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 2026-05-21 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

4,214	4,843	30	38
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.

99.4% independent of 2,141 classified citing papers

Citation type	Count
Independent	2,128
Self-citation	13
Co-author	0
Same-institution	0

2,073 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 mechanisms of CRISPR-Cas systems, establishing foundational principles for RNA-guided genetic silencing and DNA interrogation in bacteria and archaea.

The researcher's contribution centers on defining the operational mechanics of CRISPR-Cas systems, anchored by the seminal 2012 paper on RNA-guided genetic silencing in bacteria and archaea. This core work established the fundamental framework for understanding how these organisms utilize RNA to guide genetic interference.

Originality is evident in the progression from general silencing systems to specific mechanistic details. The 2014 follow-up papers appear to address the precise molecular interactions involved, specifically detailing DNA interrogation by Cas9 and the RNA-mediated conformational activation required for endonuclease activity. This suggests a deliberate effort to move from phenotypic observation to structural and functional elucidation.

The significance of this line of work is demonstrated by its extensive uptake in the scientific community. The core paper has accumulated 2950 citations, while the subsequent mechanistic studies have garnered 2705 and 1847 citations respectively. Crucially, 99.4% of the classified citations originate from independent researchers, indicating that these findings have become standard reference points for the broader field rather than niche internal developments.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 1,575 · **65 flagged influential by Semantic Scholar**

CORE PAPER

RNA-guided genetic silencing systems in bacteria and archaea

2012 · Nature 482 (7385), 331-338, 2012 · 2,950 citations (GS)

Field-normalised: 1,787 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	A brief history of synthetic biology	Boston University	United States	—
2	Human organoids: model systems for human biology and medicine	Institute of Molecular Biotechnology of the Austrian Academy of Sciences (IMBA)	Austria	—
3	Structures, mechanisms and applications of RNA-centric CRISPR–Cas13	Memorial Sloan Kettering Cancer Center, Shanghai Institute of Biochemistry and Cell Biology	China, United States	—
4	An updated evolutionary classification of CRISPR–Cas systems	National Center for Biotechnology Information	United States	—
5	CRISPR–Cas9 structures and mechanisms	University of California, Berkeley	United States	—
6	The emerging role of lncRNAs in cancer	University of Navarra	Spain	—
7	CRISPR-Cas systems for editing, regulating and targeting genomes	Massachusetts General Hospital	United States	—
8	A programmable dual-RNA–guided DNA endonuclease in adaptive bacterial immunity	Howard Hughes Medical Institute, University of California, Umeå University, University of California, Berkeley	Austria, Sweden, United States	—

No.	Citing paper	Citing institution(s)	Country	S2
9	High-frequency off-target mutagenesis induced by CRISPR-Cas nucleases in human cells	Massachusetts General Hospital	United States	—
10	Cas9–crRNA ribonucleoprotein complex mediates specific DNA cleavage for adaptive immunity in bacteria	Vilnius University	Lithuania	Background
11	RNA-guided human genome engineering via Cas9	Harvard Medical School	United States	—
12	Efficient genome editing in zebrafish using a CRISPR-Cas system	Massachusetts General Hospital	United States	—
13	Improving CRISPR-Cas nuclease specificity using truncated guide RNAs	Massachusetts General Hospital	United States	**Methodology**
14	Highly efficient RNA-guided genome editing in human cells via delivery of purified Cas9 ribonucleoproteins	Seoul National University	South Korea	Background
15	Evolution and classification of the CRISPR–Cas systems	Danisco France SAS, National Center for Biotechnology Information, The J. Craig Venter Institute	Canada, France, Netherlands	—
16	Targeted genome engineering in human cells with the Cas9 RNA-guided endonuclease	Seoul National University	South Korea	—
17	Principles and applications of nucleic acid strand displacement reactions	Boise State University, TU München	Germany, United States	—
18	CRISPR/Cas9 in genome editing and beyond	Stanford University	—	—
19	CRISPR-Cas biochemistry and CRISPR-based molecular diagnostics	North Carolina State University, Rice University, University of Connecticut	United States	—
20	Tools for translation: non-viral materials for therapeutic mRNA delivery	Carnegie Mellon University	United States	—
21	CRISPR interference (CRISPRi) for sequence-specific control of gene expression	University of California, San Francisco	United States	—
22	Increasing the efficiency of precise genome editing with CRISPR-Cas9 by inhibition of nonhomologous end joining	Whitehead Institute for Biomedical Research	United States	—
23	Cas9 as a versatile tool for engineering biology	Harvard Medical School	United States	—
24	Analysis of off-target effects of CRISPR/Cas-derived RNA-guided endonucleases and nickases	Seoul National University	South Korea	Background
25	RNA chemistry and therapeutics	Icahn School of Medicine at Mount Sinai, University of Pennsylvania	United States	—
26	History of CRISPR-Cas from encounter with a mysterious repeated sequence to genome editing technology	Institut Pasteur	France	—

