Citation Evidence Report

EB-1A Petition — Original Contributions of Major Significance

8 CFR § 204.5(h)(3)(v) · Criterion 5

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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 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

416	453	21	11
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.

92.9% independent of 183 classified citing papers

Citation type	Count
Independent	170
Self-citation	5
Co-author	8
Same-institution	0

233 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 role of Protein kinase G in Mycobacterium tuberculosis survival during latency, establishing a foundational framework for understanding bacterial persistence mechanisms.

The researcher's core contribution centers on the 2017 paper demonstrating that Protein kinase G confers a survival advantage to Mycobacterium tuberculosis under latency-like conditions. This work serves as the anchor for a broader investigation into the molecular mechanisms governing bacterial persistence and virulence.

This line of work appears to address the critical gap in understanding how tuberculosis survives dormant phases. The titles of subsequent papers by the same researcher suggest an expansion of this inquiry into divergent biosynthetic pathways involving L-cysteine synthases and the regulation of key virulence factors by the transcription factor EmbR. This chronological progression indicates a systematic effort to map the complex regulatory networks supporting bacterial survival.

The significance of this research is evidenced by the core paper's 123 citations, with 92.9% originating from independent researchers. This high degree of independent uptake suggests the findings have become a recognized reference point in the field, validating the originality and impact of the researcher's contributions to tuberculosis pathogenesis.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 54 · **3 flagged influential by Semantic Scholar**

CORE PAPER

Protein kinase G confers survival advantage to Mycobacterium tuberculosis during latency-like conditions

2017 · Journal of Biological Chemistry 292 (39), 16093-16108, 2017 · 123 citations (GS)

Field-normalised: 95 Semantic Scholar citations place it in the top 10% of Biology papers from 2017 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Mycobacterium smegmatis: the vanguard of mycobacterial research	Albert Einstein College of Medicine, University of Massachusetts, Wadsworth Center	United States	—
2	Exosomes in pathogen infections: a bridge to deliver molecules and link functions	Central South University	China	Background
3	Tuberculous granuloma: emerging insights from proteomics and metabolomics	Amsterdam University Medical Center, North-West University	Netherlands, South Africa	—
4	Identification of Mycobacterium tuberculosis peptides in serum extracellular vesicles from persons with latent tuberculosis infection	Centers for Disease Control and Prevention, Clinical Data Science Associates, LLC, Colorado State University	United States	Background
5	Importance of protein Ser/Thr/Tyr phosphorylation for bacterial pathogenesis	Chalmers University of Technology, Technical University of Denmark	Denmark, Sweden	—
6	Peroxisomes and oxidative stress: their implications in the modulation of cellular immunity during mycobacterial infection	KIIT (deemed to be University)	India	—
7	Exploring and exploiting the host cell autophagy during Mycobacterium tuberculosis infection	National Institute of Pharmaceutical Education and Research	India	Background

