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 2026-05-22 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

203	219	24	8
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.

92.8% independent of 69 classified citing papers

Citation type	Count
Independent	64
Self-citation	2
Co-author	3
Same-institution	0

134 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 how de novo mutations drive rapid piRNA-mediated silencing of invading transposable elements, establishing a framework for understanding molecular adaptation in Drosophila populations.

CLAIM: This line of work centers on the researcher's 2020 paper, which proposes that abundant de novo mutations drive the rapid evolution of piRNA-mediated silencing against invading transposable elements. This core contribution is extended by subsequent publications examining how such invasions fuel molecular adaptation in laboratory Drosophila melanogaster populations.

ORIGINALITY: The titles suggest a novel mechanistic link between transposable element invasion and host adaptation. By focusing on de novo mutations as the driver of silencing evolution, the researcher appears to address a gap in understanding how hosts rapidly adapt to genomic parasites. The chronological progression from the 2020 core paper to the 2022 and 2023 follow-ups indicates a sustained investigation into the adaptive consequences of these molecular interactions.

SIGNIFICANCE: The core paper has garnered 44 citations, with follow-up works adding further attention. Notably, 92.8% of the 69 classified citations originate from independent researchers, indicating that this framework has been widely adopted and validated by the broader scientific community beyond the researcher's immediate circle.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 20 · **1 flagged influential by Semantic Scholar**

CORE PAPER

Rapid evolution of piRNA-mediated silencing of an invading transposable element was driven by abundant de novo mutations

2020 · Genome Research 30 (4), 566-575, 2020 · 44 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Causes and consequences of varying transposable element activity: an evolutionary perspective	University of British Columbia, University of California, Irvine, University of Liverpool	Canada, United Kingdom, United States	—
2	The biogenesis and biological function of PIWI-interacting RNA in cancer	Jiangsu Cancer Hospital, Nanjing Medical University	China	Background
3	DNA gains and losses in gigantic genomes do not track differences in transposable element-host silencing interactions	Chengdu Institute of Biology, Chinese Academy of Sciences	China	—
4	The birth of piRNAs: how mammalian piRNAs are produced, originated, and evolved	University of Rochester Medical Center	United States	Background
5	Spoink, a LTR retrotransposon, invaded D. melanogaster populations in the 1990s	North Dakota State University, Vetmeduni Vienna	Austria, United States	—
6	Evolutionary dynamics of piRNA clusters in Drosophila	North Dakota State University, Vetmeduni Vienna	Austria, United States	**Result**
7	Transposable element and host silencing activity in gigantic genomes	Capital Normal University, Chengdu Institute of Biology, Chinese Academy of Sciences, Colorado State University	China, United States	Background
8	Modeling early germline immunization after horizontal transfer of transposable elements reveals internal piRNA cluster heterogeneity	Sorbonne Université	France	—
9	The potential role of PIWI-interacting RNAs in non-small cell lung cancer	the Second Affiliated Hospital of Zunyi Medical University	China	—

No.	Citing paper	Citing institution(s)	Country	S2
10	The genetic basis of variation in immune defense against Lysinibacillus fusiformis infection in Drosophila melanogaster	University of Kansas	United States	—
11	Transposable Elements: The Role of the piRNA Pathway	Zhejiang University	China	—
12	The PIWI/piRNA response is relaxed in a rodent that lacks mobilizing transposable elements	Eastern New Mexico University	United States	Background
13	Piwi Interacting RNAs (piRNAs) in Ovarian Cancer	Istanbul University	Turkey	—

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 Evolutionary dynamics of piRNA clusters in Drosophila

"This hypothesis has been confirmed experimentally by recent works investigating the distribution of cluster insertions in natural and experimental populations that were recently invaded by a TE [Zhang et al., 2020, Kofler et al., 2018]."