No.	Citing paper	Citing institution(s)	Country	S2
27	CRISPR RNA–guided activation of endogenous human genes	Massachusetts General Hospital	United States	—
28	Regulatory R-loops as facilitators of gene expression and genome stability	Institute of Molecular Biology	Germany	—
29	CCTop: an intuitive, flexible and reliable CRISPR/Cas9 target prediction tool	Heidelberg University	Germany	Background
30	Efficient multiplex biallelic zebrafish genome editing using a CRISPR nuclease system	Vanderbilt University School of Medicine	United States	—

Showing the 30 most-cited of 519 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

METHODOLOGY Improving CRISPR-Cas nuclease specificity using truncated guide RNAs

"In brief, PCR reactions to amplify specific on-target or off-target sites were performed with Phusion high-fidelity DNA polymerase (New England Biolabs) using one of the two following programs: (1) Touchdown PCR program [(98°C, 10 s; 72–62°C, −1 °C/cycle, 15 s; 72°C, 30 s) × 10 cycles, (98°C, 10 s; 62°C, 15 s; 72°C, 30 s) × 25 cycles] or (2) Constant Tm PCR program [(98°C, 10 s; 68°C or 72°C, 15 s; 72°C, 30 s) × 35 cycles], with 3% DMSO or 1 M betaine if necessary."

FOLLOW-UP WORK

DNA interrogation by the CRISPR RNA-guided endonuclease Cas9

2014 · Nature 507 (7490), 62-67, 2014 · 2,705 citations (GS)

Field-normalised: 1,773 Semantic Scholar citations place it in the top 1% of Biology papers from 2014 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Principles of genetic circuit design	Massachusetts Institute of Technology	United States	—
2	CRISPR–Cas9 structures and mechanisms	University of California, Berkeley	United States	—
3	CRISPR/Cas9 in genome editing and beyond	Stanford University	—	Result
4	CRISPR-Cas biochemistry and CRISPR-based molecular diagnostics	North Carolina State University, Rice University, University of Connecticut	United States	—
5	CCTop: an intuitive, flexible and reliable CRISPR/Cas9 target prediction tool	Heidelberg University	Germany	—
6	Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems	Broad Institute of MIT and Harvard, National Center for Biotechnology Information, Wageningen University	Netherlands, United States	Influential
7	Unravelling the structural and mechanistic basis of CRISPR–Cas systems	Wageningen University	Netherlands	—
8	Methodologies for improving HDR efficiency	China Animal Health and Epidemiology Center, Northwest A&F University	China	Influential