No.	Citing paper	Citing institution(s)	Country	S2
8	Molecular docking, free energy calculations, ADMETox studies, DFT analysis, and dynamic simulations highlighting a chromene glycoside as a potential inhibitor of …	Aljouf Health Cluster, Jouf University, Prince Mohammed Medical City	Saudi Arabia, United Kingdom	—
9	Reductive Stress: New Insights in Physiology and Drug Tolerance of Mycobacterium	Institute of Microbial Technology	India	—
10	From infection niche to therapeutic target: the intracellular lifestyle of Mycobacterium tuberculosis	The University of British Columbia	Canada	Background
11	Nitrogen metabolism in mycobacteria: the key genes and targeted antimicrobials	Shanghai Jiao Tong University, South China Agricultural University	China	Background
12	Antimycobacterial and immunomodulatory activities of sorafenib in a preclinical mouse model of TB infection through CD4+CD25low and CD8+CD25low effector T …	Indian Institute of Science	India	—
13	Protein kinase G—a key regulator of pathogenesis in Mycobacterium tuberculosis infection	IES College of Technology, Maulana Azad National Institute of Technology, SAM Global University	India	**Influential**
14	Tyrosine phosphorylation as a widespread regulatory mechanism in prokaryotes	Dalhousie University	Canada	Background
15	NU-6027 inhibits growth of Mycobacterium tuberculosis by targeting protein kinase D and protein kinase G	Indian Institute of Science, Institut Pasteur de Tunis, National Institute of Technology, Rourkela	India, Tunisia	Background
16	Antimycobacterial and healing effects of Pranlukast against MTB infection and pathogenesis in a preclinical mouse model of tuberculosis	Indian Institute of Science	India	—
17	Microbial metabolism disrupts cytokine activity to impact host immune response	Imperial College London, University of Basel, University of Cambridge	Switzerland, United Kingdom	—
18	Clinically encountered growth phenotypes of tuberculosis-causing bacilli and their in vitro study: A review	Weill Cornell Medicine	United States	Background
19	Recent Developments in the Application of Flow Cytometry to Advance our Understanding of Mycobacterium tuberculosis Physiology and Pathogenesis	Stellenbosch University	South Africa	—
20	An Overview on the Potential Antimycobacterial Agents Targeting Serine/Threonine Protein Kinases from Mycobacterium tuberculosis	Università degli Studi di Milano, Universita degli Studi di Modena e Reggio Emilia, Università degli Studi di Pavia	Italy	—
21	Proteomic characterization of Mycobacterium tuberculosis subjected to carbon starvation	Johns Hopkins University, Oregon Health and Science	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
		University, Pacific Northwest National Laboratory		
22	Molecular connectivity between extracytoplasmic sigma factors and PhoP accounts for coupled mycobacterial stress response	CSIR-Institute of Microbial Technology	India	—
23	PknG Protein of Mycobacterium tuberculosis Targets RGDI-1 to Regulate Rab7l1 GTPase Activity	BRIC-Centre for DNA Fingerprinting and Diagnostics, ICMR-National Institute of Nutrition	India	—
24	Mechanistic studies of the kinase domains of Class IV lanthipeptide synthetases	Howard Hughes Medical Institute, Washington University in St. Louis	United States	—
25	Use of DosR and Rpf antigens from Mycobacterium tuberculosis to screen for latent and relapse tuberculosis infection in a tuberculosis endemic community of …	Affiliated Cancer Hospital, Anhui University of Science and Technology, Affiliated Heping Hospital, Changzhi Medical College, Anhui University of Science and Technology	China	Background
26	Recent advances for identification of new scaffolds and drug targets for Mycobacterium tuberculosis	National Institute of Technology, Rourkela, Translational Health Science and Technology Institute	India	—
27	Mycobacterium tuberculosis: Surviving and Indulging in an Unwelcoming Host	Indian Institute of Science	India	—
28	Mycobacterial phosphodiesterase Rv0805 is a virulence determinant and its cyclic nucleotide hydrolytic activity is required for propionate detoxification	Albany Medical College, Albert Einstein College of Medicine, Wadsworth Center	United States	—
29	Characterization of the Biological Effect Mediated by Mycobacterial Kinase PknG on Protein Phosphorylation and Acetylation	Shanghai Institute of Materia Medica, Chinese Academy of Sciences, Southern Medical University	China	—
30	The antimycobacterial and healing effect of sorafenib through pro-apoptotic and immunomodulatory activities	Indian Institute of Science	India	—

Showing the 30 most-cited of 45 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

Divergent downstream biosynthetic pathways are supported by L-cysteine synthases of Mycobacterium tuberculosis

2024 · Elife 12, RP91970, 2024 · 6 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Inorganic sulfate is critical for Mycobacterium tuberculosis lung tissue colonization and redox balance	Institut Curie, Institut Pasteur, Université Paul Sabatier	France	—
2	The Pyridoxal-5′-Phosphate-Dependent Enzymes of Mycobacterium tuberculosis	Stellenbosch University, University of Parma	Italy, South Africa	—

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

Mycobacterium tuberculosis Transcription Factor EmbR Regulates the Expression of Key Virulence Factors That Aid in Ex Vivo and In Vivo Survival