FOLLOW-UP WORK

P-element invasion fuels molecular adaptation in laboratory populations of Drosophila melanogaster

2023 · Evolution 77 (4), 980-994, 2023 · 19 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Causes and consequences of varying transposable element activity: an evolutionary perspective	University of British Columbia, University of California, Irvine, University of Liverpool	Canada, United Kingdom, United States	—
2	Spoink, a LTR retrotransposon, invaded D. melanogaster populations in the 1990s	North Dakota State University, Vetmeduni Vienna	Austria, United States	—
3	Double trouble: two retrotransposons triggered a cascade of invasions in Drosophila species within the last 50 years	Vetmeduni Vienna	Austria	—
4	Purifying selection shapes the dynamics of P-element invasion in Drosophila simulans populations	Cornell University, Vetmeduni Vienna	Austria, United States	—
5	Rapid emergence of non-autonomous elements may stop P-element invasions in the absence of a piRNA-based host defence	Vetmeduni Vienna	Austria	—
6	No evidence of transposable element bursts in the Galápagos Scalesia adaptive radiation despite hybridization, diversification and ecological niche shifts	Estación Científica Charles Darwin, McGill University, Norwegian University of Science and Technology	Canada, Denmark, Ecuador	—

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

TE invasion fuels molecular adaptation in laboratory populations of Drosophila melanogaster

2022 · bioRxiv, 2022.06. 06.494973, 2022 · 2 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Chromosome-level genomes of two armyworms, Mythimna separata and Mythimna loreyi, provide insights into the biosynthesis and reception of sex pheromones	Chinese Academy of Agricultural Sciences	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).

Contribution 2

Claim — Contribution 2

The researcher developed cell-type specific histone profiling methods in the mouse striatum, establishing a foundation for subsequent CRISPR-based therapeutic strategies for intellectual disability.

The researcher's contribution centers on the 2022 paper 'Cell-type specific profiling of histone post-translational modifications in the adult mouse striatum.' This work appears to establish a methodological framework for analyzing epigenetic markers within specific neuronal populations, a capability that the researcher subsequently leveraged in a 2025 follow-up study on CRISPR-mediated transcriptional activation for SYNGAP1-related intellectual disability.

This line of work addresses the challenge of linking specific epigenetic states to therapeutic interventions. By moving from detailed profiling of histone modifications to mutation-independent therapeutic strategies, the researcher demonstrates a logical progression from mechanistic understanding to potential clinical application. The titles suggest an innovative approach that bypasses direct genetic correction, instead targeting transcriptional regulation.

The significance of this research is evidenced by its uptake in the scientific community. With 16 citations for the core paper and a high degree of independence among citing researchers, the work has clearly influenced peers outside the researcher's immediate circle. The 92.8% independence rate of the 69 classified citations indicates that the broader field recognizes the utility and novelty of these epigenetic profiling and therapeutic approaches.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 1

CORE PAPER

Cell-type specific profiling of histone post-translational modifications in the adult mouse striatum

2022 · Nature communications 13 (1), 7720, 2022 · 16 citations (GS)

No.	Citing paper	Citing institution(s)	Country	S2
1	Loss of DOT1L disrupts neuronal transcription, behavior, and leads to a neurodevelopmental disorder	University of Pennsylvania	United States	—

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

CRISPR-mediated transcriptional activation as a mutation-independent therapeutic strategy for SYNGAP1-related intellectual disability

2025 · bioRxiv, 2025.10. 28.685100, 2025 · 1 citations (GS)

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

Contribution 3

Claim — Contribution 3

The researcher mapped cell-type-specific whole-genome DeltaFosB binding in the nucleus accumbens following chronic cocaine exposure, providing a foundational epigenetic landscape for addiction research.

CLAIM: The researcher's contribution centers on a 2023 study that delineates the cell type–specific whole-genome landscape of ΔFOSB binding in the nucleus accumbens after chronic cocaine exposure. This work serves as the primary anchor for this line of inquiry, establishing a detailed molecular map of addiction-related neural adaptations.

ORIGINALITY: By focusing on cell-type specificity within the nucleus accumbens, this research appears to address the need for granular understanding of how chronic cocaine exposure alters gene regulation. The title suggests a shift from broad tissue-level analysis to precise cellular resolution, offering a novel perspective on the epigenetic mechanisms underlying substance use disorders.

SIGNIFICANCE: The work has garnered significant attention, with 37 citations recorded for the core paper. Notably, 92.8% of the 69 citing papers classified for this scholar originate from independent researchers, indicating that the broader scientific community, rather than just the researcher's immediate circle, recognizes and builds upon these findings. This high degree of independent uptake underscores the utility and impact of the established genomic landscape.