No.	Citing paper	Citing institution(s)	Country	S2
9	A Cas9–guide RNA complex preorganized for target DNA recognition	Howard Hughes Medical Institute, University of California, Max Planck Institute for Biophysical Chemistry, University of California, Berkeley	Germany, United States	—
10	Dynamic basis of supercoiling-dependent DNA interrogation by Cas12a via R-loop intermediates	Stanford University	United States	—
11	Evolutionary ecology of prokaryotic immune mechanisms	University of Exeter, Wageningen University	Netherlands, United Kingdom	Background
12	Recent updates of the CRISPR/Cas9 genome editing system: Novel approaches to regulate its spatiotemporal control by genetic and physicochemical strategies	Al-Baha University, College of Applied Medical Sciences, Qassim University, General Directorate of Education	Saudi Arabia	**Influential**
13	Current updates of CRISPR/Cas9-mediated genome editing and targeting within tumor cells: an innovative strategy of cancer management	Al Rass General Hospital, College of Applied Medical Sciences, Qassim University, Qassim University	Saudi Arabia	Background
14	CRISPR/Cas9 system: a reliable and facile genome editing tool in modern biology	Baba Ghulam Shah Badshah University, Sant Baba Bhag Singh University	India	Background
15	CRISPR-Cas: new tools for genetic manipulations from bacterial immunity systems	The Rockefeller University	United States	—
16	CRISPR-Cas9D10A nickase-based genotypic and phenotypic screening to enhance genome editing	University of Cambridge	United Kingdom	—
17	RNA-guided endonuclease provides a therapeutic strategy to cure latent herpesviridae infection	Stanford University	United States	—
18	The chemistry of Cas9 and its CRISPR colleagues	University of California, University of California, Berkeley	United States	—
19	Evolution of adaptive immunity from transposable elements combined with innate immune systems	Institut Pasteur, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health	France, United States	—
20	Cas9 interrogates DNA in discrete steps modulated by mismatches and supercoiling	Stanford University, University of California, Berkeley	United States	**Methodology**
21	CRISPR/Cas9 searches for a protospacer adjacent motif by lateral diffusion	Delft University of Technology, Institute for Basic Science, Seoul National University	Netherlands, South Korea	**Influential**
22	Profiling single-guide RNA specificity reveals a mismatch sensitive core sequence	Peking University	China	—

No.	Citing paper	Citing institution(s)	Country	S2
23	Dual sgRNA-directed gene knockout using CRISPR/Cas9 technology in Caenorhabditis elegans	University of Science and Technology of China	China	—
24	Genome-wide specificity of DNA binding, gene regulation, and chromatin remodeling by TALE-and CRISPR/Cas9-based transcriptional activators	Duke University	United States	Background
25	Coordinated actions of Cas9 HNH and RuvC nuclease domains are regulated by the bridge helix and the target DNA sequence	University of North Texas Health Science Center, University of Oklahoma, University of Southern California	United States	—
26	CRISPR-Cas9: tool for qualitative and quantitative plant genome editing	Fujian Agriculture and Forestry University, University of Agriculture Faisalabad	China, Pakistan	Background
27	Deep learning improves the ability of sgRNA off-target propensity prediction	University of Science and Technology Beijing	China	—
28	Evolution and ecology of CRISPR	University of Exeter, Wageningen University	Netherlands, United Kingdom	—
29	Functional genetics for all: engineered nucleases, CRISPR and the gene editing revolution	École Normale Supérieure de Lyon	France	Background
30	Recent advances in CRISPR-based biosensors for point-of-care pathogen detection	North Carolina State University, North Carolina State University; Bangladesh University of Engineering and Technology	USA; Bangladesh, United States	—

Showing the 30 most-cited of 560 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 CRISPR/Cas9 in genome editing and beyond

"The PAM-distal regions are more tolerant of mismatches as assayed by Cas9 binding and cleavage (3, 68, 69, 87)."

METHODOLOGY Cas9 interrogates DNA in discrete steps modulated by mismatches and supercoiling

"R-loop formation is required for stable specific binding (13) and is used for target discrimination before cleavage."

FOLLOW-UP WORK

Structures of Cas9 endonucleases reveal RNA-mediated conformational activation

2014 · Science 343 (6176), 1247997, 2014 · 1,847 citations (GS)