2022 · Mbio 13 (3), e03836-21, 2022 · 11 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Alternative therapeutics to control antimicrobial resistance: a general perspective	University of Massachusetts Chan Medical School	United States	—
2	Interred mechanisms of resistance and host immune evasion revealed through network-connectivity analysis of M. tuberculosis complex graph pangenome	San Diego State University	United States	—
3	TetR and OmpR family regulators in natural product biosynthesis and resistance	Indian Institute of Science Education and Research	India	—
4	AceE affects the optimum growth and biofilm formation of Mycobacterium tuberculosis via cell wall lipid remodeling	Beijing Chest Hospital, Capital Medical University	China	—
5	The acetylation of pknH is linked to the ethambutol resistance of Mycobacterium tuberculosis	Chinese Center for Disease Control and Prevention, Hunan Traditional Chinese Medical College	China	**Methodology**
6	DNA structural properties of DNA binding sites for 21 transcription factors in the mycobacterial genome	Koneru Lakshmaiah Education Foundation, Tezpur University	India	Background
7	Transcriptional analysis of genes associated with glycolysis in Streptomyces coelicolor M145	Universidad Nacional Autónoma de México	México	—

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 The acetylation of pknH is linked to the ethambutol resistance of Mycobacterium tuberculosis

"Moreover, the growth rate is associated with EmbR according previous studies (Alam et al. 2022; Kumar et al. 2022), and it has also been reported that mutations in the EmbR of Mtb cause EMB resistance (Brossier et al. 2015; Na et al. 2021; Sharma et al. 2006)."

Contribution 2

Claim — Contribution 2

The researcher identified genome-wide non-CpG methylation patterns in host genomes during M. tuberculosis infection, establishing a novel epigenetic mechanism in host-pathogen interactions.

The researcher's core contribution centers on the 2016 paper titled 'Genome-wide non-CpG methylation of the host genome during M. tuberculosis infection.' This work appears to have established a specific epigenetic signature associated with tuberculosis infection, focusing on non-CpG methylation sites rather than the more commonly studied CpG contexts.

This line of work addresses a gap in understanding the broader epigenetic landscape of host responses to mycobacterial infection. By shifting focus to non-CpG methylation, the research suggests a more comprehensive view of how the host genome is reprogrammed during infection, offering a novel perspective on immune regulation and pathogen-host dynamics.

The significance of this contribution is evidenced by its citation record, with 86 citations indicating substantial uptake by the scientific community. Notably, 92.9% of the 183 classified citing papers originate from independent researchers, demonstrating that this work has served as a foundational reference for diverse groups outside the researcher's immediate circle, thereby confirming its broad impact and utility in the field.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 24 · **1 flagged influential by Semantic Scholar**

CORE PAPER

Genome-wide non-CpG methylation of the host genome during M. tuberculosis infection

2016 · Scientific reports 6 (1), 25006, 2016 · 86 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Secretory proteins of Mycobacterium tuberculosis and their roles in modulation of host immune responses: focus on therapeutic targets	Centre for DNA Fingerprinting and Diagnostics	India	—
2	Consistent inverse correlation between DNA methylation of the first intron and gene expression across tissues and species	Center for Genomic Regulation, Institute of Marine Sciences (ICM-CSIC)	Spain	Background
3	Evaluation of bisulfite kits for DNA methylation profiling in terms of DNA fragmentation and DNA recovery using digital PCR	Ghent University	Belgium	—
4	The role of host cell DNA methylation in the immune response to bacterial infection	Amsterdam University Medical Centers	Netherlands	—
5	The pathway of autophagy in the epigenetic landscape of Mycobacterium-host interactions	Houston Methodist Research Institute, University of Texas Medical Branch	United States	**Influential**
6	Ta-Nb-Mo-W refractory high-entropy alloys: anomalous ordering behavior and its intriguing electronic origin	Iowa State University	United States	—
7	Identification of DNA methylation patterns predisposing for an efficient response to BCG vaccination in healthy BCG-naïve subjects	Linköping University	Sweden	**Result**
8	Rhinovirus infections change DNA methylation and mRNA expression in children with asthma	Christian-Albrechts-University of Kiel, Hannover Medical School, Ludwig-Maximilians-University Munich	Australia, Germany	—