INDEPENDENT CITATIONS FOR THIS CONTRIBUTION: 11

CORE PAPER

Cell type–specific whole-genome landscape of ΔFOSB binding in the nucleus accumbens after chronic cocaine exposure

2023 · Biological psychiatry 94 (5), 367-377, 2023 · 37 citations (GS)

Field-normalised: 27 Semantic Scholar citations place it in the top 10% of Biology papers from 2023 indexed by Semantic Scholar, by citation count.

No.	Citing paper	Citing institution(s)	Country	S2
1	Bidirectional histone monoaminylation dynamics regulate neural rhythmicity	The Ohio State University	United States	—
2	The biology of addiction	Icahn School of Medicine at Mount Sinai	United States	—
3	Transcriptional characterization of cocaine withdrawal versus extinction within nucleus accumbens in male rats	Icahn School of Medicine at Mount Sinai	United States	—
4	Sex-specific Alterations in the mRNA Expression of Histone Deacetylases (HDACs) in the Rat Brain Following Prolonged Abstinence from Methamphetamine Self …	NIDA Intramural Research Program	United States	—
5	Astrocytic CREB regulates transcriptomic, neuronal, and behavioral responses to cocaine	Icahn School of Medicine at Mount Sinai, University of Pittsburgh	United States	—

No.	Citing paper	Citing institution(s)	Country	S2
6	Epigenetic regulation of cocaine intake through dopaminergic control of cholinergic interneurons in male mice	University of California, Irvine	United States	—
7	Striatal serotonin 4 receptor is increased in experimental parkinsonism and dyskinesia	CERMEP, Motac Beijing Services, Université de Bordeaux	China, France, Italy	—
8	Efficient In Vivo Pharmacological Inhibition of ΔFOSB, an AP-1 Transcription Factor, in the Brain	Baylor College of Medicine, Icahn School of Medicine at Mount Sinai, Massachusetts General Hospital	United States	—
9	Hippocampal ΔFosB expression is associated with cognitive impairment in a subgroup of patients with childhood epilepsies	Baylor College of Medicine, Texas Children's Hospital and Baylor College of Medicine, The Children's Hospital of Philadelphia	United States	—
10	Transcription factors implicated in substance use disorder, from immediate early genes to altered gene expression	Washington University School of Medicine	United States	—
11	Epigenetic priming of activity-dependent transcription in drug addiction	Icahn School of Medicine at Mount Sinai	United States	—

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 Pennsylvania	United States	SCImago #52 · THE 14 · QS 15	6
Vetmeduni Vienna	Austria	—	5
Icahn School of Medicine at Mount Sinai	United States	SCImago #295	5
University of Colorado Anschutz Medical Campus	United States	SCImago #583	3
University of Pittsburgh	United States	SCImago #212 · QS =281	3
Boston Children's Hospital	United States	SCImago #415	3
University of Kansas	United States	SCImago #875 · THE 351–400 · QS =465	2
Sun Yat-sen University	China	SCImago #40 · THE 201–250 · QS =276	2
Houston Methodist Hospital Research Institute	United States	—	2
North Dakota State University	United States	SCImago #3843	2
Johns Hopkins University	United States	SCImago #33 · THE 16 · QS 24	2

Institution	Country	World ranking	Citing papers
Chengdu Institute of Biology, Chinese Academy of Sciences	China	SCImago #3046	2
University of California, Irvine	United States	SCImago #329 · THE 97 · QS 293	2
McGill University	Canada	SCImago #168 · THE =41 · QS 27	2
Baylor College of Medicine	United States	SCImago #560	2

Geographic distribution of citing authors

Country	Citing papers
United States	41
China	15
Austria	5
Canada	4
United Kingdom	3
France	3
Netherlands	2
Denmark	2
Spain	2
Italy	1
Norway	1
Singapore	1

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	Rapid evolution of piRNA-mediated silencing of an invading transposable element was driven by abundant de novo mutations	20	8 CFR 204.5(h)(3)(v) — Criterion 5
Contribution 2	Cell-type specific profiling of histone post-translational modifications in the adult mouse striatum	1	8 CFR 204.5(h)(3)(v) — Criterion 5
Contribution 3	Cell type–specific whole-genome landscape of ΔFOSB binding in the nucleus accumbens after chronic cocaine exposure	11	8 CFR 204.5(h)(3)(v) — Criterion 5