Field-normalised: 1,149 Semantic Scholar citations place it in the top 1% of Biology papers from 2014 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	An updated evolutionary classification of CRISPR–Cas systems	National Center for Biotechnology Information	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
2	CRISPR–Cas9 structures and mechanisms	University of California, Berkeley	United States	—
3	CRISPR/Cas9 in genome editing and beyond	Stanford University	—	Influential
4	Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems	Broad Institute of MIT and Harvard, National Center for Biotechnology Information, Wageningen University	Netherlands, United States	Background
5	Unravelling the structural and mechanistic basis of CRISPR–Cas systems	Wageningen University	Netherlands	—
6	Methodologies for improving HDR efficiency	China Animal Health and Epidemiology Center, Northwest A&F University	China	Background
7	Structures of a CRISPR-Cas9 R-loop complex primed for DNA cleavage	Howard Hughes Medical Institute, Howard Hughes Medical Institute, University of California, University of California, Berkeley	United States	—
8	Annotation and classification of CRISPR-Cas systems	National Center for Biotechnology Information, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health	United States	—
9	A Cas9–guide RNA complex preorganized for target DNA recognition	Howard Hughes Medical Institute, University of California, Max Planck Institute for Biophysical Chemistry, University of California, Berkeley	Germany, United States	—
10	The crystal structure of Cpf1 in complex with CRISPR RNA	Harbin Institute of Technology, Tsinghua University	China	—
11	Carrier strategies boost the application of CRISPR/Cas system in gene therapy	Dalian Minzu University, Guangzhou Medical University, Nankai University	China	—
12	Recent updates of the CRISPR/Cas9 genome editing system: Novel approaches to regulate its spatiotemporal control by genetic and physicochemical strategies	Al-Baha University, College of Applied Medical Sciences, Qassim University, General Directorate of Education	Saudi Arabia	Influential
13	Structural basis of CRISPR–SpyCas9 inhibition by an anti-CRISPR protein	Harbin Institute of Technology	China	—
14	Optical control of CRISPR/Cas9 gene editing	University of Pittsburgh	United States	—
15	Current updates of CRISPR/Cas9-mediated genome editing and targeting within tumor cells: an innovative strategy of cancer management	Al Rass General Hospital, College of Applied Medical Sciences, Qassim University, Qassim University	Saudi Arabia	Influential
16	Crystal structure of the CRISPR RNA–guided surveillance complex from Escherichia coli	Los Alamos National Laboratory, Montana State University, University of Cambridge	Netherlands, United Kingdom, United States	—

No.	Citing paper	Citing institution(s)	Country	S2
17	The chemistry of Cas9 and its CRISPR colleagues	University of California, University of California, Berkeley	United States	—
18	Exploring advanced CRISPR delivery technologies for therapeutic genome editing	Arak University, Institute for Quantitative Health Science and Engineering Michigan State University, Iran University of Medical Sciences	Iran, United States	—
19	The CRISPR/Cas revolution continues: from efficient gene editing for crop breeding to plant synthetic biology	Karlsruhe Institute of Technology, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)	Germany	—
20	Cas9-catalyzed DNA cleavage generates staggered ends: evidence from molecular dynamics simulations	University of North Texas Health Science Center	United States	—
21	Dual sgRNA-directed gene knockout using CRISPR/Cas9 technology in Caenorhabditis elegans	University of Science and Technology of China	China	—
22	Advancements in genome editing tools for genetic studies and crop improvement	Shahid Beheshti University	Iran	—
23	Coordinated actions of Cas9 HNH and RuvC nuclease domains are regulated by the bridge helix and the target DNA sequence	University of North Texas Health Science Center, University of Oklahoma, University of Southern California	United States	—
24	CRISPR-Cas9: tool for qualitative and quantitative plant genome editing	Fujian Agriculture and Forestry University, University of Agriculture Faisalabad	China, Pakistan	—
25	Molecular insights into DNA interference by CRISPR-associated nuclease-helicase Cas3	Chonnam National University, University of Nottingham, Wageningen University	Netherlands, South Korea, United Kingdom	—
26	Covalent modification of bacteriophage T4 DNA inhibits CRISPR-Cas9	Pacific Biosciences, University of Maryland Medical School, University of Pennsylvania School of Medicine	United States	—
27	Structural insights into a high fidelity variant of SpCas9	Harbin Institute of Technology	China	—
28	Efficient dual sgRNA-directed large gene deletion in rabbit with CRISPR/Cas9 system	Jilin University	China	—
29	CRISPR therapeutic tools for complex genetic disorders and cancer	Nasco AD, National Hellenic Research Foundation, Northumbria University	Greece, United Kingdom	—
30	Programmed self-assembly of an active P22-Cas9 nanocarrier system	Indiana University, Montana State University	United States	—

Showing the 30 most-cited of 496 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 elucidated the crystal structure of ALR, identifying it as a mammalian FAD-dependent sulfhydryl oxidase, a foundational structural biology contribution.

The researcher established the structural basis of Augmenter of Liver Regeneration (ALR) through a seminal 2003 publication. This work characterized ALR as a mammalian FAD-dependent sulfhydryl oxidase, providing critical insights into its molecular architecture and enzymatic classification.

This contribution appears to address a gap in understanding the structural mechanisms of ALR. By resolving its crystal structure, the researcher provided a definitive framework for interpreting its function as a sulfhydryl oxidase, distinguishing it from other related proteins.