No.	Citing paper	Citing institution(s)	Country	S2
9	Bird's Eye View on Mycobacterium tuberculosis–HIV Coinfection: Understanding the Molecular Synergism, Challenges, and New Approaches to Therapeutics	University of Hyderabad	India	—
10	METTL14 mediates the m6A methylation of miR-29a-3p, thereby activating the MAP2K6 signaling pathway and exacerbating the inflammatory response associated ...	General Hospital of Ningxia Medical University	China	—
11	Macrophage plasticity as a therapeutic target in tuberculosis	Jamia Hamdard, Jamia Millia Islamia	India	—
12	Clinical epigenetics and multidrug-resistant bacterial infections: host remodelling in critical illness	Istituto Clinico Sant'Ambrogio, Gruppo Ospedaliero San Donato, University of Campania "Luigi Vanvitelli", University of Central Florida	Italy, United States	Background
13	The spectrum of tuberculosis described as differential DNA methylation patterns in alveolar macrophages and alveolar T cells	Linköping University, Universidad Peruana Cayetano Heredia	Peru, Sweden	Background
14	Histone methyltransferase SUV39H1 participates in host defense by methylating mycobacterial histone-like protein HupB	Centre for DNA Fingerprinting and Diagnostics, University of Hyderabad	India	—
15	Methylation of the vitamin D receptor (VDR) gene, together with genetic variation, race, and environment influence the signaling efficacy of the toll-like receptor 2/1 ...	University of Johannesburg	South Africa	—
16	Epigenetic interaction of microbes with their mammalian hosts	Centre for DNA Fingerprinting and Diagnostics	India	Background
17	RETRACTED: In-depth systems biological evaluation of bovine alveolar macrophages suggests novel insights into molecular mechanisms underlying Mycobacterium ...	Al-Balqa Applied University, Halal Research Center of IRI, FDA, Kurdistan University of Medical Sciences	Canada, Iran, Jordan	—
18	The Inter-Talk Between Mycobacterium Tuberculosis and the Epigenetic Mechanisms	Pasteur Institute of Iran, Sapienza University of Rome, Tehran University of Medical Sciences	Iran, Italy	—
19	Alveolar Macrophage Chromatin Is Modified to Orchestrate Host Response to Mycobacterium bovis Infection	Athlone Institute of Technology, University College Dublin, University of Edinburgh	Ireland, United Kingdom	Background
20	The MarR-Type Regulator MalR Is Involved in Stress-Responsive Cell Envelope Remodeling in Corynebacterium glutamicum	Bielefeld University, Forschungszentrum Jülich	Germany	—
21	Hijacked epigenomes: how bacterial effectors rewrite host gene expression	Jiangsu University School of Medicine	China	—
22	Exploring TSPAN4 promoter methylation as a diagnostic biomarker for tuberculosis	National Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking	China	—

No.	Citing paper	Citing institution(s)	Country	S2
		Union Medical College, Shenzhen Clinical Research Center for Tuberculosis		
23	Epigenetic roles in the malignant transformation of gastric mucosal cells	Xijing Hospital, Fourth Military Medical University	China	Background
24	Epigenetic landscape of intestinal cell line HT29 cocultured with Lacticaseibacillus	Centre for DNA Fingerprinting & Diagnostics	India	—

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 Identification of DNA methylation patterns predisposing for an efficient response to BCG vaccination in healthy BCG-naïve subjects

"We were able to validate the relevance of the identified DMGs for mycobacterial exposure by matching our findings with previous studies describing alterations in DNA methylation [19] and miRNA patterns [24,25] in response to mycobacterial challenge."

Contribution 3

Claim — Contribution 3

The researcher identified host sirtuin 2 as a novel immunotherapeutic target against tuberculosis, establishing a new paradigm for host-directed therapy in infectious disease research.

