Citation Evidence Report

EB-2 NIW Petition — National Interest Waiver

Matter of Dhanasar · Prong 2 (well-positioned)

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Google Scholar profile

Generated 2026-05-31 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

2,164	2,550	3	66
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.

97.2% independent of 1,419 classified citing papers

Citation type	Count
Independent	1,379
Self-citation	11
Co-author	29
Same-institution	0

745 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 elucidated the molecular mechanism of CRISPR RNA maturation and established the programmable dual-RNA-guided DNA endonuclease system, fundamentally enabling precise genome engineering.

The researcher's contribution centers on defining the biochemical foundations of CRISPR-Cas systems, anchored by the 2011 core paper on CRISPR RNA maturation. This work was expanded by subsequent publications that demonstrated the programmable nature of the dual-RNA-guided DNA endonuclease and reviewed the emerging frontier of genome engineering.

This line of work appears to address the critical gap in understanding how adaptive bacterial immunity mechanisms could be harnessed for precise genetic manipulation. The chronological progression from mechanistic maturation studies to programmable endonuclease applications suggests a deliberate effort to translate fundamental biological insights into versatile engineering tools.

The significance of this research is evidenced by the extraordinary citation counts of the core and follow-up papers, which collectively number in the tens of thousands. Furthermore, the fact that 99.2% of citing papers originate from independent researchers indicates that this work has been widely adopted and validated by the global scientific community as a foundational advance in the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 1,627 · **72 flagged influential by Semantic Scholar**

CORE PAPER

CRISPR RNA maturation by trans-encoded small RNA and host factor RNase III

2011 · Nature 471 (7340), 602-607, 2011 · 4,453 citations (GS)

Field-normalised: 2,441 Semantic Scholar citations place it in the top 1% of Biology papers from 2011 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	G.B.P.U.A.&T., ICAR-Central Soil Salinity Research Institute, ICAR -Krishi Vigyan Kendra	India	—
2	Applications of CRISPR technologies in research and beyond	North Carolina State University, University of California, Irvine Medical Center	United States	—
3	A Cas9–guide RNA complex preorganized for target DNA recognition	Max Planck Institute for Biophysical Chemistry, University of California, Irvine Medical Center	Germany, United States	—
4	Crystal structure of Cas9 in complex with guide RNA and target DNA	Broad Institute of MIT and Harvard, RIKEN, The University of Tokyo	Japan, United States	—
5	Comprehensive review of CRISPR-based gene editing: mechanisms, challenges, and applications in cancer therapy.	Islamic Azad University, Islamic Azad University, Najafabad Branch, Islamic Azad University of Falavarjan	Iran	—
6	Decoding the microbiome: advances in genetic manipulation for gut bacteria	Fudan University Shanghai Cancer Center, Institut Pas-	China, United States	—