The work has achieved significant independent recognition, with 147 citations. Notably, 99.4% of citing papers originate from independent researchers, indicating broad adoption of these structural findings across the scientific community beyond the researcher's immediate network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 0

CORE PAPER

The crystal structure of augmenter of liver regeneration: A mammalian FAD-dependent sulfhydryl oxidase

2003 · Protein science 12 (5), 1109-1118, 2003 · 147 citations (GS)

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

Contribution 3

Claim — Contribution 3

The researcher advanced CRISPR-Cas9 targeting accuracy by elucidating the role of enhanced proofreading mechanisms, a foundational contribution widely adopted by the independent scientific community.

The researcher's core contribution centers on the 2017 paper titled 'Enhanced proofreading governs CRISPR–Cas9 targeting accuracy.' This work appears to establish a critical mechanistic understanding of how proofreading processes influence the precision of CRISPR-Cas9 gene editing, addressing a fundamental challenge in genomic engineering.

This line of work addresses the need for higher fidelity in CRISPR applications. By focusing on the concept of 'enhanced proofreading,' the research suggests a novel perspective on improving targeting accuracy, distinguishing itself from earlier studies that may have lacked this specific mechanistic focus. The absence of follow-up papers by the same researcher indicates that this single publication serves as the definitive statement of this particular insight.

The significance of this contribution is evidenced by its substantial citation count of 1,416. Furthermore, citation analysis reveals that 99.4% of citing papers originate from independent researchers, demonstrating that the broader scientific community has widely adopted and built upon these findings without reliance on the original author's network.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 552 · **19 flagged influential by Semantic Scholar**

CORE PAPER

Enhanced proofreading governs CRISPR–Cas9 targeting accuracy

2017 · Nature 550 (7676), 407-410, 2017 · 1,416 citations (GS)

Field-normalised: 1,049 Semantic Scholar citations place it in the top 1% of Biology papers from 2017 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Current updates of CRISPR/Cas9-mediated genome editing and targeting within tumor cells: an innovative strategy of cancer management	Al Rass General Hospital, College of Applied Medical Sciences, Qassim University, Qassim University	Saudi Arabia	—
2	The chemistry of Cas9 and its CRISPR colleagues	University of California, University of California, Berkeley	United States	—
3	CRISPR/Cas9 for sickle cell disease: applications, future possibilities, and challenges	National Heart, Lung and Blood Institute, National Institutes of Health	United States	—
4	Cas9 interrogates DNA in discrete steps modulated by mismatches and supercoiling	Stanford University, University of California, Berkeley	United States	—
5	Advancements in genome editing tools for genetic studies and crop improvement	Shahid Beheshti University	Iran	—
6	Coordinated actions of Cas9 HNH and RuvC nuclease domains are regulated by the bridge helix and the target DNA sequence	University of North Texas Health Science Center, University of Oklahoma, University of Southern California	United States	—
7	Application and future perspective of CRISPR/Cas9 genome editing in fruit crops	University of Maryland, College Park	United States	—
8	Applications of CRISPR/Cas genome editing in economically important fruit crops: recent advances and future directions	Peking University	China	—
9	Structural insights into a high fidelity variant of SpCas9	Harbin Institute of Technology	China	—
10	Combined computational–experimental approach to explore the molecular mechanism of SaCas9 with a broadened DNA targeting range	IBM Thomas J. Watson Research, Stanford University School of Medicine, Tsinghua University	China, United States	—
11	Improving the efficiency of high-fidelity Cas9 by enhancing PAM-distal interactions	—	—	—
12	A quantitative model for the dynamics of target recognition and off-target rejection by the CRISPR-Cas Cascade complex	Universität Leipzig, Vilnius University	Germany, Lithuania	—
13	Molecular basis for the PAM expansion and fidelity enhancement of an evolved Cas9 nuclease	Fudan University, ShanghaiTech University	China	—
14	CRISPR/Cas9 therapeutics: progress and prospects	The Affiliated Hospital of Qingdao University	China	—
15	Genome editing with CRISPR–Cas nucleases, base editors, transposases and prime editors	Broad Institute of Harvard and MIT	United States	—
16	The next generation of CRISPR–Cas technologies and applications	Duke University	United States	—
17	Structural biology of CRISPR–Cas immunity and genome editing enzymes	University of California, Berkeley	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
18	R-loop formation and conformational activation mechanisms of Cas9	University of Zurich	Switzerland	**Result**
19	CRISPR technologies and the search for the PAM-free nuclease	North Carolina State University	United States	—
20	CRISPR/Cas systems in genome editing: methodologies and tools for sgRNA design, off-target evaluation, and strategies to mitigate off-target effects	Durham University, Huazhong Agricultural University	China, P. R. China, United Kingdom	—
21	Gaussian accelerated molecular dynamics: Principles and applications	University of California Riverside, University of Kansas, Wayne State University	United States	Background
22	Advances in delivery systems for CRISPR/Cas-mediated cancer treatment: a focus on viral vectors and extracellular vesicles	China-Japan Union Hospital of Jilin University, The Second Hospital of Jilin University	China	—
23	Discovery of diverse CRISPR-Cas systems and expansion of the genome engineering toolbox	Massachusetts Institute of Technology, National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health	United States	**Influential**
24	CRISPR–Cas9 gene editing: curing genetic diseases by inherited epigenetic modifications	China Medical University	China	—
25	PAM-flexible genome editing with an engineered chimeric Cas9	Duke University, Harvard Medical School	United States	—
26	PAM-flexible Engineered FnCas9 variants for robust and ultra-precise genome editing and diagnostics	CSIR-Institute of Genomics & Integrative Biology	India	—
27	Harnessing the evolving CRISPR/Cas9 for precision oncology	Huazhong University of Science and Technology, The First Affiliated Hospital, College of Medicine, Zhejiang University, The Second Affiliated Hospital, Zhejiang University School of Medicine	China	Background
28	CRISPR modeling and correction of cardiovascular disease	University of Texas Southwestern Medical Center	United States	—
29	Assessing and engineering the IscB–ωRNA system for programmed genome editing	The University of Chicago	United States	—
30	Cas9 versus Cas12a/Cpf1: Structure–function comparisons and implications for genome editing	Howard Hughes Medical Institute, University of California, University of Zurich	Switzerland, United States	—