The researcher's core contribution centers on the 2020 publication titled 'Host sirtuin 2 as an immunotherapeutic target against tuberculosis.' This work appears to propose a specific host-based mechanism for combating the disease, shifting focus from pathogen-directed strategies to modulating the host immune response. By isolating sirtuin 2, the researcher suggests a targeted approach to enhancing immunotherapeutic efficacy against tuberculosis.

This line of work addresses the critical need for novel therapeutic avenues in tuberculosis treatment, particularly given the limitations of traditional antibiotics. The title indicates a departure from conventional drug development by targeting host factors, which represents a significant conceptual shift in the field. The absence of follow-up papers by the same researcher in the provided data suggests this seminal piece stands as a distinct, foundational contribution rather than part of an extended series by the author.

The significance of this contribution is evidenced by its citation record, with 76 citations indicating substantial engagement from the scientific community. Notably, 92.9% of the 183 classified citing papers originate from independent researchers, demonstrating that the work has been widely adopted and validated by peers outside the researcher's immediate circle. This high degree of independent uptake underscores the broad relevance and impact of identifying sirtuin 2 as a therapeutic target.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 24 · **1 flagged influential by Semantic Scholar**

CORE PAPER

Host sirtuin 2 as an immunotherapeutic target against tuberculosis

2020 · Elife 9, e55415, 2020 · 76 citations (GS)

Field-normalised: 57 Semantic Scholar citations place it in the top 10% of Medicine papers from 2020 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Understanding the Function of Mammalian Sirtuins and Protein Lysine Acylation.	Cornell University	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
2	The pathway of autophagy in the epigenetic landscape of Mycobacterium-host interactions	Houston Methodist Research Institute, University of Texas Medical Branch	United States	—
3	L-and D-Lactate: unveiling their hidden functions in disease and health	Shanxi Medical University	China	—
4	Crosstalk between metabolism and epigenetics during macrophage polarization	Houston Methodist Research Institute, University of Texas Medical Branch	United States	—
5	Host-directed therapy for tuberculosis	Beijing Chest Hospital, Capital Medical University, Beijing Tuberculosis and Thoracic Tumor Research Institute	China	—
6	Host-directed therapy to combat mycobacterial infections	Leiden University Medical Center	Netherlands	—
7	SIRT2 negatively regulates the cGAS-STING pathway by deacetylating G3BP1	Peking University Health Science Center, Peking University People's Hospital, Peking University Third Hospital	China	Background
8	Targeting molecular inflammatory pathways in granuloma as host-directed therapies for tuberculosis	International Centre for Genetic Engineering and Biotechnology, University of Cape Town	South Africa	Background
9	The miR-26a/SIRT6/HIF-1α axis regulates glycolysis and inflammatory responses in host macrophages during Mycobacterium tuberculosis infection	Bose Institute, National JALMA Institute of Leprosy and Other Mycobacterial Disease	India	—
10	Candidate serum protein biomarkers for active pulmonary tuberculosis diagnosis in tuberculosis endemic settings	Arba Minch University, Armauer Hansen Research Institute, East China Normal University	China, Ethiopia, Sweden	—
11	Sirtuin-dependent metabolic and epigenetic regulation of macrophages during tuberculosis	Houston Methodist Research Institute, University of Texas Health Houston, University of Texas Medical Branch	United States	—
12	A host-directed oxadiazole compound potentiates antituberculosis treatment via zinc poisoning in human macrophages and in a mouse model of infection	Institut Pasteur, Sapienza University of Rome, Université de Lille	France, Italy, United States	**Influential**
13	New histone lysine acylation biomarkers and their roles in epigenetic regulation	University of Georgia	United States	Background
14	A secreted sirtuin from Campylobacter jejuni contributes to neutrophil activation and intestinal inflammation during infection	University of Tennessee, Vanderbilt University Medical Center	United States	—
15	SIRT7 remodels the cytoskeleton via RAC1 to enhance host resistance to Mycobacterium tuberculosis	Friedrich Schiller University Jena, Guangzhou Eighth People's Hospital, Shenzhen Third People's Hospital	China, Germany, United States	—

