia National Laboratories	United States	Background
30	Genome-scale CRISPR-Cas9 knockout and transcriptional activation screening (2017)	Broad Institute of MIT and Harvard, Massachusetts Institute of Technology	United States	—

Showing the 30 most-cited of 593 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 2

Claim — Contribution 2

The researcher advanced genome engineering by publishing a seminal 2014 Science review on CRISPR-Cas9, establishing a foundational framework that has garnered nearly 10,000 citations from independent scholars.

The researcher's primary contribution lies in the publication of a seminal 2014 review in Science titled 'The new frontier of genome engineering with CRISPR-Cas9.' This work serves as the cornerstone of the presented evidence, defining the scope and potential of this transformative technology for the broader scientific community.

This line of work appears to address the critical need for a comprehensive synthesis of emerging CRISPR-Cas9 methodologies at a pivotal moment in the field. By framing the technology as a 'new frontier,' the researcher likely helped consolidate disparate findings and articulate the broader implications for genome engineering, thereby accelerating its adoption and understanding across diverse disciplines.

The significance of this contribution is underscored by its exceptional citation record, with the core paper accumulating 9,823 citations. Furthermore, citation analysis reveals that 99.0% of these citations originate from independent researchers, indicating that the work has had a profound and widespread impact on the global scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 783 **· 16 flagged influential by Semantic Scholar**

CORE PAPER

The new frontier of genome engineering with CRISPR-Cas9

2014 · Science · 9,823 citations (GS)

Field-normalised: 5,929 Semantic Scholar citations place it in the top 1% of Engineering papers from 2014 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	The emerging role of mass spectrometry-based proteomics in drug discovery (2022)	Cellzome GmbH, Max Planck Institute of Biochemistry, University of Guelph	Canada, Germany	—
2	Breeding crops to feed 10 billion (2019)	Chinese Academy of Sciences, InterGrain Pty Ltd, John Innes Centre	Australia, China, Saudi Arabia	—
3	Correction of a pathogenic gene mutation in human embryos (2017)	Capital Medical University, Institute for Basic Science, Oregon Health & Science University	United States	—
4	Applications of genome editing technology in the targeted therapy of human diseases: mechanisms, advances and prospects (2020)	Sichuan University, University of North Dakota	China, P. R. China, United States	—
5	A CRISPR–Cas9-triggered strand displacement amplification method for ultrasensitive DNA detection (2018)	City University of Hong Kong, Imperial College London, Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences	China, United Kingdom	—
6	Chemically induced proximity in biology and medicine (2018)	Stanford University School of Medicine	United States	Background
7	Machine Learning and Deep Learning in Synthetic Biology: Key Architectures, Applications, and Challenges. (2024)	University of Wisconsin-Green Bay, Manitowoc	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
8	Synthetic and Biogenic Materials for Oral Delivery of Biologics: From Bench to Bedside. (2025)	Columbia University, University of Pennsylvania	United States	—
9	Recent developments in (2025)	Geisel School of Medicine at Dartmouth	United States	—
10	A Survey of Scientific Large Language Models: From Data Foundations to Agent Frontiers (2025)	Alibaba Group, Beijing Institute of Technology, Beijing Jiaotong University	Australia, China, Hong Kong	—
11	Stem Cell Models of Human Brain Development (2016)	MRC Laboratory of Molecular Biology	United Kingdom	—
12	PROTACs: great opportunities for academia and industry (an update from 2020 to 2021) (2022)	Tsinghua University, Zhengzhou University	China	—
13	CRISPR/Cas9 therapeutics: progress and prospects (2023)	Linyi Center for Disease Control and Prevention, People's Hospital of Rizhao, Qingdao University	China	—
14	Targeted genome-modification tools and their advanced applications in crop breeding (2024)	Chinese Academy of Sciences, Hainan Yazhou Bay Seed Laboratory	China	—
15	Selective organ targeting (SORT) nanoparticles for tissue-specific mRNA delivery and CRISPR–Cas gene editing (2020)	Peking University, University of Texas Southwestern Medical Center	China, United States	—
16	Current applications and future perspective of CRISPR/Cas9 gene editing in cancer. (2022)	Fudan University	China	—
17	The CRISPR tool kit for genome editing and beyond (2018)	University of Virginia	United States	—
18	Base editing: precision chemistry on the genome and transcriptome of living cells (2018)	—	—	—
19	Evolved Cas9 variants with broad PAM compatibility and high DNA specificity (2018)	Broad Institute of MIT and Harvard	United States	—
20	Gene therapy comes of age. (2018)	Massachusetts General Hospital and Harvard Medical School, Memorial Sloan Kettering Cancer Center, National Heart, Lung and Blood Institute	Japan, United States	—
21	CRISPR-GPT for agentic automation of gene-editing experiments (2025)	Google DeepMind, Princeton University, Stanford University School of Medicine	United States	—
22	CRISPR-Cas-Based Antimicrobials: Design, Challenges, and Bacterial Mechanisms of Resistance. (2023)	Universidad San Francisco de Quito, Universidad UTE	Ecuador	—
23	Transcriptome Engineering with RNA-Targeting Type VI-D CRISPR Effectors (2018)	Salk Institute for Biological Studies	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
24	Induced protein degradation: an emerging drug discovery paradigm (2017)	Yale University	United States	—
25	DNA repair pathway choices in CRISPR-Cas9-mediated genome editing (2021)	Columbia University	United States	—
26	Engineered CRISPR-Cas9 nucleases with altered PAM specificities (2015)	Massachusetts General Hospital	United States	—
27	Genetically modified crops: current status and future prospects. (2020)	Indian Institute of Maize Research, National Institute for Research in Environmental Health	India	—
28	Advances in CRISPR-Cas technology and its applications: revolutionising precision medicine. (2024)	Erbil Polytechnic University, Salahaddin University, Uppsala University	Iraq, Sweden	—
29	CRISPR-Based Technologies for the Manipulation of Eukaryotic Genomes (2017)	Harvard University, The Broad Institute of MIT and Harvard	United States	—
30	A high-fidelity Cas9 mutant delivered as a ribonucleoprotein complex enables efficient gene editing in human hematopoietic stem and progenitor cells (2018)	Aarhus University, Integrated DNA Technologies, Inc., Rice University	Denmark, United States	—