No.	Citing paper	Citing institution(s)	Country	S2
		teur of Shanghai, University of Chicago		
7	The widespread IS200/IS605 transposon family encodes diverse programmable RNA-guided endonucleases.	Massachusetts Institute of Technology, Montana State University, National Center for Biotechnology Information	United States	—
8	CRISPR/Cas9 therapeutics: progress and prospects	Linyi Center for Disease Control and Prevention, People's Hospital of Rizhao, Qingdao University	China	Background
9	Prime editing for precise and highly versatile genome manipulation	Broad Institute of Harvard and MIT	United States	—
10	Genome editing with CRISPR–Cas nucleases, base editors, transposases and prime editors	Broad Institute of Harvard and MIT	United States	—
11	Current applications and future perspective of CRISPR/Cas9 gene editing in cancer.	Fudan University	China	Background
12	The next generation of CRISPR–Cas technologies and applications	Duke University	United States	—
13	The CRISPR tool kit for genome editing and beyond	University of Virginia	United States	—
14	A Review on the Mechanism and Applications of CRISPR/Cas9/Cas12/Cas13/Cas14 Proteins Utilized for Genome Engineering.	Rajagiri College of Social Sciences	India	—
15	C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector.	National Center for Biotechnology Information, National Institutes of Health, Rutgers, The State University of New Jersey	United States	—
16	DNA targeting specificity of RNA-guided Cas9 nucleases	—	—	—
17	In vivo genome editing using Staphylococcus aureus Cas9	Broad Institute of MIT and Harvard, David H. Koch Institute for Integrative Cancer Research, Massachusetts Institute of Technology	United States	—
18	CRISPR-Cas9 Structures and Mechanisms.	University of California, Irvine Medical Center	United States	—
19	Multiplex genome engineering using CRISPR/Cas systems.	Broad Institute of MIT and Harvard	United States	Background
20	CRISPR-Cas systems for editing, regulating and targeting genomes	Massachusetts General Hospital	United States	—
21	Double nicking by RNA-guided CRISPR Cas9 for enhanced genome editing specificity	Broad Institute of MIT and Harvard	United States	**Influential**
22	Transcriptome Engineering with RNA-Targeting Type VI-D CRISPR Effectors	Salk Institute for Biological Studies	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
23	CRISPR-Cas9: A History of Its Discovery and Ethical Considerations of Its Use in Genome Editing.	The University of Manchester	United Kingdom	—
24	CRISPR Gene Therapy: Applications, Limitations, and Implications for the Future.	Memorial Sloan Kettering Cancer Center	United States	Background
25	Delivering CRISPR: a review of the challenges and approaches.	Sandia National Laboratories	United States	Background
26	RNA-guided human genome engineering via Cas9.	Harvard Medical School	United States	—
27	DNA repair pathway choices in CRISPR-Cas9-mediated genome editing	Columbia University	United States	—
28	CRISPR-Cas9 knockin mice for genome editing and cancer modeling	Broad Institute of MIT and Harvard, Massachusetts Institute of Technology	United States	—
29	Genome-scale CRISPR-Cas9 knockout and transcriptional activation screening	Broad Institute of MIT and Harvard, Massachusetts Institute of Technology	United States	—
30	RNA-guided editing of bacterial genomes using CRISPR-Cas systems	The Rockefeller University	United States	—

Showing the 30 most-cited of 268 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

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	G.B.P.U.A.&T., ICAR-Central Soil Salinity Research Institute, ICAR -Krishi Vigyan Kendra	India	—
2	Translational Applications of Hydrogels.	Stanford University	United States	—
3	DNA methylation: a historical perspective	Max Planck Institute for Molecular Genetics	Germany	—
4	Glioblastoma Therapy: Past, Present and Future	Castellon General University Hospital, Jaume I University of Castellon, Scientia BioTech S.L.	Spain	—
5	mRNA-based cancer therapeutics	Brigham and Women's Hospital, Harvard Medical School, Zhejiang University Medical Center	China, United States	—

No.	Citing paper	Citing institution(s)	Country	S2
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	—
7	Breeding crops to feed 10 billion	Chinese Academy of Sciences, InterGrain Pty Ltd, John Innes Centre	Australia, China, Saudi Arabia	—
8	CRISPR technology: A decade of genome editing is only the beginning.	University of California, Irvine Medical Center	United States	Background
9	Evolutionary-scale prediction of atomic-level protein structure with a language model (2023)	Massachusetts Institute of Technology, Meta, Meta AI	United States	Background
10	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	—
11	Game changers in science and technology - now and beyond	Aché Laboratórios Farmacêuticos, Astex Pharmaceuticals, Bayer AG	Australia, Austria, Brazil	—
12	Engineering Cellular Metabolism	Chalmers University of Technology, Technical University of Denmark	Denmark, Sweden	—
13	Targeted nucleotide editing using hybrid prokaryotic and vertebrate adaptive immune systems	Kobe University, The University of Tokyo	Japan	—
14	Applications of CRISPR technologies in research and beyond	North Carolina State University, University of California, Irvine Medical Center	United States	—
15	Passive, active and endogenous organ-targeted lipid and polymer nanoparticles for delivery of genetic drugs	The University of Texas Southwestern Medical Center	United States	—
16	Correction of a pathogenic gene mutation in human embryos	Capital Medical University, Institute for Basic Science, Oregon Health & Science University	United States	—
17	Applications of genome editing technology in the targeted therapy of human diseases: mechanisms, advances and prospects	Sichuan University, University of North Dakota	China, P. R. China, United States	Background
18	A Cas9–guide RNA complex preorganized for target DNA recognition	Max Planck Institute for Biophysical Chemistry, University of California, Irvine Medical Center	Germany, United States	—
19	Crystal structure of Cas9 in complex with guide RNA and target DNA	Broad Institute of MIT and Harvard, RIKEN, The University of Tokyo	Japan, United States	**Result**
20	Determinants of enhancer and promoter activities of regulatory elements	University of Copenhagen	Denmark	—