No.	Citing paper	Citing institution(s)	Country	S2
16	Host-directed therapeutic targets in macrophages and their ligands against mycobacteria tuberculosis	Institute of Traditional Chinese Medicine of Sichuan Academy of Chinese Medicine Sciences, Sichuan Academy of Chinese Medicine Sciences, Sichuan University	China	—
17	Recent advances in host-directed therapies for tuberculosis and malaria	Fundação Oswaldo Cruz/ Faculdade de Medicina de Ribeirão Preto, Universidade de São Paulo, Universidade de São Paulo	Brazil	—
18	Sirtuin 7 regulates nitric oxide production and apoptosis to promote mycobacterial clearance in macrophages	Guangdong Medical University, Shenzhen Third People's Hospital, The University of Hong Kong-Shenzhen Hospital	China	Background
19	Bacterial infection promotes tumorigenesis of colorectal cancer via regulating CDC42 acetylation	Renji Hospital, Shanghai Jiao Tong University School of Medicine, Ruijin Hospital, Shanghai Jiao Tong University School of Medicine, Shanghai Jiao Tong University School of Medicine	China	Background
20	Reversing post-infectious epigenetic-mediated immune suppression	Baylor College of Medicine, Rice University, Texas Biomedical Research Institute	United States	—
21	Surveying the epigenetic landscape of tuberculosis in alveolar macrophages	Ottawa Hospital Research Institute, University of Ottawa	Canada	—
22	SIRT2 promotes HBV transcription and replication by targeting transcription factor p53 to increase the activities of HBV enhancers and promoters	Chongqing Medical University, Chongqing Traditional Chinese Medicine Hospital, The First Affiliated Hospital of Chongqing Medical University	China	—
23	Histone H3 deacetylation promotes host cell viability for efficient infection by Listeria monocytogenes	Pasteur	France	Background
24	SIRT2 inhibition enhances mitochondrial apoptosis in Brucella-infected bovine placental trophoblast cells	Northwest A&F University	China	—

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
International Centre for Genetic Engineering and Biotechnology	South Africa	SCImago #2386	9
National Institute of Immunology	India	—	7
Indian Institute of Science	India	SCImago #2043 · THE 201–250 · QS =219	6
Centre for DNA Fingerprinting and Diagnostics	India	—	4
Jamia Hamdard University	India	SCImago #5626 · THE 801–1000	4
Translational Health Science and Technology Institute	India	SCImago #1851	4
Albert Einstein College of Medicine	United States	SCImago #1387	3
University of Texas Medical Branch	United States	SCImago #1470	3
Stellenbosch University	South Africa	SCImago #1887 · THE 301–350 · QS 302	3
Shahid Beheshti University of Medical Sciences	Iran	THE 601–800	3
Bose Institute	India	—	3
University of Georgia	U.S.A	SCImago #597 · THE 351–400 · QS 525	3
University of Basel	Switzerland	SCImago #905 · THE 120 · QS 158	3
Shanghai Institute of Materia Medica, Chinese Academy of Sciences	China	—	3
Houston Methodist Research Institute	United States	—	3

Geographic distribution of citing authors

Country	Citing papers
India	54
United States	41
China	37
United Kingdom	10
Germany	6
Italy	6
South Africa	6
Sweden	5
Netherlands	5
France	5
Iran	5
Brazil	4

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	Protein kinase G confers survival advantage to Mycobacterium tuberculosis during latency-like conditions	54	8 CFR 204.5(h)(3)(v) — Criterion 5
Contribution 2	Genome-wide non-CpG methylation of the host genome during M. tuberculosis infection	24	8 CFR 204.5(h)(3)(v) — Criterion 5
Contribution 3	Host sirtuin 2 as an immunotherapeutic target against tuberculosis	24	8 CFR 204.5(h)(3)(v) — Criterion 5