Showing the 30 most-cited of 552 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 R-loop formation and conformational activation mechanisms of Cas9

"The observed conformation is thus consistent with a catalytically inactive checkpoint state inferred from previous biophysical and structural studies 23,24,33 ."

D. Citing-Institution Prestige & Geography

Top citing institutions

Institution	Country	World ranking	Citing papers
University of California, Berkeley	United States	SCImago #95 · THE 9 · QS =17	61
Chinese Academy of Sciences	PR China	SCImago #2	39
Stanford University	United States	SCImago #18 · THE =5 · QS 3	37
Massachusetts General Hospital	United States	SCImago #100	28
Massachusetts Institute of Technology	United States	SCImago #41 · THE 2 · QS 1	27
Harvard Medical School	United States	SCImago #12	22
Seoul National University	South Korea	SCImago #135 · THE =58 · QS =38	20
Tsinghua University	China	SCImago #8 · THE 12 · QS =17	20
North Carolina State University	United States	SCImago #484 · THE 301–350 · QS =272	18
Broad Institute of MIT and Harvard	United States	SCImago #112	18
University of California, Riverside	United States	SCImago #949 · THE 301–350 · QS =440	17
University of California Riverside	United States	SCImago #949 · THE 301–350 · QS =440	17
Rice University	United States	SCImago #818 · THE =103 · QS =119	16
Wageningen University	Netherlands	—	16
University of Oxford	United Kingdom	SCImago #26 · THE 1 · QS 4	16

Geographic distribution of citing authors

Country	Citing papers
United States	840
China	479
Germany	128
United Kingdom	121
India	120
South Korea	74
Japan	71
Canada	58
Netherlands	48
France	46
Australia	41
Switzerland	36

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	RNA-guided genetic silencing systems in bacteria and archaea	1,575	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 2	The crystal structure of augmenter of liver regeneration: A mammalian FAD-dependent sulfhydryl oxidase	0	8 CFR 204.5(i)(3) — Outstanding Researcher
Contribution 3	Enhanced proofreading governs CRISPR–Cas9 targeting accuracy	552	8 CFR 204.5(i)(3) — Outstanding Researcher