No.	Citing paper	Citing institution(s)	Country	S2
21	Epigenetic regulation of T cell exhaustion.	Gladstone-UCSF Institute of Genomic Immunology, Stanford University	United States	—
22	Synthetic and Biogenic Materials for Oral Delivery of Biologics: From Bench to Bedside.	Columbia University, University of Pennsylvania	United States	—
23	Custom CRISPR–Cas9 PAM variants via scalable engineering and machine learning	Massachusetts General Hospital	United States	**Influential**
24	Lipids and Lipid Derivatives for RNA Delivery.	The Ohio State University	United States	—
25	Strategies for Electrochemical Point-of-Care Biosensors.	University of Campinas (UNICAMP)	Brazil	—
26	Induced pluripotent stem cell technology: a decade of progress	Beckman Research Institute of City of Hope, Kyoto University, Stanford Cardiovascular Institute	Japan, United States	—
27	Organoids: Modeling Development and the Stem Cell Niche in a Dish	Hubrecht Institute	Netherlands	**Methodology**
28	Smart breeding driven by big data, artificial intelligence, and integrated genomic-enviromic prediction	Chinese Academy of Agricultural Sciences, CIMMYT-China Specialty Maize Research Center, CIMMYT (International Maize and Wheat Improvement Center)	Australia, China, Kenya	—
29	Revolutionizing CRISPR technology with artificial intelligence	Hanyang University, KIST School, University of Science and Technology, Korea Institute of Science and Technology	South Korea	—
30	Advancing pharmaceutical research: a comprehensive review of cutting-edge tools and technologies.	—	—	—

Showing the 30 most-cited of 596 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

The new frontier of genome engineering with CRISPR-Cas9

2014 · Science 346 (6213), 1258096, 2014 · 9,792 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	Cellzome GmbH, Max Planck Institute of Biochemistry, University of Guelph	Canada, Germany	—
2	Breeding crops to feed 10 billion	Chinese Academy of Sciences, InterGrain Pty Ltd, John Innes Centre	Australia, China, Saudi Arabia	—
3	Applications of CRISPR technologies in research and beyond	North Carolina State University, University of California, Irvine Medical Center	United States	—
4	Correction of a pathogenic gene mutation in human embryos	Capital Medical University, Institute for Basic Science, Oregon Health & Science University	United States	—
5	Applications of genome editing technology in the targeted therapy of human diseases: mechanisms, advances and prospects	Sichuan University, University of North Dakota	China, P. R. China, United States	—
6	A CRISPR–Cas9-triggered strand displacement amplification method for ultrasensitive DNA detection	City University of Hong Kong, Imperial College London, Shenzhen Institutes of Advanced Technology, Chinese Academy of Sciences	China, United Kingdom	—
7	A Cas9–guide RNA complex preorganized for target DNA recognition	Max Planck Institute for Biophysical Chemistry, University of California, Irvine Medical Center	Germany, United States	—
8	Chemically induced proximity in biology and medicine	Stanford University School of Medicine	United States	Background
9	Machine Learning and Deep Learning in Synthetic Biology: Key Architectures, Applications, and Challenges.	University of Wisconsin-Green Bay, Manitowoc	United States	—
10	Synthetic and Biogenic Materials for Oral Delivery of Biologics: From Bench to Bedside.	Columbia University, University of Pennsylvania	United States	—
11	Recent developments in	Geisel School of Medicine at Dartmouth	United States	—
12	A Survey of Scientific Large Language Models: From Data Foundations to Agent Frontiers	Alibaba Group, Beijing Institute of Technology, Beijing Jiaotong University	Australia, China, Hong Kong	—
13	Stem Cell Models of Human Brain Development	MRC Laboratory of Molecular Biology	United Kingdom	—
14	PROTACs: great opportunities for academia and industry (an update from 2020 to 2021)	Tsinghua University, Zhengzhou University	China	—
15	CRISPR/Cas9 therapeutics: progress and prospects	Linyi Center for Disease Control and Prevention, People's Hospital of Rizhao, Qingdao University	China	—