Showing the 30 most-cited of 783 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 California, Irvine Medical Center	United States	—	126
Broad Institute of MIT and Harvard	United States	SCImago #112	45
Massachusetts Institute of Technology	United States	SCImago #41 · THE 2 · QS 1	45
Stanford University	United States	SCImago #18 · THE =5 · QS 3	40
Chinese Academy of Sciences	PR China	SCImago #2	37
Harvard Medical School	United States	SCImago #12	35
Harvard University	United States	SCImago #4 · THE =5 · QS 5	21
University of Pennsylvania	United States	SCImago #52 · THE 14 · QS 15	19
Massachusetts General Hospital	United States	SCImago #100	18
University of Minnesota	United States	SCImago #165 · THE 88 · QS 210	17
National Institutes of Health	United States	SCImago #44	16
University of Texas Southwestern Medical Center	United States	SCImago #562	16

Institution	Country	World ranking	Citing papers
King Abdullah University of Science and Technology	Saudi Arabia	SCImago #680	16
University of Toronto	Canada	SCImago #39 · THE 21 · QS 29	15
Columbia University	United States	SCImago #65 · THE 20 · QS =38	14

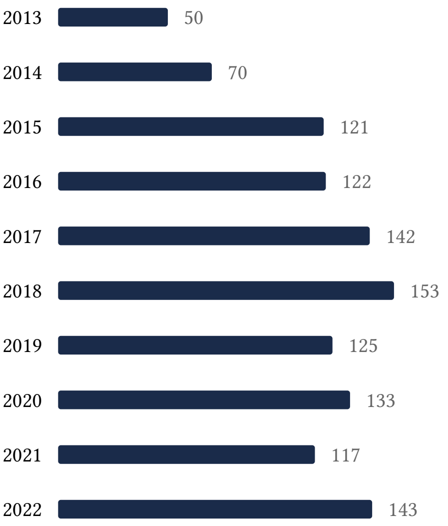
Geographic distribution of citing authors

Country	Citing papers
United States	802
China	344
Germany	98
United Kingdom	91
India	72
Canada	62
South Korea	57
Australia	51
Switzerland	47
Netherlands	38
Japan	38
France	35

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	A programmable dual-RNA–guided DNA endonuclease in adaptive bacterial immunity	1,188	8 CFR 204.5(h)(3)(v) — Criterion 5
Contribution 2	The new frontier of genome engineering with CRISPR-Cas9	783	8 CFR 204.5(h)(3)(v) — Criterion 5