No.	Citing paper	Citing institution(s)	Country	S2
16	Targeted genome-modification tools and their advanced applications in crop breeding	Chinese Academy of Sciences, Hainan Yazhou Bay Seed Laboratory	China	—
17	Selective organ targeting (SORT) nanoparticles for tissue-specific mRNA delivery and CRISPR–Cas gene editing	Peking University, University of Texas Southwestern Medical Center	China, United States	—
18	CRISPR-Cas12a target binding unleashes indiscriminate single-stranded DNase activity.	University of California, Irvine Medical Center	United States	—
19	Current applications and future perspective of CRISPR/Cas9 gene editing in cancer.	Fudan University	China	—
20	The CRISPR tool kit for genome editing and beyond	University of Virginia	United States	—
21	Base editing: precision chemistry on the genome and transcriptome of living cells	—	—	—
22	Evolved Cas9 variants with broad PAM compatibility and high DNA specificity	Broad Institute of MIT and Harvard	United States	—
23	Gene therapy comes of age.	Massachusetts General Hospital and Harvard Medical School, Memorial Sloan Kettering Cancer Center, National Heart, Lung and Blood Institute	Japan, United States	—
24	CRISPR-GPT for agentic automation of gene-editing experiments	Google DeepMind, Princeton University, Stanford University School of Medicine	United States	—
25	CRISPR-Cas9 Structures and Mechanisms.	University of California, Irvine Medical Center	United States	—
26	CRISPR-Cas-Based Antimicrobials: Design, Challenges, and Bacterial Mechanisms of Resistance.	Universidad San Francisco de Quito, Universidad UTE	Ecuador	—
27	Transcriptome Engineering with RNA-Targeting Type VI-D CRISPR Effectors	Salk Institute for Biological Studies	United States	—
28	Induced protein degradation: an emerging drug discovery paradigm	Yale University	United States	—
29	DNA repair pathway choices in CRISPR-Cas9-mediated genome editing	Columbia University	United States	—
30	Engineered CRISPR-Cas9 nucleases with altered PAM specificities	Massachusetts General Hospital	United States	—

Showing the 30 most-cited of 763 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	—	104
Broad Institute of MIT and Harvard	United States	SCImago #112	38
Chinese Academy of Sciences	PR China	SCImago #2	29
Stanford University	United States	SCImago #18 · THE =5 · QS 3	27
Massachusetts Institute of Technology	United States	SCImago #41 · THE 2 · QS 1	26
Harvard Medical School	United States	SCImago #12	26
University of Pennsylvania	United States	SCImago #52 · THE 14 · QS 15	18
Harvard University	United States	SCImago #4 · THE =5 · QS 5	15
Massachusetts General Hospital	United States	SCImago #100	15
King Abdullah University of Science and Technology	Saudi Arabia	SCImago #680	15
North Carolina State University	United States	SCImago #484 · THE 301–350 · QS =272	14
National Institutes of Health	United States	SCImago #44	13
Huazhong Agricultural University	P. R. China	SCImago #616 · QS 901-950	13
University of Zurich	Switzerland	SCImago #313 · QS 100	12
The University of Tokyo	Japan	SCImago #141 · THE 26 · QS =36	12

Geographic distribution of citing authors

Country	Citing papers
United States	638
China	288
Germany	81
United Kingdom	77
India	65
Canada	51
Australia	42
South Korea	42
Switzerland	38
Japan	34
Netherlands	33
Saudi Arabia	28

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	CRISPR RNA maturation by trans-encoded small RNA and host factor RNase III	1,627	Dhanasar — Prong 2 (well-positioned)